

GenCore version 5.1.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 22:15:05 ; Search time 2159 Seconds
(without alignments)
1079.473 Million cell updates/sec

Title: US-09-904-968A-1_N3336_COPY_3300_3340
Perfect score: 41
Sequence: 1 aagctccgagtgccagtc.....tcctcgctggcccgncgcg 41

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

prior ant dbs

Seq 1, "N" at 3336

searched nt 3300-3340

using "identity-nucdx" matrix.

(Matches to 'N' are marked with a colon [:]; N in query seq considered a match to anything in db seq)

Pred. No. is the number of
score greater than or equa
and is derived by analysis

SUMMARIES							
Result No.	Score	Query Match	Length DB ID	Description			
C 1	41	100.0	164 10	HSA248385	AJ248385	Homo sapi	
C 2	41	100.0	31571 6	I59642	I59642	Sequence 1	
C 3	41	100.0	34934 14	AC141442	AC141442	Homo sapi	
4	41	100.0	37244 14	AC140806	AC140806	Homo sapi	
5	41	100.0	37279 14	AC140702	AC140702	Homo sapi	
6	41	100.0	38849 8	AC005346	AC005346	Homo sapi	
C 7	41	100.0	39322 14	AC140703	AC140703	Homo sapi	
8	41	100.0	40673 14	AC140704	AC140704	Homo sapi	
9	41	100.0	41489 14	AC142549	AC142549	Homo sapi	
10	41	100.0	47934 8	HSU24498	HSU24498	Human autos	
11	41	100.0	53522 6	AX440497	AX440497	Sequence	
12	41	100.0	53522 8	HUMPKD1GEN	L39891	Homo sapien	
13	41	100.0	53526 6	AR097326	AR097326	Sequence	
14	41	100.0	53526 6	BD128573	BD128573	Polycysti	
15	41	100.0	53577 6	AR097325	AR097325	Sequence	
16	41	100.0	53577 6	BD128572	BD128572	Polycysti	
17	41	100.0	53577 6	AR643858	AR643858	Sequence	
18	41	100.0	84562 14	AC140700	AC140700	Homo sapi	

C 19	41	100.0	84928	14	AC141231	AC141231	Homo sapi
C 20	41	100.0	89599	14	AC138966	AC138966	Homo sapi
C 21	41	100.0	109340	8	AC010488	AC010488	Homo sapi
C 22	41	100.0	127485	8	HUAC002039	HUAC002039	Homo sapi
C 23	41	100.0	131353	14	AC137642	AC137642	Homo sapi
C 24	41	100.0	145971	8	AC136427	AC136427	Homo sapi
C 25	41	100.0	147573	14	AC133566	AC133566	Homo sapi
C 26	41	100.0	148930	14	AC138949	AC138949	Homo sapi
C 27	41	100.0	152171	14	AC138892	AC138892	Homo sapi
C 28	41	100.0	162264	14	AC139266	AC139266	Homo sapi
C 29	41	100.0	167184	14	AC138888	AC138888	Homo sapi
C 30	41	100.0	168230	14	AC138901	AC138901	Homo sapi
C 31	41	100.0	168408	14	AC139265	AC139265	Homo sapi
C 32	41	100.0	172474	14	AC142081	AC142081	Homo sapi
C 33	41	100.0	173775	14	AC141410	AC141410	Homo sapi
C 34	41	100.0	177920	14	AC137806	AC137806	Homo sapi
C 35	41	100.0	179399	14	AC141465	AC141465	Homo sapi
C 36	41	100.0	179399	14	AC141465	AC141465	Homo sapi
C 37	41	100.0	179754	14	AC141616	AC141616	Homo sapi
C 38	41	100.0	180798	8	AC138932	AC138932	Homo sapi
C 39	41	100.0	181231	14	AC138903	AC138903	Homo sapi
C 40	41	100.0	183215	14	AC142195	AC142195	Homo sapi
C 41	41	100.0	183537	14	AC141266	AC141266	Homo sapi
C 42	41	100.0	187226	14	AC139258	AC139258	Homo sapi
C 43	41	100.0	188734	14	AC141304	AC141304	Homo sapi
C 44	41	100.0	194670	14	AC141613	AC141613	Homo sapi
C 45	41	100.0	199759	8	AC009065	AC009065	Homo sapi
C 46	41	100.0	202656	14	AC141468	AC141468	Homo sapi
C 47	41	100.0	202882	14	AC141411	AC141411	Homo sapi
C 48	41	100.0	204500	14	AC141267	AC141267	Homo sapi
C 49	41	100.0	204638	14	AC141253	AC141253	Homo sapi
C 50	41	100.0	215974	14	AC141607	AC141607	Homo sapi
C 51	41	100.0	216759	8	AC138969	AC138969	Homo sapi
C 52	41	100.0	223432	8	AC126755	AC126755	Homo sapi
C 53	39.4	96.1	865	8	HSA323057	HSA323057	Homo sapi
C 54	39.4	96.1	38848	14	AC141236	AC141236	Homo sapi
C 55	39.4	96.1	129473	14	AC040158	AC040158	Homo sapi
C 56	39.4	96.1	144161	14	AC141602	AC141602	Homo sapi
C 57	39.4	96.1	183396	14	AC154112	AC154112	Pan trogl
C 58	39.4	96.1	184891	8	AC092137	AC092137	Homo sapi
C 59	39.4	96.1	187721	8	AC126763	AC126763	Homo sapi
C 60	39.4	96.1	189770	14	AC139281	AC139281	Homo sapi
C 61	39.4	96.1	196687	14	AC136442	AC136442	Homo sapi
C 62	39.4	96.1	215222	14	AC141467	AC141467	Homo sapi
C 63	39.4	96.1	215960	14	AC144881	AC144881	Gorilla g
C 64	39.4	96.1	218593	14	AC141303	AC141303	Homo sapi
C 65	37.8	92.2	192549	14	AC141401	AC141401	Homo sapi
C 66	36.4	88.8	131818	14	AC138872	AC138872	Homo sapi
C 67	36.2	88.3	51437	14	AC140805	AC140805	Homo sapi
C 68	36.2	88.3	162696	14	AC148537	AC148537	Pan trogl
C 69	36.2	88.3	166278	14	AC141276	AC141276	Homo sapi
C 70	35.4	86.3	198295	14	AC141080	AC141080	Homo sapi
C 71	34.6	84.4	202023	14	AC141270	AC141270	Homo sapi
C 72	30.4	74.1	159468	14	AC140888	AC140888	Homo sapi
C 73	29.8	72.7	6423	6	AX281458	AX281458	Sequence
C 74	29.8	72.7	6423	6	AX348742	AX348742	Sequence
C 75	29	70.7	187328	14	AC150732	AC150732	Papio anu
C 76	28.4	69.3	110000	1	AY596297	AY596297	Continuation (28 o
C 77	25.2	61.5	173370	14	AC116286	AC116286	Rattus no
C 78	25.2	61.5	192405	14	AC126160	AC126160	Rattus no
C 79	25	61.0	371	3	AY574424	AY574424	Unculture
C 80	24.6	60.0	1424	6	AR621724	AR621724	Sequence
C 81	24.6	60.0	15268	6	AR619747	AR619747	Sequence
C 82	24.2	59.0	2202	6	CQ615018	CQ615018	Sequence
C 83	24.2	59.0	5083	6	CQ615017	CQ615017	Sequence
C 84	24.2	59.0	12393	1	AE012414	AE012414	Xanthomon
C 85	24.2	59.0	33483	14	AC020333	AC020333	Drosophil
C 86	24.2	59.0	110000	1	BA000400	BA000400	Continuation (72 o
C 87	24.2	59.0	110000	1	CP000050	CP000050	Continuation (14 o
C 88	24.2	59.0	167344	2	AC093438	AC093438	Drosophil
C 89	24.2	59.0	170988	2	AC091223	AC091223	Drosophil
C 90	24.2	59.0	254095	14	AC108990	AC108990	Rattus no
C 91	24.2	59.0	265524	2	AE003541	AE003541	Drosophil

92	24	58.5	110000	1	BA000030_05	Continuation (6 of
93	24	58.5	110000	15	AP008208_271	Continuation (272
C	94	58.5	132830	14	AC011051	AC011051 Homo sapi
95	24	58.5	137841	15	AP005055	AP005055 Oryza sat
96	24	58.5	155431	15	AP004858	AP004858 Oryza sat
97	24	58.5	236171	14	AC160739	AC160739 Bos tauru
C	98	58.0	95614	14	AC012890	AC012890 Drosophil
99	23.8	58.0	108924	2	AC005889	AC005889 Drosophil
100	23.8	58.0	110000	1	CP000076_54	Continuation (55 o
101	23.8	58.0	170053	2	AC009197	AC009197 Drosophil
102	23.8	58.0	270771	2	AE003624	AE003624 Drosophil
C	103	57.6	281	8	S81084S01	S81084 glucose pho
104	23.6	57.6	622	15	AY489244	AY489244 Halosarci
C	105	57.6	2418	8	HUMGPI1	M55538 Homo sapien
C	106	57.6	110000	1	AE006470_03	Continuation (4 of
107	23.6	57.6	110000	1	CP000027_02	Continuation (3 of
108	23.6	57.6	110000	1	CP000027_08	Continuation (9 of
C	109	57.6	122000	8	AC003093	AC003093 Human BAC
C	110	57.6	234326	14	AC159346	AC159346 Bos tauru
C	111	57.1	606	3	AF376430	AF376430 Unculture
C	112	57.1	611	3	AF376443	AF376443 Unculture
C	113	57.1	110000	14	CT005263_0	CT005263 Leishmani
C	114	57.1	194474	14	AC137536	AC137536 Sus scrof
C	115	56.6	371	9	MUSSCG04	L20262 Mouse SCG10
C	116	56.6	110000	1	BA000012_67	Continuation (68 o
C	117	56.6	110000	1	BA000040_59	Continuation (60 o
118	23.2	56.6	110000	15	AP008215_001	Continuation (2 of
119	23.2	56.6	127560	15	AP006059	AP006059 Oryza sat
C	120	56.6	142304	14	AC099529	AC099529 Felis cat
C	121	56.6	153455	14	AC145260	AC145260 Felis cat
C	122	56.6	157738	9	AC140333	AC140333 Mus muscu
123	23.2	56.6	190143	15	AP006058	AP006058 Oryza sat
124	23.2	56.6	191481	9	AC124554	AC124554 Mus muscu
125	23.2	56.6	246827	14	AC150314	AC150314 Mus muscu
126	23	56.1	89672	8	AC005872	AC005872 Homo sapi
C	127	56.1	110000	1	BA000035_26	Continuation (27 o
128	23	56.1	110000	1	BA000040_30	Continuation (31 o
C	129	56.1	110292	14	AC150196	AC150196 Gallus ga
130	23	56.1	112077	14	AC159579	AC159579 Dasyypus n
C	131	56.1	113124	14	AC150076	AC150076 Gallus ga
C	132	56.1	122543	8	AC012470	AC012470 Homo sapi
C	133	56.1	134370	14	AC159175	AC159175 Dasyypus n
C	134	56.1	135492	14	AC150123	AC150123 Gallus ga
C	135	56.1	137506	8	AC004824	AC004824 Homo sapi
136	23	56.1	145463	14	AC151507	AC151507 Dasyypus n
137	23	56.1	169982	14	AC145237	AC145237 Pan trogl
138	23	56.1	172146	14	AC130272	AC130272 Papio anu
C	139	56.1	172206	14	AC144495	AC144495 Pan trogl
140	23	56.1	177364	14	AC150041	AC150041 Gallus ga
C	141	56.1	194396	14	AC151087	AC151087 Bos tauru
142	23	56.1	207790	14	AC150166	AC150166 Gallus ga
143	23	56.1	304450	1	BX294134	BX294134 pirellula
144	22.8	55.6	110000	1	BA000035_13	Continuation (14 o
145	22.8	55.6	195741	14	AC166017	AC166017 Oryctolag
146	22.6	55.1	369	6	AR502847	AR502847 Sequence
147	22.6	55.1	369	6	AR518129	AR518129 Sequence
C	148	55.1	1020	6	CQ737027	CQ737027 Sequence
C	149	55.1	2213	6	CQ850708	CQ850708 Sequence
C	150	55.1	2213	8	AK128810	AK128810 Homo sapi
151	22.6	55.1	2232	15	AY299654	AY299654 Taeniathe
152	22.6	55.1	2454	15	TTI306976	AJ306976 Triticum
C	153	55.1	12730	1	AE005055	AE005055 Halobacte
154	22.6	55.1	22715	6	AX695743	AX695743 Sequence
155	22.6	55.1	48109	14	AC151741	AC151741 Rattus no
156	22.6	55.1	65905	14	AC069492	AC069492 Homo sapi
157	22.6	55.1	110000	1	CP000075_51	Continuation (52 o
158	22.6	55.1	110000	14	CT005251_1	Continuation (2 of
C	159	55.1	110000	14	LMFLCHR32_12	Continuation (13 o
C	160	55.1	110000	15	AP008207_204	Continuation (205
C	161	55.1	126083	8	AC105337	AC105337 Homo sapi
C	162	55.1	127719	14	AC153338	AC153338 Loxodonta
163	22.6	55.1	139609	14	AC166033	AC166033 Loxodonta
C	164	55.1	141230	15	AP004614	AP004614 Oryza sat

C	165	22.6	55.1	145631	14	AC087460
C	166	22.6	55.1	151559	8	AL390294
	167	22.6	55.1	173660	8	AC084693
	168	22.6	55.1	175137	14	AC018670
169	22.6	55.1	176708	8	AC039056	
170	22.6	55.1	190891	14	AC058800	
C	171	22.6	55.1	197643	14	AC113790
172	22.6	55.1	199827	14	AC026373	
C	173	22.6	55.1	215313	8	AC100791
C	174	22.6	55.1	232931	14	AC094067
175	22.6	55.1	238437	14	AC158053	
C	176	22.6	55.1	254939	14	AC099076
177	22.6	55.1	300933	1	AE016791	
178	22.4	54.6	622	8	HUMSCN4A14	
179	22.4	54.6	3723	6	AX823170	
C	180	22.4	54.6	11871	1	AE004625
C	181	22.4	54.6	37115	14	AC139098
182	22.4	54.6	41839	8	AC104815	
183	22.4	54.6	61095	8	AL390780	
C	184	22.4	54.6	69488	14	AC165863
C	185	22.4	54.6	72279	14	AC124320
186	22.4	54.6	88655	8	AC079135	
C	187	22.4	54.6	110000	1	AP008226_17
188	22.4	54.6	110000	1	AP008231_00	
C	189	22.4	54.6	110000	14	AC150790_2
C	190	22.4	54.6	110000	14	CR954204_6
191	22.4	54.6	126253	8	AC004934	
C	192	22.4	54.6	152428	8	AC114490
193	22.4	54.6	162361	14	AC023779	
194	22.4	54.6	163218	8	AC005837	
195	22.4	54.6	165516	8	AC005912	
C	196	22.4	54.6	169621	9	AL627093
C	197	22.4	54.6	187433	14	AC024195
198	22.4	54.6	196976	9	AL845528	
C	199	22.4	54.6	226174	8	AY796304
200	22.4	54.6	240099	14	AC098398	
C	201	22.4	54.6	245499	14	AC107173
C	202	22.4	54.6	276289	1	AE017306
203	22.2	54.1	8301	6	AX153792	
204	22.2	54.1	10378	1	AE011854	
205	22.2	54.1	34071	6	AX153790	
C	206	22.2	54.1	36567	1	AF521015
C	207	22.2	54.1	42717	6	AX153789
208	22.2	54.1	110000	14	AC114623_1	
209	22.2	54.1	156422	9	AC102896	
C	210	22.2	54.1	192812	9	AC115303
C	211	22.2	54.1	198590	9	AC113983
C	212	22.2	54.1	226170	8	AC008761
213	22.2	54.1	229390	14	AC097700	
C	214	22.2	54.1	258635	14	AC106208
215	22	53.7	298	15	ATAK15	
216	22	53.7	614	10	BV629652	
C	217	22	53.7	619	10	BV213089
218	22	53.7	636	10	BV346059	
219	22	53.7	1281	6	AR625795	
C	220	22	53.7	2069	9	RNU92010
221	22	53.7	2979	6	AX505353	
222	22	53.7	3462	1	AF111945	
223	22	53.7	6175	1	AF064527	
C	224	22	53.7	6430	6	AR619274
225	22	53.7	11528	1	AE002068	
C	226	22	53.7	11856	1	AY786992
227	22	53.7	34503	14	AC151612	
C	228	22	53.7	44913	8	AC005786
C	229	22	53.7	70797	7	AY129339
230	22	53.7	106921	8	AC004263	
C	231	22	53.7	107529	8	AL357936
232	22	53.7	110000	14	CT005271_01	
C	233	22	53.7	110000	15	AP008215_167
C	234	22	53.7	110000	15	AP008208_244
235	22	53.7	110000	15	AP008213_152	
236	22	53.7	111945	15	ATF1C12	
237	22	53.7	127559	1	AY787762	

238	22	53.7	139961	15	AP004668	AP004668 Oryza sat	c	311	21.8	53.2	138819	14	AC155467	AC155467 Zea mays
c 239	22	53.7	141649	15	AP004097	AP004097 Oryza sat		312	21.8	53.2	141394	14	AC155221	AC155221 Dromaius
240	22	53.7	147890	15	AP004395	AP004395 Oryza sat	c	313	21.8	53.2	141511	14	AC155475	AC155475 Zea mays
c 241	22	53.7	158798	15	AP005308	AP005308 Oryza sat		314	21.8	53.2	143192	8	AL954247	AL954247 Pan trogl
242	22	53.7	165122	8	AC011448	AC011448 Homo sapi	c	315	21.8	53.2	144601	15	AC104709	AC104709 Oryza sat
243	22	53.7	165867	14	AL3533609	AL3535609 Homo sapi		316	21.8	53.2	145050	1	AL627275	AL627275 Salmonell
244	22	53.7	166054	8	CNS06C71	AL389895 Human chr		317	21.8	53.2	153921	15	AP004570	AP004570 Oryza sat
245	22	53.7	169511	8	AC146026	AC146026 Pan trogl	c	318	21.8	53.2	157171	14	AC155454	AC155454 Zea mays
c 246	22	53.7	173213	14	AC073865	AC073865 Homo sapi		319	21.8	53.2	162839	8	AL137846	AL137846 Human DNA
247	22	53.7	180035	14	AC125819	AC125819 Rattus no	c	320	21.8	53.2	169118	14	AC155595	AC155595 Zea mays
248	22	53.7	189729	14	AC073930	AC073930 Homo sapi		321	21.8	53.2	169627	14	AC155528	AC155528 Zea mays
c 249	22	53.7	189884	14	AC024440	AC024440 Homo sapi		322	21.8	53.2	170072	14	AC155589	AC155589 Zea mays
250	22	53.7	198427	15	ATCHRIV52	AL161552 Arabidops	c	323	21.8	53.2	174864	14	AC155530	AC155530 Zea mays
251	22	53.7	217841	14	AC095995	AC095995 Rattus no		324	21.8	53.2	184752	14	AC155597	AC155597 Zea mays
252	22	53.7	241206	14	AC120484	AC120484 Rattus no	c	325	21.8	53.2	185534	14	AC145481	AC145481 Zea mays
253	22	53.7	241627	14	AC128374	AC128374 Rattus no		326	21.8	53.2	195859	13	AF281817	AF281817 Tupaia he
c 254	22	53.7	244292	14	AC098749	AC098749 Rattus no		327	21.8	53.2	196249	14	AY542797	AY542797 Zea mays
c 255	22	53.7	264270	14	AC156048	AC156048 Bos tauru	c	328	21.8	53.2	197030	14	AY542797	AY542797 Zea mays
c 256	22	53.7	289308	1	AE017242	AE017242 Mycobacte		329	21.8	53.2	201041	14	AC154139	AC154139 Zea mays
c 257	22	53.7	300100	1	SCO939123	AL939123 Streptomy	c	330	21.8	53.2	203498	2	AC011697	AC011697 Drosophil
258	22	53.7	300242	1	AE016790	AE016790 Pseudomon		331	21.8	53.2	238578	14	AC110968	AC110968 Rattus no
c 259	22	53.7	301617	1	AE016911	AE016911 Chromobac		332	21.8	53.2	239030	9	AC131323	AC131323 Mus muscu
c 260	22	53.7	304282	1	AE016910	AE016910 Chromobac		333	21.8	53.2	300431	1	AE016835	AE016835 Salmonell
c 261	21.8	53.2	289	6	AR249266	AR249266 Sequence	c	334	21.8	53.2	303855	1	AE017230	AE017230 Mycobacte
c 262	21.8	53.2	371	3	AY574505	AY574505 Unculture		335	21.8	53.2	304450	1	BE294134	BE294134 Pirellula
c 263	21.8	53.2	500	3	AJ812177	AJ812177 Unculture	c	336	21.8	53.2	314743	2	AE003495	AE003495 Drosophil
c 264	21.8	53.2	676	3	AY343244	AY343244 Unculture		337	21.8	53.2	349980	6	AX044029	AX044029 Sequence
c 265	21.8	53.2	684	15	AY341385	AY341385 Hibiscus	c	338	21.6	52.7	230	6	AR128560	AR128560 Sequence
266	21.8	53.2	687	6	AR627479	AR627479 Sequence		339	21.6	52.7	731	10	BV043867	BV043867 S212P6603
c 267	21.8	53.2	705	15	AJ616326	AJ616326 Nuxia con	c	340	21.6	52.7	1689	6	AR621946	AR621946 Sequence
c 268	21.8	53.2	1035	3	AY920133	AY920133 Unculture		341	21.6	52.7	2400	1	AB051407	AB051407 Burkholde
c 269	21.8	53.2	1057	15	AK059797	AK059797 Oryza sat	c	342	21.6	52.7	2649	15	AK107362	AK107362 Oryza sat
270	21.8	53.2	1263	2	BT021428	BT021428 Drosophil		343	21.6	52.7	3028	1	AB117721	AB117721 Rhodococc
c 271	21.8	53.2	1349	3	AF376229	AF376229 Unculture	c	344	21.6	52.7	3216	15	AB168090	AB168090 Chlamydom
c 272	21.8	53.2	1350	3	AY986095	AY986095 Unculture		345	21.6	52.7	16651	15	AB168089	AB168089 Chlamydom
c 273	21.8	53.2	1397	15	AF233583	AF233583 Coriolus	c	346	21.6	52.7	18537	6	AR619762	AR619762 Sequence
c 274	21.8	53.2	1458	15	BT016254	BT016254 Zea mays		347	21.6	52.7	66938	14	AC165266	AC165266 Mus muscu
c 275	21.8	53.2	1484	1	BBA270471	AJ270471 Butyrate-	c	348	21.6	52.7	87093	1	AP006620	AP006620 Nocardia
c 276	21.8	53.2	2188	2	AY491261	AY491261 Neomantis		349	21.6	52.7	90398	14	AC164167	AC164167 Mus muscu
c 277	21.8	53.2	2436	15	OSA427971	AJ427971 Oryza sat	c	350	21.6	52.7	110000	1	AE014295_06	Continuation (7 of
c 278	21.8	53.2	3162	15	AK109999	AK109999 Oryza sat		351	21.6	52.7	110000	1	AP008231_08	Continuation (9 of
c 279	21.8	53.2	5189	15	OSA427976	AJ427976 Oryza sat	c	352	21.6	52.7	110000	1	BA000030_09	Continuation (10 o
c 280	21.8	53.2	5284	1	ECORAF	M27273 E.coli rafa		353	21.6	52.7	110000	1	BA000045_43	Continuation (44 o
281	21.8	53.2	6423	6	AX281457	AX281457 Sequence	c	354	21.6	52.7	110000	1	CP000009_06	Continuation (45 o
282	21.8	53.2	6423	6	AX348741	AX348741 Sequence		355	21.6	52.7	110000	1	CP000009_06	Continuation (7 of
283	21.8	53.2	6492	6	CQ573363	CQ573363 Sequence	c	356	21.6	52.7	110000	14	CT005263_3	Continuation (4 of
c 284	21.8	53.2	10029	1	AE015726	AE015726 Shewanell		357	21.6	52.7	110000	15	CR382132_22	Continuation (23 o
c 285	21.8	53.2	10528	6	AR619550	AR619550 Sequence	c	358	21.6	52.7	110000	15	AE016816_2	Continuation (3 of
c 286	21.8	53.2	10570	1	AE005005	AE005005 Halobacte		359	21.6	52.7	118497	14	AC134479	AC134479 Rattus no
287	21.8	53.2	16105	6	CQ573362	CQ573362 Sequence	c	360	21.6	52.7	133801	8	AC004585	AC004585 Homo sapi
288	21.8	53.2	16657	2	AF174134	AF174134 Drosophil		361	21.6	52.7	145127	9	AC136730	AC136730 Mus muscu
289	21.8	53.2	23865	1	AE008812	AE008812 Salmonell	c	362	21.6	52.7	146086	9	AL935056	AL935056 Mouse DNA
c 290	21.8	53.2	34946	14	AC014947	AC014947 Drosophil		363	21.6	52.7	161944	14	AC156785	AC156785 Rhinolph
c 291	21.8	53.2	102662	14	AC158288	AC158288 Dasyypus n	c	364	21.6	52.7	166234	8	AC018629	AC018629 Homo sapi
c 292	21.8	53.2	104992	14	AP004016	AP004016 Oryza sat		365	21.6	52.7	174630	14	AC150723	AC150723 Callithri
293	21.8	53.2	110000	1	AE002098_03	Continuation (4 of	c	366	21.6	52.7	175797	8	AL390760	AL390760 Human DNA
c 294	21.8	53.2	110000	1	CP000091_23	Continuation (24 o		367	21.6	52.7	177521	14	AC166236	AC166236 Rhinolph
c 295	21.8	53.2	110000	1	AE017220_03	Continuation (4 of	c	368	21.6	52.7	179736	14	AC163277	AC163277 Mus muscu
296	21.8	53.2	110000	1	AE017220_26	Continuation (27 o	c	369	21.6	52.7	180101	14	AC148583	AC148583 Gasterost
297	21.8	53.2	110000	1	AP006618_13	Continuation (14 o		370	21.6	52.7	183402	14	AC126231	AC126231 Bos tauru
298	21.8	53.2	110000	1	AP006618_14	Continuation (15 o	c	371	21.6	52.7	187220	14	AC150827	AC150827 Callithri
299	21.8	53.2	110000	1	BA000030_78	Continuation (79 o		372	21.6	52.7	187666	9	AC137157	AC137157 Mus muscu
300	21.8	53.2	110000	1	BA000030_89	Continuation (90 o	c	373	21.6	52.7	188740	9	AC163221	AC163221 Mus muscu
301	21.8	53.2	110000	1	BA000040_67	Continuation (68 o		374	21.6	52.7	189381	14	AC126920	AC126920 Bos tauru
302	21.8	53.2	110000	1	BA000040_83	Continuation (84 o	c	375	21.6	52.7	189405	14	AC127051	AC127051 Rattus no
c 303	21.8	53.2	110000	1	CP000026_04	Continuation (5 of		376	21.6	52.7	193347	14	AC125884	AC125884 Rattus no
c 304	21.8	53.2	110000	14	AC125726_1	Continuation (2 of	c	377	21.6	52.7	198050	1	AL646061	AL646061 Ralstonia
c 305	21.8	53.2	110000	15	AP008211_274	Continuation (275		378	21.6	52.7	200858	9	AC118255	AC118255 Mus muscu
306	21.8	53.2	110000	15	AP008213_282	Continuation (283	c	379	21.6	52.7	203483	14	AC164979	AC164979 Mus muscu
307	21.8	53.2	122177	14	AC152468	AL152468 Dasyypus n		380	21.6	52.7	206646	9	AC154598	AC154598 Mus muscu
308	21.8	53.2	131466	8	AL603650	AL603650 Human DNA	c	381	21.6	52.7	207514	9	AC142455	AC142455 Mus muscu
309	21.8	53.2	131547	14	AP003982	AP003982 Oryza sat		382	21.6	52.7	213925	14	AC150641	AC150641 Bos tauru
310	21.8	53.2	134299	14	AC155474	AC155474 Zea mays	c	383	21.6	52.7	224779	14	AC163810	AC163810 Bos tauru

C 384	21.6	52.7	226640	14	AC097833	AC097833 Rattus no
C 385	21.6	52.7	228864	14	AC155755	AC155755 Bos tauru
C 386	21.6	52.7	234949	5	BX936298	BX936298 Zebrafish
C 387	21.6	52.7	271034	14	AC102996	AC102996 Rattus no
C 388	21.6	52.7	277307	14	AC105149	AC105149 Rattus no
C 389	21.6	52.7	302007	1	SCO939132	AL939132 Streptomy
C 390	21.6	52.7	349980	6	AX492784	AX492784 Sequence
C 391	21.6	52.7	349980	6	AX553951	AX553951 Sequence
C 392	21.4	52.2	409	6	AR623837	AR623837 Sequence
C 393	21.4	52.2	438	9	MMFGF6E1	X51552 Mouse FGF-6
C 394	21.4	52.2	447	15	BT009578	BT009578 Triticum
C 395	21.4	52.2	572	6	CQ178247	CQ178247 Sequence
C 396	21.4	52.2	572	6	CQ338404	CQ338404 Sequence
C 397	21.4	52.2	627	9	AB079674	AB079674 Rattus no
C 398	21.4	52.2	630	6	E26527	E26527 Sugar chain
C 399	21.4	52.2	642	11	AY657572	AY657572 Synthetic
C 400	21.4	52.2	670	10	BV218271	BV218271 S233P626R
C 401	21.4	52.2	747	6	CQ740186	CQ740186 Sequence
C 402	21.4	52.2	1038	15	AK061213	AK061213 Oryza sat
C 403	21.4	52.2	1098	11	AY659060	AY659060 Synthetic
C 404	21.4	52.2	1182	9	AB035383	AB035383 Mus muscu
C 405	21.4	52.2	1224	9	BC063748	BC063748 Mus muscu
C 406	21.4	52.2	1305	6	AX659744	AX659744 Sequence
C 407	21.4	52.2	1532	6	AR507090	AR507090 Sequence
C 408	21.4	52.2	1578	15	AY570713	AY570713 Ostreococ
C 409	21.4	52.2	1602	15	BT017987	BT017987 Zea mays
C 410	21.4	52.2	1719	1	CSU16275	U16275 Comamonas s
C 411	21.4	52.2	1739	1	AF031149	AF031149 Chromatiu
C 412	21.4	52.2	1861	6	CQ598842	CQ598842 Sequence
C 413	21.4	52.2	2069	9	BC025585	BC025585 Mus muscu
C 414	21.4	52.2	2113	1	AB000508	AB000508 Comamonas
C 415	21.4	52.2	2266	6	CQ573282	CQ573282 Sequence
C 416	21.4	52.2	2303	2	AF145614	AF145614 Drosophil
C 417	21.4	52.2	2303	15	AK071363	AK071363 Oryza sat
C 418	21.4	52.2	2328	2	AF342986	AF342986 Caenorhab
C 419	21.4	52.2	3792	2	BT009935	BT009935 Drosophil
C 420	21.4	52.2	4236	6	AR623966	AR623966 Sequence
C 421	21.4	52.2	4339	15	AY081008	AY081008 Aspergill
C 422	21.4	52.2	4607	9	MUSFGFAB	M92416 Mus musculu
C 423	21.4	52.2	5888	1	AF038578	AF038578 Pseudomon
C 424	21.4	52.2	5998	1	AB032524	AB032524 Streptomy
C 425	21.4	52.2	6037	6	CQ573281	CQ573281 Sequence
C 426	21.4	52.2	6323	6	CQ598841	CQ598841 Sequence
C 427	21.4	52.2	6683	9	RNU24070	U24070 Rattus norv
C 428	21.4	52.2	10647	1	AE004518	AE004518 Pseudomon
C 429	21.4	52.2	10773	1	AE012272	AE012272 Xanthomon
C 430	21.4	52.2	10965	1	AE004740	AE004740 Pseudomon
C 431	21.4	52.2	11854	6	AR619642	AR619642 Sequence
C 432	21.4	52.2	20776	2	CEK03D10	Z81561 Caenorhabdi
C 433	21.4	52.2	34662	6	AR619866	AR619866 Sequence
C 434	21.4	52.2	39200	8	AC024584	AC024584 Homo sapi
C 435	21.4	52.2	39263	3	AY281354	AY281354 Unculture
C 436	21.4	52.2	39360	1	AY943953	AY943953 Streptomy
C 437	21.4	52.2	44567	6	AX695371	AX695371 Sequence
C 438	21.4	52.2	47618	14	AC166904	AC166904 Bos tauru
C 439	21.4	52.2	55578	1	PPS304453	AJ304453 Plasmid p
C 440	21.4	52.2	66093	14	AC125991_4	Continuation (5 of
C 441	21.4	52.2	76345	14	AC165120_	AC165120 Bos tauru
C 442	21.4	52.2	78065	8	AC005355	AC005355 Homo sapi
C 443	21.4	52.2	91170	14	AC014779	AC014779 Drosophil
C 444	21.4	52.2	104561	1	AE017282_32	Continuation (33 o
C 445	21.4	52.2	110000	1	AE006470_07	Continuation (8 of
C 446	21.4	52.2	110000	1	AP006618_21	Continuation (22 o
C 447	21.4	52.2	110000	1	AP006618_25	Continuation (26 o
C 448	21.4	52.2	110000	1	AP006618_36	Continuation (37 o
C 449	21.4	52.2	110000	1	BA000030_11	Continuation (12 o
C 450	21.4	52.2	110000	1	BA000030_27	Continuation (28 o
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C 454	21.4	52.2	110000	1	BA000030_85	Continuation (86 o
C 455	21.4	52.2	110000	1	CP000050_30	Continuation (31 o
C 456	21.4	52.2	110000	1	CP000058_45	Continuation (46 o

457	21.4	52.2	110000	1	CP000076_33	Continuation (34 o
458	21.4	52.2	110000	1	CP000076_39	Continuation (40 o
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460	21.4	52.2	110000	1	CP000076_61	Continuation (62 o
461	21.4	52.2	110000	2	CP000078_2	Continuation (3 of
462	21.4	52.2	110000	14	AC125991_3	Continuation (4 of
463	21.4	52.2	110000	14	BX255276_13	Continuation (14 o
464	21.4	52.2	110000	14	CEY105E8_0	AL022594 Caenorhab
C 465	21.4	52.2	110000	14	CR954213_1	Continuation (2 of
C 466	21.4	52.2	110000	15	AP008214_097	Continuation (98 o
C 467	21.4	52.2	110000	15	AP008218_093	Continuation (94 o
C 468	21.4	52.2	110000	15	AP008209_168	Continuation (169
C 469	21.4	52.2	110000	15	AP008210_171	Continuation (172
C 470	21.4	52.2	110000	15	AP008211_251	Continuation (252
C 471	21.4	52.2	110000	15	AP008212_050	Continuation (51 o
472	21.4	52.2	112351	8	AC011484	AC011484 Homo sapi
C 473	21.4	52.2	113266	15	AC092262	AC092262 Oryza sat
C 474	21.4	52.2	127490	14	AC163683	AC163683 Mus muscu
C 475	21.4	52.2	130712	14	AC141789	AC141789 Apis mell
C 476	21.4	52.2	130748	14	AP005906	AP005906 Oryza sat
477	21.4	52.2	131141	14	AC153085	AC153085 Ornithorh
478	21.4	52.2	132781	14	AC141265	AC141265 Homo sapi
479	21.4	52.2	132830	14	AC148864	AC148864 Canis fam
C 480	21.4	52.2	134059	14	AC016284	AC016284 Homo sapi
481	21.4	52.2	134184	14	AC150028	AC150028 Canis fam
C 482	21.4	52.2	143427	8	AC002432	AC002432 Homo sapi
C 483	21.4	52.2	146712	15	AC130604	AC130604 Oryza sat
484	21.4	52.2	152945	14	AC130606	AC130606 Oryza sat
C 485	21.4	52.2	154440	14	AC108176	AC108176 Bos tauru
486	21.4	52.2	155649	14	AC015874	AC015874 Homo sapi
487	21.4	52.2	157493	14	AC022175	AC022175 Homo sapi
C 488	21.4	52.2	158892	14	AC108175	AC108175 Bos tauru
489	21.4	52.2	162727	8	HS467L1	Z98884 Human DNA s
C 490	21.4	52.2	162772	15	AC108873	AC108873 Oryza sat
C 491	21.4	52.2	163162	14	AC139311	AC139311 Bos tauru
492	21.4	52.2	163741	2	AC007821	AC007821 Drosophil
C 493	21.4	52.2	164632	14	AC025624	AC025624 Homo sapi
494	21.4	52.2	165902	8	AC106763	AC106763 Homo sapi
C 495	21.4	52.2	168076	14	AC013304	AC013304 Homo sapi
496	21.4	52.2	168243	14	AC011269	AC011269 Homo sapi
C 497	21.4	52.2	169509	14	AC150713	AC150713 Bos tauru
498	21.4	52.2	169559	15	OSJN00159	AL662956 Oryza sat
499	21.4	52.2	170453	15	AP005095	AP005095 Oryza sat
500	21.4	52.2	170652	14	AC092934	AC092934 Homo sapi

ALIGNMENTS

RESULT 1	HSA248385	164 bp	DNA	linear	STS 08-MAR-2000
LOCUS	HSA248385	Homo sapiens STS J-210R, sequence tagged site.			
DEFINITION	AJ248385				
ACCESSION	AJ248385.1	GI:5514723			
VERSION	STS.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 164)				
AUTHORS	Sulimova,G.E., Udina,I.G., Kunizheva,S.S. and Kompaniytzev,A.A.				
TITLE	Creating NotI-STS Markers for Human Chromosome 3				
JOURNAL	Mol. Biol. 33, 698-703 (1999)				
REFERENCE	2 (bases 1 to 164)				
AUTHORS	Sulimova,G.E.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-JUN-1999) Sulimova G.E., Laboratory of Comparative Animal Genetics, N.I.Vavilov Institute of General Genetics RAS, Gubkin Str. 3, Moscow B-333, 117809 GSP-1, RUSSIA				
COMMENT	The STS markers registered were developed to clones from NotI library of human chromosome				

3 received by E.R. Zabarovsky (Karolinska Institute, Sweden) as a result of collaborative research work with Engelhardt Molecular Biology Institute of the Russian Academy of Sciences. The NotI clones were used to construct NotI map of human chromosome 3 by FISH and mapping by a somatic cell hybrid panel.

FEATURES

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complement(144. .164)
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STS

primer_bind

ORIGIN

Query Match 100.0%; Score 41; DB 10; Length 164;
Best Local Similarity 97.6%; Pred. No. 0.046; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
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Db 131 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 91

RESULT 2
I59642/c

LOCUS I59642 31571 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5654170.
ACCESSION I59642
VERSION I59642.1 GI:2478274
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31571)
AUTHORS Klingner,K.W., Landes,G.M., Burn,T.C., Connors,T.D., Dackowski,W.,
Germino,G. and Qian,F.
TITLE Polycystic kidney disease gene
JOURNAL Patent: US 5654170-A 1 05-AUG-1997;
FEATURES Location/Qualifiers
source
1. .31571
/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 41; DB 6; Length 31571;
Best Local Similarity 97.6%; Pred. No. 0.017; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
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Db 3633 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 3593

RESULT 3
AC141442/c

LOCUS AC141442 34934 bp DNA linear HTG 16-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-371H10, WORKING DRAFT
SEQUENCE, 4 unordered pieces.

ACCESSION

AC141442 AC141442.1 GI:28974995
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 34934)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished

REFERENCE

2 (bases 1 to 34934)
DOE Joint Genome Institute.
Direct Submission
Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

JOURNAL

COMMENT

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1222782
Center clone name: LANL-16c_371H10

Summary Statistics

Consensus quality: 33115 bases at least Q40
Consensus quality: 33242 bases at least Q30
Consensus quality: 33298 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 34634; sum-of-contigs estimation
Quality coverage: 15.87 in Q20 bases; agarose-fp estimation
Quality coverage: 18.32 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1026: contig of 1026 bp in length
* 1027 1126: gap of unknown length
* 1127 2407: contig of 1281 bp in length
* 2408 2507: gap of unknown length
* 2508 7632: contig of 5125 bp in length
* 7633 7732: gap of unknown length
* 7733 34934: contig of 27202 bp in length.

FEATURES

source
1. .34934
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16c-371H10"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
1027. .1126
/estimated_length=unknown
2408. .2507
/estimated_length=unknown
7633. .7732
/estimated_length=unknown

gap
1027. .1126
/estimated_length=unknown
2408. .2507
/estimated_length=unknown
7633. .7732
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 34934;
Best Local Similarity 97.6%; Pred. No. 0.017; Indels 0; Gaps 0;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
|||||

Db 24319 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 24279

RESULT 4
AC140806 37244 bp DNA linear HTG 03-MAR-2003
LOCUS Homo sapiens chromosome 16 clone LA16C-379A4, WORKING DRAFT
DEFINITION SEQUENCE, 2 unordered pieces.
AC140806
ACCESSION AC140806.1 GI:28631187
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 37244)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 37244)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1223460
Center clone name: LANL-16C_379A4

Summary Statistics
Consensus quality: 36406 bases at least Q40
Consensus quality: 36465 bases at least Q30
Consensus quality: 36556 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 37144; sum-of-contigs estimation
Quality coverage: 9.59 in Q20 bases; agarose-fp estimation
Quality coverage: 10.33 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 17558: contig of 17558 bp in length
* 17559 17658: gap of unknown length
* 17659 37244: contig of 19586 bp in length.
FEATURES
source
1. .37244
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16C-379A4"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
17559. .17658
gap
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 37244;
Best Local Similarity 97.6%; Pred. No. 0.017;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
|||||
Db 16992 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 17032
|||||

RESULT 5
AC140702 37279 bp DNA linear HTG 28-FEB-2003
LOCUS Homo sapiens chromosome 16 clone LA16C-317A11, WORKING DRAFT
DEFINITION SEQUENCE, 2 unordered pieces.
AC140702
ACCESSION AC140702.1 GI:28603918
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 37279)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 37279)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1217515
Center clone name: LANL-16C_317A11

Summary Statistics
Consensus quality: 36867 bases at least Q40
Consensus quality: 37083 bases at least Q30
Consensus quality: 37153 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 37179; sum-of-contigs estimation
Quality coverage: 15.56 in Q20 bases; agarose-fp estimation
Quality coverage: 16.74 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2057: contig of 2057 bp in length
* 2058 2157: gap of unknown length
* 2158 37279: contig of 35122 bp in length.
FEATURES
source
1. .37279
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16C-317A11"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
2058. .2157
gap
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 37279;
Best Local Similarity 97.6%; Pred. No. 0.017;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
|||||
Db 37099 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 37139
|||||

RESULT 6
AC005346
LOCUS
DEFINITION Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete
sequence.
ACCESSION AC005346
VERSION AC005346.1 GI:3366566
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 38849)
AUTHORS Ricke,D.O.
TITLE Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 38849)
AUTHORS Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S.,
Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J.,
White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M.,
Misra,M. and Deaven,L.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-1998) Center for Human Genome Studies, DOE Joint
Genome Institute, Los Alamos National Laboratory, MS M888, Los
Alamos, NM 87545, USA
FEATURES
source Location/Qualifiers
1..38849
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"
/clone="2H2"
complement(join(544..637,2772..2834,4702..4832))
/note="100% identity EST zt53d08.s1"
/db_xref="dbEST:AA399469"
complement(join(544..637,2772..2834,4719..4823))
/note="85% identity mouse EST mj33h06.r1"
/db_xref="dbEST:AA048697"
complement(544..635)
/note="GRAIL 2 excellent exon, frame 2"
2023..2291
/rpt_family="Alu"
complement(2776..2833)
/note="GRAIL 2 excellent exon, frame 0"
join(2868..3015,3611..3712,3884..3999,4552..4795)
/note="97% identity dbEST:H86633 & H86545 yt04f02"
complement(5954..6098)
/note="GRAIL 2 excellent exon, frame 0"
12312..12503
/rpt_family="MER20"
join(13385..13572,13788..13910)
/note="96% identity dbEST:W60179 & W60180 zd28b11"
complement(14071..14338)
/rpt_family="Alu"
14071..14090
/note="(T)20"
/rpt_type=tandem
/rpt_unit="t"
complement(14995..15137)
/note="GRAIL 2 excellent exon, frame 2"
complement(15261..15398)

/note="83% identity me96a10.r1"
/db_xref="dbEST:W82874"
complement(join(15275..15398,15492..15587,18689..18805))
/standard_name="Rab26 (Rat homolog)"
complement(join(15301..15398,15512..15571,15826..15898))
/note="97%, 100%, & 100% identity EST AA984064 am76b10.s1"
complement(15493..15601)
/note="GRAIL 2 excellent exon, frame 0"
complement(15786..15895)
/note="GRAIL 2 excellent exon, frame 1"
15999..16022
/note="(T)24"
/rpt_type=tandem
/rpt_unit="t"
complement(16005..16528)
/rpt_family="Alu"
complement(16808..16860)
/note="GRAIL 2 excellent exon, frame 1"
complement(17106..17147)
/note="GRAIL 2 excellent exon, frame 0"
17508..17576
/rpt_family="Alu"
complement(18689..18799)
/note="100% identity L48770 (clone exon trap 44.2)"
complement(18689..18799)
/note="GRAIL 2 excellent exon, frame 1"
19415..19436
/note="(A)22"
/rpt_type=tandem
/rpt_unit="a"
complement(19762..19956)
/note="GRAIL 2 excellent exon, frame 2"
20058..20093
/note="(GGC)12"
/rpt_type=tandem
/rpt_unit="ggc"
22264..22545
/rpt_family="Alu"
23196..23760
/rpt_family="Alu"
25104..25127
/note="GRAIL 2 excellent exon, frame 2"
complement(25572..26174)
/rpt_family="Alu"
25875..25898
/note="(T)24"
/rpt_type=tandem
/rpt_unit="t"
26184..26205
/note="(T)22"
/rpt_type=tandem
/rpt_unit="t"
complement(26188..26461)
/rpt_family="Alu"
complement(27153..27447)
/rpt_family="Alu"
complement(27494..27773)
/rpt_family="Alu"
complement(28010..28315)
/rpt_family="Alu"
28478..28777
/rpt_family="Alu"
complement(28795..28971)
/rpt_family="Alu"
28995..29301
/rpt_family="Alu"
complement(29325..29382)
/rpt_family="Alu"
complement(29421..29487)
/rpt_family="Alu"
complement(29647..29950)
/rpt_family="Alu"
30100..30123
repeat_region

```

/note="(T)24"
/rpt_type=tandem
/rpt_unit="t"
complement(30106. .30688)
/rpt_family="Alu"
complement(30881. .31183)
/rpt_family="Alu"
complement(31488. .31754)
/rpt_family="Alu"
complement(31673. .38849)
/note="L39891 overlap"
complement(31787. .32068)
/rpt_family="Alu"
35647. .35670
/note="(T)24"
/rpt_type=tandem
/rpt_unit="t"
complement(35653. .35942)
/rpt_family="Alu"
complement(36161. .36779)
/rpt_family="Alu"
complement(36922. .37194)
/rpt_family="Alu"
37212. .37235
/note="(ATT)6"
/rpt_type=tandem
/rpt_unit="attt"
complement(37242. .37514)
/rpt_family="Alu"

ORIGIN
Query Match      100.0%;   Score 41;   DB 8;   Length 38849;
Best Local Similarity 97.6%;   Pred. No. 0.017;
Matches 40;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1  AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db      32714 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 32754

RESULT 7
AC140703/c
LOCUS      AC140703      39322 bp      DNA      linear      HTG 28-FEB-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-320A3, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
ACCESSION      AC140703
VERSION      AC140703.1 GI:28603919
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE      1 (bases 1 to 39322)
AUTHORS      DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 16
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 39322)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (28-FEB-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1217795
Center clone name: LANL-16c_320A3
-----
Summary Statistics
Consensus quality: 38784 bases at least Q40
```

```

Consensus quality: 38986 bases at least Q30
Consensus quality: 39072 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 39222; sum-of-contigs estimation
Quality coverage: 16.68 in Q20 bases; agarose-fp estimation
Quality coverage: 17.02 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*      1 10022: contig of 10022 bp in length
*      10023 10122: gap of unknown length
*      10123 39322: contig of 29200 bp in length.

FEATURES
source
1.39322
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16c-320A3"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
10023. .10122
/estimated_length=unknown

gap

ORIGIN
Query Match      100.0%;   Score 41;   DB 14;   Length 39322;
Best Local Similarity 97.6%;   Pred. No. 0.016;
Matches 40;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1  AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db      10416 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 10376

RESULT 8
AC140704
LOCUS      AC140704      40673 bp      DNA      linear      HTG 28-FEB-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-326B6, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
ACCESSION      AC140704
VERSION      AC140704.1 GI:28603920
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE      1 (bases 1 to 40673)
AUTHORS      DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 16
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 40673)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (28-FEB-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1218386
Center clone name: LANL-16c_326B6
-----
Summary Statistics
Consensus quality: 38913 bases at least Q40
Consensus quality: 39592 bases at least Q30
```


Consensus quality: 39957 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 40573; sum-of-contigs estimation
Quality coverage: 15.02 in Q20 bases; agarose-fp estimation
Quality coverage: 14.8 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 14666: contig of 14666 bp in length
14667 14766: gap of unknown length
14767 40673: contig of 25907 bp in length.

Location/Qualifiers
1. .40673
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16C-326B6"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
14667. .14766
/estimated_length=unknown

gap

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 40673;
Best Local Similarity 97.6%; Pred. No. 0.016;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||

Db 24348 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 24388

RESULT 9
AC142549 41489 bp DNA linear HTG 04-APR-2003
LOCUS Homo sapiens chromosome 16 clone XXfos-81795G9, WORKING DRAFT
DEFINITION SEQUENCE, 5 unordered pieces.
AC142549
AC142549.1 GI:29540584
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 41489)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 41489)
DOE Joint Genome Institute.
Direct Submission
Submitted (04-APR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 3436195
Center clone name: WF-81795G9

Summary Statistics
Consensus quality: 39376 bases at least Q40
Consensus quality: 39697 bases at least Q30
Consensus quality: 39943 bases at least Q20

Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 41089; sum-of-contigs estimation
Quality coverage: 8.2 in Q20 bases; agarose-fp estimation
Quality coverage: 7.98 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1669: contig of 1669 bp in length
1670 1769: gap of unknown length
1770 4523: contig of 2754 bp in length
4524 4623: gap of unknown length
4624 17325: contig of 12702 bp in length
17326 17425: gap of unknown length
17426 24658: contig of 7233 bp in length
24659 24758: gap of unknown length
24759 41489: contig of 16731 bp in length.

FEATURES
Location/Qualifiers
1. .41489
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="XXfos-81795G9"
1670. .1769
/estimated_length=unknown
4524. .4623
/estimated_length=unknown
17326. .17425
/estimated_length=unknown
24659. .24758
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 41489;
Best Local Similarity 97.6%; Pred. No. 0.016;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 41
|||||

Db 24485 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG 24525

RESULT 10
HSU24498 47934 bp DNA linear PRI 09-MAY-2002
LOCUS Human autosomal dominant polycystic kidney disease protein 1 (PKD1)
DEFINITION gene.
ACCESSION U24498
VERSION U24498.1 GI:794297
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 47934)
The International Polycystic Kidney Disease Consortium.
Polycystic kidney disease: the complete structure of the PKD1 gene
and its protein
Cell 81 (2), 289-298 (1995)
7736581
REFERENCE 2 (bases 1 to 47934)
AUTHORS Glucksmann-Kuis,M.A.
TITLE Direct Submission
JOURNAL Submitted (10-APR-1995) M. Alexandra Glucksmann-Kuis, Genomics,
Millennium Pharmaceuticals, 640 Memorial Drive, Cambridge, MA
02139, USA
Location/Qualifiers

```

source
1. .47934
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"

ORIGIN
Query Match      100.0%;   Score 41;   DB 8;   Length 47934;
Best Local Similarity 97.6%;   Pred. No. 0.016;
Matches 40;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCCGNCGCG 41
|||||
724 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCCGTCGCG 764

RESULT 11
AX440497
LOCUS      AX440497      53522 bp      DNA      linear      PAT 28-JUN-2002
DEFINITION Sequence 1 from Patent WO0206529.
ACCESSION  AX440497
VERSION     AX440497.1   GI:21665301
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1
AUTHORS    Germino,G.G., Watnick,T.J. and Phakdeekitcharoen,B.
TITLE      Detection and treatment of polycystic kidney disease
JOURNAL    Patent: WO 0206529-A 1 24-JAN-2002;
            The Johns Hopkins University School of Medicine (US)
FEATURES
source
1. .53522
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match      100.0%;   Score 41;   DB 6;   Length 53522;
Best Local Similarity 97.6%;   Pred. No. 0.016;
Matches 40;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCCGNCGCG 41
|||||
3300 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCCGTCGCG 3340

Db

RESULT 12
HUMPKD1GEN
LOCUS      HUMPKD1GEN      53522 bp      DNA      linear      PRI 10-MAY-2002
DEFINITION Homo sapiens polycystic kidney disease-associated protein (PKD1)
            gene, complete cds.
ACCESSION  L39891
VERSION    L39891.1   GI:790818
KEYWORDS   polycystic kidney disease.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (sites)
AUTHORS    Ward,C.J., Peral,B., Hughes,J., Thomas,S., Gamble,V.,
            MacCarthy,A.B., Sloane-Stanley,J., Buckle,V.J., Kearney,L.,
            Higgs,D.R., Ratcliffe,P.J., Harris,P.C., Roelfsema,J.H.,
            Spruit,L.L., Saris,J.J., Dauwerse,H.G., Peters,D.J.M.,
            Breuning,M.H., Nellist,M., Brook-Carter,P.T., Maheshwar,M.M.,
            Cordeiro,I., Santos,H., Cabral,P., Sampson,J.R., Janssen,B.,
            Hesselting-Janssen,A.L.W., van den Ouweland,A.M.W., Eussen,B.,
            Verhoef,S., Lindhout,D. and Hallley,D.J.J.
            The polycystic kidney disease 1 gene encodes a 14 kb transcript and
TITLE
```

```

lies within a duplicated region on chromosome 16. The European
Polycystic Kidney Disease Consortium [published erratum appears in
Cell 1994 Aug 26;78(4):following 724]
Cell 77 (6), 881-894 (1994)
8004675
2 (bases 1 to 53522)
Burn,T.C., Connors,T.D., Dackowski,W.R., Petry,L.R., Van Raay,T.J.,
Millholland,J., Venet,M., Miller,G., Hakim,R.M., Doggett,N.A.,
Landes,G.M., Klinger,K.W., Qian,F., Onuchic,L.F., Watnick,T. and
Germino,G.G.
Analysis of the genomic sequence for the autosomal dominant
polycystic kidney disease (PKD1) gene predicts the presence of a
leucine-rich repeat. The American PKD1 Consortium (APKD1
Consortium)
Hum. Mol. Genet. 4 (4), 575-582 (1995)
7633406

JOURNAL
PUBMED
REFERENCE
AUTHORS

TITLE
Analysis of the genomic sequence for the autosomal dominant
polycystic kidney disease (PKD1) gene predicts the presence of a
leucine-rich repeat. The American PKD1 Consortium (APKD1
Consortium)
Hum. Mol. Genet. 4 (4), 575-582 (1995)
7633406

JOURNAL
PUBMED
FEATURES
source
Location/Qualifiers
1. .53522
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complement(236. .524)
/rpt_family="Alu"
complement(704. .940)
/rpt_family="Alu"
complement(998. .1287)
/rpt_family="Alu"
complement(1483. .1771)
/rpt_family="Alu"
complement(2081. .2352)
/rpt_family="Alu"
complement(2423. .2666)
/rpt_family="Alu"
3096. .4204
/note="CpG island; putative"
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25989. .26120,26318. .26493,26808. .26941,27407. .27525,
27628. .28683,29126. .29875,30419. .31024,31244. .31393,
32328. .32471,32599. .32878,32972. .33185,33251. .33410,
33848. .33952,36954. .37098,37701. .38330,38624. .38780,
38961. .39213,39338. .39533,41028. .41198,41285. .41428,
41523. .41733,41824. .41950,43610. .43726,43817. .43866,
44091. .44275,44353. .44446,47384. .47502,47581. .47783,
47856. .48050,48501. .48640,49002. .49114,49406. .49547,
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/gene="PKD1"
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/gene="PKD1"
/codon_start=1
/product="polycystic kidney disease-associated protein"
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/db_xref="GI:790819"
/translation="MPPAAPARLALALGLWLGLAGSPGRGCGPPEPCLCGPAPG
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RESULT 14
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LOCUS BD128573 53526 bp DNA linear PAT 18-SEP-2002
DEFINITION Polycystic kidney disease gene.
ACCESSION BD128573
VERSION BD128573.1 GI:23223518
KEYWORDS JP 2002503952-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 53526)
AUTHORS Klinger,K., Burn,T., Connors,T., Dackowski,W., Germino,G. and Qian,F.
TITLE Polycystic kidney disease gene
JOURNAL Patent: JP 2002503952-A 2 05-FEB-2002;
GENZYME CORP
COMMENT OS Unidentified
PN JP 2002503952-A/2
PD 05-FEB-2002
PF 22-MAY-1997 JP 1997542784
PR 24-MAY-1996 US 08/655360,03-JUN-1996 US 08/658136 PI
KATHERINE KLINGER,TIMOTHY BURN,TIMOTHY CONNORS,WILLIAM PI
DACKOWSKI,
PI GREGORY GERMINO,FENG QIAN
PC C12N15/12,C12N15/11,C07K14/47,C12N5/10,C12Q1/68,G01N33/68, PC
G01N33/53,
PC C07K16/18,A61K48/00,A61K38/17,A01K67/027,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Polycystic kidney disease gene
FH key Location/Qualifiers
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Query Match 100.0%; Score 41; DB 6; Length 53526;
Best Local Similarity 97.6%; Pred. No. 0.016;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|||||
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGTCCGCG 3340
RESULT 15
AR097325
LOCUS AR097325 53577 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6071717.
ACCESSION AR097325
VERSION AR097325.1 GI:12806055
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53577)
AUTHORS Klinger,K., Burn,T., Connors,T., Dackowski,W., Germino,G., Qian,F. and Landes,G.
TITLE Polycystic kidney disease gene and protein
JOURNAL Patent: US 6071717-A 1 06-JUN-2000;
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source 1..53577
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 41; DB 6; Length 53577;
Best Local Similarity 97.6%; Pred. No. 0.016;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|||||
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGTCCGCG 3340
RESULT 16
BD128572
LOCUS BD128572 53577 bp DNA linear PAT 18-SEP-2002
DEFINITION Polycystic kidney disease gene.
ACCESSION BD128572
VERSION BD128572.1 GI:23223517
KEYWORDS JP 2002503952-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 53577)
AUTHORS Klinger,K., Burn,T., Connors,T., Dackowski,W., Germino,G. and Qian,F.
TITLE Polycystic kidney disease gene
JOURNAL Patent: JP 2002503952-A 1 05-FEB-2002;
GENZYME CORP
COMMENT OS Unidentified
PN JP 2002503952-A/1
PD 05-FEB-2002
PF 22-MAY-1997 JP 1997542784
PR 24-MAY-1996 US 08/655360,03-JUN-1996 US 08/658136 PI
KATHERINE KLINGER,TIMOTHY BURN,TIMOTHY CONNORS,WILLIAM PI
DACKOWSKI,
PI GREGORY GERMINO,FENG QIAN
PC C12N15/12,C12N15/11,C07K14/47,C12N5/10,C12Q1/68,G01N33/68, PC
G01N33/53,
PC C07K16/18,A61K48/00,A61K38/17,A01K67/027,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Polycystic kidney disease gene
FH key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 41; DB 6; Length 53577;
Best Local Similarity 97.6%; Pred. No. 0.016;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|||||
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGTCCGCG 3340
RESULT 17
AR643858
LOCUS AR643858 53577 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 1 from patent US 6867288.
ACCESSION AR643858
VERSION AR643858.1 GI:62782487
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 53577)
AUTHORS Klinger,K.W., Landes,G.M., Burn,T.C., Connors,T.D., Dackowski,W., Germino,G. and Qian,F.
TITLE Polycystic kidney disease gene
JOURNAL Patent: US 6867288-A 1 15-MAR-2005;
GENZYME Corporation and Johns Hopkins University; Cambridge, MA
FEATURES
source 1..53577

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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 41; DB 6; Length 53577;
Best Local Similarity 97.6%; Pred. No. 0.016;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 41
    |||||
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 3340

RESULT 18
AC140700
LOCUS      AC140700      84562 bp      DNA      linear      HTG 28-FEB-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-304D8, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
AC140700
ACCESSION  AC140700.1 GI:28603916
VERSION     HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 84562)
AUTHORS    DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 16
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 84562)
AUTHORS    DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL    Submitted (28-FEB-2003) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1216300
Center clone name: LANL-16c_304D8

Summary Statistics
Consensus quality: 83255 bases at least Q40
Consensus quality: 83860 bases at least Q30
Consensus quality: 84027 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Quality coverage: 15.89 in Q20 bases; agarose-fp estimation
Quality coverage: 7.55 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 3092: contig of 3092 bp in length
* 3093 3192: gap of unknown length
* 3193 19478: contig of 16286 bp in length
* 19479 19578: gap of unknown length
* 19579 36789: contig of 17211 bp in length
* 36790 36889: gap of unknown length
* 36890 57552: contig of 20663 bp in length
* 57553 57652: gap of unknown length
* 57653 84562: contig of 26910 bp in length.
            Location/Qualifiers
            1. .84562
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            /mol_type="genomic DNA"

/db xref="taxon:9606"
/chromosome="16"
/clone="LA16c-304D8"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
3093. .3192
/estimated_length=unknown
19479. .19578
/estimated_length=unknown
36790. .36889
/estimated_length=unknown
57553. .57652
/estimated_length=unknown

ORIGIN
Query Match      100.0%; Score 41; DB 14; Length 84562;
Best Local Similarity 97.6%; Pred. No. 0.014;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 41
    |||||
Db 84456 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 84496

RESULT 19
AC141231/c
LOCUS      AC141231      84928 bp      DNA      linear      HTG 11-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-339B10, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
AC141231
ACCESSION  AC141231.1 GI:28913011
VERSION     HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 84928)
AUTHORS    DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 16
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 84928)
AUTHORS    DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL    Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1219638
Center clone name: LANL-16c_339B10

Summary Statistics
Consensus quality: 83944 bases at least Q40
Consensus quality: 84247 bases at least Q30
Consensus quality: 84389 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Quality coverage: 18.18 in Q20 bases; agarose-fp estimation
Quality coverage: 8.59 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2589: contig of 2589 bp in length
* 2590 2689: gap of unknown length
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* 2690 19595: contig of 16906 bp in length
* 19596 19695: gap of unknown length
* 19696 46734: contig of 27039 bp in length
* 46735 46834: gap of unknown length
* 46835 84928: contig of 38094 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16C-339B10"
/libraries; LA16NC01 and LA16NC02"
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/estimated_length=unknown
19596. .19695
/estimated_length=unknown
46735. .46834
/estimated_length=unknown
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Query Match 100.0%; Score 41; DB 14; Length 84928;
Best Local Similarity 97.6%; Pred.No. 0.014;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 19931 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTGC 19891
AC138966 89599 bp DNA linear HTG 21-JAN-2003
Homo sapiens chromosome 16 clone RP11-921M23, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
AC138966
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 89599)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 89599)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1648479
Center clone name: RPCI-11_921M23

Summary Statistics
Consensus quality: 85343 bases at least Q40
Consensus quality: 86141 bases at least Q30
Consensus quality: 86639 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 88799; sum-of-contigs estimation
Quality coverage: 8.26 in Q20 bases; agarose-fp estimation
Quality coverage: 16.74 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1131: contig of 1131 bp in length
* 1132 1231: gap of unknown length
* 1232 3226: contig of 1995 bp in length
* 3227 3326: gap of unknown length
* 3327 7532: contig of 4206 bp in length
* 7533 7632: gap of unknown length
* 7633 19088: contig of 11456 bp in length
* 19089 19188: gap of unknown length
* 19189 35501: contig of 16313 bp in length
* 35502 35601: gap of unknown length
* 35602 44325: contig of 8724 bp in length
* 44326 44425: gap of unknown length
* 44426 52214: contig of 7789 bp in length
* 52215 52314: gap of unknown length
* 52315 70546: contig of 18232 bp in length
* 70547 70646: gap of unknown length
* 70647 89599: contig of 18953 bp in length.
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/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-921M23"
/clone_lib="RPCI human BAC library 11"
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3227. .3326
/estimated_length=unknown
7533. .7632
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19089. .19188
/estimated_length=unknown
35502. .35601
/estimated_length=unknown
44326. .44425
/estimated_length=unknown
52215. .52314
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70547. .70646
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ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 89599;
Best Local Similarity 97.6%; Pred.No. 0.014;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 7144 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTGC 7184
RESULT 21
AC010488/c
LOCUS AC010488 109340 bp DNA linear PRI 07-APR-2003
DEFINITION Homo sapiens chromosome 16 clone CTD-2332D4, complete sequence.
ACCESSION AC010488
VERSION AC010488.7 GI:28973804
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 109340)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 109340)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 109340)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 109340)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 15, 2003 this sequence version replaced gi:16924086.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
NOTE: Unsure number of dinucleotide repeats from 25789 to 26208.
Forced join at 26030. The number of missing bases by PCR is 100.
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/clone="CTD-2332D4"
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25789 to 26208. Forced join at 26030. The number of
missing bases by PCR is 100."
ORIGIN
Query Match 100.0%; Score 41; DB 8; Length 109340;
Best Local Similarity 97.6%; Pred. No. 0.014;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
|||||
Db 42483 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGTCGCG 42443
RESULT 22
HUAC002039
LOCUS Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 PRI 30-OCT-2002
DEFINITION genomic sequence, complete sequence.
ACCESSION AC002039
VERSION AC002039.1 GI:2342716
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 127485)
AUTHORS Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,
Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S.,
Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
TITLE Genome duplications and other features in 12 Mb of DNA sequence
from human chromosome 16p and 16q
JOURNAL Genomics 60 (3), 295-308 (1999)
PUBMED 10493829
REFERENCE 2 (bases 1 to 127485)

AUTHORS Adams,M.D., Loftus,B.J., Zhou,L., LaBombard,M., Fuhrmann,J.,
Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
TITLE Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 #complete
genomic sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 127485)
AUTHORS Adams,M.D. and Loftus,B.J.
TITLE Direct Submission
JOURNAL Submitted (29-APR-1997) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
REFERENCE 4 (bases 1 to 127485)
AUTHORS Adams,M.D.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1997) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
COMMENT On Aug 26, 1997 this sequence version replaced gi:2341053.
Address all correspondence to:
Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr,
Rockville, MD 20850,USAE-mail address: mdadams@tigr.org. The bac
location is on chromosome BAC clone is located on human chromosome
16p13.11 . The orientation of the sequence is from SP6 end to T7
end.Genes were identified by a combination of five methods
including: XGRAIL (available by anonymous ftp from
arthur.epm.ornl.gov), Genefinder (Phil Green, University of
Washington), Genscan (Chris Burge,
http://gnomic.stanford.edu/~chris/GENSCANW.html
)
searches of the complete sequence against a peptide database, and
the Human gene Index database at TIGR
(http://www.tigr.org/tdb/hgi/hgi.html). A gene with homology to
another protein is annotated as the isolog of that protein. Genes
without peptide homology having spliced EST hits are termed
'unknown protein'. Genes encoding tRNAs are predicted by
tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
FEATURES
Location/Qualifiers
source
1..127485
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.11"
/clone="A-13F4"
847..1095
/note="GB|G19453|G19453"
complement(945..967)
/rpt_family="AT_rich"
1022..1156
STS
/note="GB|G15446|G15446"
complement(2687..2979)
/rpt_family="AluSg"
complement(3206..3337)
/rpt_family="FLAM_C"
complement(3428..3480)
/rpt_family="(CA)n"
complement(3620..3827)
/rpt_family="MIR"
4270..4672
/rpt_family="MLT1P"
4840..4932
/rpt_family="MLT1P"
5688..5977
/rpt_family="AluSc"
complement(6249..6556)
/rpt_family="AluJo"
complement(7173..7355)
/rpt_family="MER58A"
complement(7358..7658)
/rpt_family="AluSx"
complement(7725..8865)
/rpt_family="LINE2"
8892..8946
repeat_region

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repeat_region /rpt_family="(TGGA)n"
repeat_region 9149. .9249
repeat_region /rpt_family="L1MC3"
repeat_region 9318. .9749
repeat_region /rpt_family="L1MC3"
repeat_region complement(9750. .10056)
repeat_region /rpt_family="AluSx"
repeat_region 10058. .10491
repeat_region /rpt_family="L1MC3"
repeat_region 10494. .10797
repeat_region /rpt_family="AluJb"
repeat_region 10798. .10967
repeat_region /rpt_family="AluJo"
repeat_region 11014. .11078
repeat_region /rpt_family="L1MC3"
repeat_region complement(11370. .11574)
repeat_region /rpt_family="MER58A"
repeat_region complement(11668. .11970)
repeat_region /rpt_family="AluSg"
repeat_region complement(13440. .13559)
repeat_region /rpt_family="(CA)n"
repeat_region complement(14144. .14572)
repeat_region /rpt_family="MER57A"
repeat_region complement(14676. .14832)
repeat_region /rpt_family="MIR"
repeat_region complement(15113. .15410)
repeat_region /rpt_family="AluSx"
repeat_region complement(15426. .15723)
repeat_region /rpt_family="AluJb"
repeat_region 15725. .15822
repeat_region /rpt_family="MIR"
repeat_region complement(15865. .15950)
repeat_region /rpt_family="(GA)n"
repeat_region complement(16406. .16663)
repeat_region /rpt_family="GC_rich"
repeat_region 16335. .16585
misc_feature /note="Unresolved region of approximately 1000bp
containing GC repeat"
repeat_region 16845. .16870
repeat_region /rpt_family="GC_rich"
repeat_region complement(17362. .17470)
repeat_region /rpt_family="MIR"
repeat_region complement(19001. .19299)
repeat_region /rpt_family="AluSp"
repeat_region complement(19504. .19810)
repeat_region /rpt_family="AluSc"
repeat_region complement(19833. .20130)
repeat_region /rpt_family="AluSp"
STS 19926. .20043
repeat_region /note="GB|G02122|G02122"
repeat_region complement(20155. .20251)
repeat_region /rpt_family="HY3"
repeat_region complement(20261. .20551)
repeat_region /rpt_family="AluSx"
repeat_region complement(20576. .20872)
repeat_region /rpt_family="AluY"
repeat_region complement(20889. .21164)
repeat_region /rpt_family="AluJo"
misc_feature 21000. .59000
/note="Large duplication of approximately 38kb also
occurring between positions 60,000 and 102,000"
STS 21323. .21422
repeat_region /note="GB|G25306|G25306"
repeat_region complement(21385. .21678)
repeat_region /rpt_family="AluJo"
repeat_region 24433. .24502
repeat_region /rpt_family="MIR"
repeat_region complement(28098. .28134)
repeat_region /rpt_family="MIR"
repeat_region complement(31832. .31890)
repeat_region /rpt_family="(CAGG)n"
repeat_region complement(32323. .32447)
repeat_region /rpt_family="(GGGA)n"
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misc_feature 32358. .32408
/note="region containing unresolved CT-repeat of
approximately 400bp"
repeat_region complement(32451. .32573)
repeat_region /rpt_family="(GGA)n"
repeat_region complement(32958. .33010)
repeat_region /rpt_family="GC_rich"
misc_feature 33055. .33105
/note="Unresolved region of approximately 200 bp
containing CT repeat"
repeat_region complement(33120. .33410)
repeat_region /rpt_family="(GAA)n"
repeat_region complement(35689. .35960)
repeat_region /rpt_family="AluSx"
repeat_region 36043. .36343
repeat_region /rpt_family="AluY"
repeat_region 37805. .37919
repeat_region /rpt_family="L1"
repeat_region 38066. .38194
repeat_region /rpt_family="AluJo/FLAM"
repeat_region 38196. .38496
repeat_region /rpt_family="AluSx"
repeat_region 38498. .38621
repeat_region /rpt_family="L1"
repeat_region complement(38772. .38812)
repeat_region /rpt_family="MER3"
repeat_region 38817. .39122
repeat_region /rpt_family="AluSx"
repeat_region complement(39961. .40264)
repeat_region /rpt_family="AluSg"
repeat_region complement(40350. .40642)
repeat_region /rpt_family="AluSg"
repeat_region complement(42188. .42346)

Query Match 100.0%; Score 41; DB 8; Length 127485;
Best Local Similarity 97.6%; Pred.No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGNCGCG 41
|||||
Db 16355 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGTCGCG 16395

RESULT 23
AC137642/c AC137642 131353 bp DNA linear HTG 03-DEC-2002
LOCUS Homo sapiens chromosome 16 clone RP11-624C8, WORKING DRAFT
DEFINITION SEQUENCE, 10 unordered pieces.
ACCESSION AC137642
VERSION AC137642.2 GI:26006509
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 131353)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 131353)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 131353)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 3, 2002 this sequence version replaced gi:25698531.
-----Genome Center
Center: Joint Genome Institute
```

Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1534176
Center clone name: RPCI-11_624C8

Summary Statistics
Consensus quality: 127527 bases at least Q40
Consensus quality: 128577 bases at least Q30
Consensus quality: 129224 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 130453; sum-of-contigs estimation
Quality coverage: 8.79 in Q20 bases; agarose-fp estimation
Quality coverage: 10.78 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1566: contig of 1566 bp in length
* 1567 1666: gap of unknown length
* 1667 4256: contig of 2590 bp in length
* 4257 4356: gap of unknown length
* 4357 7659: contig of 3303 bp in length
* 7660 7759: gap of unknown length
* 7760 14250: contig of 6491 bp in length
* 14251 14350: gap of unknown length
* 14351 20962: contig of 6612 bp in length
* 20963 21062: gap of unknown length
* 21063 31690: contig of 10628 bp in length
* 31691 31790: gap of unknown length
* 31791 50658: contig of 18868 bp in length
* 50659 50758: gap of unknown length
* 50759 85243: contig of 34485 bp in length
* 85244 85343: gap of unknown length
* 85344 103268: contig of 17925 bp in length
* 103269 103368: gap of unknown length
* 103369 131353: contig of 27985 bp in length.
FEATURES
source
Location/Qualifiers
1. .131353
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RPCI-624C8"
/clone_lib="RPCI human BAC library 11"
1567. .1666
/estimated_length=unknown
4257. .4356
/estimated_length=unknown
7660. .7759
/estimated_length=unknown
14251. .14350
/estimated_length=unknown
20963. .21062
/estimated_length=unknown
31691. .31790
/estimated_length=unknown
50659. .50758
/estimated_length=unknown
85244. .85343
/estimated_length=unknown
103269. .103368
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 131353;
Best Local Similarity 97.6%; Pred. No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 51077 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 51037
|||||
RESULT 24
AC136427/c 145971 bp DNA linear PRI 18-MAR-2003
LOCUS AC136427 Homo sapiens chromosome 16 clone RP11-103G5, complete sequence.
DEFINITION AC136427
ACCESSION AC136427
VERSION AC136427.3 GI:29029243
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 145971)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 145971)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 145971)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 145971)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 18, 2003 this sequence version replaced gi:24899410.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
NOTE: Shatter libraries failed to verify the dinucleotide repeat
region 76038-76702. Unsure number of repeat copies 76038-76702.
Forced join at 76403.
FEATURES
Location/Qualifiers
source
1. .145971
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-103G5"
76038. .76702
misc_feature
/note="NOTE: Shatter libraries failed to verify the
dinucleotide repeat region 76038-76702. Unsure number of
repeat copies 76038-76702. Forced join at 76403."
ORIGIN
Query Match 100.0%; Score 41; DB 8; Length 145971;
Best Local Similarity 97.6%; Pred. No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 93003 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 92963
|||||
RESULT 25

AC133566/c
LOCUS AC133566 147573 bp DNA linear HTG 14-SEP-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-93013, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
ACCESSION AC133566
VERSION AC133566.1 GI:22857562
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 147573)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 147573)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 442426
Center clone name: RPCI-11_93013

Summary Statistics
Consensus quality: 139742 bases at least Q40
Consensus quality: 143476 bases at least Q30
Consensus quality: 145054 bases at least Q20
Estimated insert size: 145000; agarose-fp estimation
Estimated insert size: 146973; sum-of-contigs estimation
Quality coverage: 6.68 in Q20 bases; agarose-fp estimation
Quality coverage: 6.59 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1053: contig of 1053 bp in length
* 1054 1153: gap of unknown length
* 1154 2572: contig of 1419 bp in length
* 2573 2672: gap of unknown length
* 2673 12141: contig of 9469 bp in length
* 12142 12241: gap of unknown length
* 12242 20412: contig of 8171 bp in length
* 20413 20512: gap of unknown length
* 20513 33545: contig of 13033 bp in length
* 33546 33645: gap of unknown length
* 33646 68965: contig of 35320 bp in length
* 68966 69065: gap of unknown length
* 69066 147573: contig of 78508 bp in length.
Location/Qualifiers
1. .147573
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-93013"
/clone_lib="RPCI human BAC library 11"
1054. .1153
/estimated_length=unknown
2573. .2672
/estimated_length=unknown
12142. .12241
/estimated_length=unknown

gap 20413. .20512
/estimated_length=unknown
33546. .33645
/estimated_length=unknown
68966. .69065
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 147573;
Best Local Similarity 97.6%; Pred.No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 34688 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCG 34648
RESULT 26
AC138949/c
LOCUS AC138949 148930 bp DNA linear HTG 21-JAN-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-805F23, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
ACCESSION AC138949
VERSION AC138949.1 GI:27805361
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 148930)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 148930)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1603767
Center clone name: RPCI-11_805F23

Summary Statistics
Consensus quality: 143446 bases at least Q40
Consensus quality: 144466 bases at least Q30
Consensus quality: 145318 bases at least Q20
Estimated insert size: 18000; agarose-fp estimation
Estimated insert size: 147730; sum-of-contigs estimation
Quality coverage: 9.82 in Q20 bases; agarose-fp estimation
Quality coverage: 11.97 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1211: contig of 1211 bp in length
* 1212 1311: gap of unknown length
* 1312 2482: contig of 1171 bp in length
* 2483 2582: gap of unknown length
* 2583 3798: contig of 1216 bp in length
* 3799 3898: gap of unknown length
* 3899 5487: contig of 1589 bp in length
* 5488 5587: gap of unknown length
* 5588 6870: contig of 1283 bp in length

* 6871 6970: gap of unknown length
* 6971 10798: contig of 3828 bp in length
* 10799 10898: gap of unknown length
* 10899 13993: contig of 3095 bp in length
* 13994 14093: gap of unknown length
* 14094 22594: contig of 8501 bp in length
* 22595 22695: gap of unknown length
* 22695 28641: contig of 5947 bp in length
* 28642 28741: gap of unknown length
* 28742 40015: contig of 11274 bp in length
* 40016 40115: gap of unknown length
* 40116 58107: contig of 17992 bp in length
* 58108 58207: gap of unknown length
* 58208 79533: contig of 21326 bp in length
* 79534 79634: gap of unknown length
* 79634 148930: contig of 69297 bp in length.

FEATURES

source

1. 148930
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-805F23"
/clone_lib="RPCI human BAC library 11"
1212. 1311
/estimated_length=unknown
2483. 2582
/estimated_length=unknown
3799. 3898
/estimated_length=unknown
5488. 5587
/estimated_length=unknown
6871. 6970
/estimated_length=unknown
10799. 10898
/estimated_length=unknown
13994. 14093
/estimated_length=unknown
22595. 22694
/estimated_length=unknown
28642. 28741
/estimated_length=unknown
40016. 40115
/estimated_length=unknown
58108. 58207
/estimated_length=unknown
79534. 79633
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 148930;
Best Local Similarity 97.6%; Pred. No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGCG 41
|||||
Db 7189 AAGCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCG 7149
|||||

RESULT 27

AC138892

LOCUS AC138892 152171 bp DNA linear HTG 21-JAN-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-43108, WORKING DRAFT
SEQUENCE, 12 unordered pieces.

ACCESSION AC138892

VERSION AC138892.1 GI:27805304

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 152171)

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 152171)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 572213
Center clone name: RPCI-11_43108

Summary Statistics

Consensus quality: 147669 bases at least Q40
Consensus quality: 148410 bases at least Q30
Consensus quality: 149034 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Quality coverage: 12.06 in Q20 bases; agarose-fp estimation
Quality coverage: 14.37 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1087: contig of 1087 bp in length
* 1088 1187: gap of unknown length
* 1188 2506: contig of 1319 bp in length
* 2507 2606: gap of unknown length
* 2607 4415: contig of 1809 bp in length
* 4416 4515: gap of unknown length
* 4516 6448: contig of 1933 bp in length
* 6449 6549: gap of unknown length
* 6549 7689: contig of 1140 bp in length
* 7689 9094: gap of unknown length
* 9095 9195: gap of unknown length
* 9195 11683: contig of 2489 bp in length
* 11684 11783: gap of unknown length
* 11784 14476: contig of 2693 bp in length
* 14477 14576: gap of unknown length
* 14577 23842: contig of 9266 bp in length
* 23843 23942: gap of unknown length
* 23943 34968: contig of 11026 bp in length
* 34969 35069: gap of unknown length
* 35069 72126: contig of 37058 bp in length
* 72127 72226: gap of unknown length
* 72227 152171: contig of 79945 bp in length.

FEATURES

source

1. 152171
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-43108"
/clone_lib="RPCI human BAC library 11"
1088. 1187
/estimated_length=unknown
2507. 2606
/estimated_length=unknown
4416. 4515
/estimated_length=unknown
6449. 6548
/estimated_length=unknown
7689. 7788
gap
gap
gap
gap
gap

gap 7361. .7460
/estimated_length=unknown
gap 8537. .8636
/estimated_length=unknown
gap 9782. .9881
/estimated_length=unknown
gap 11067. .11166
/estimated_length=unknown
gap 12219. .12318
/estimated_length=unknown
gap 13355. .13454
/estimated_length=unknown
gap 14544. .14643
/estimated_length=unknown
gap 15847. .15946
/estimated_length=unknown
gap 17663. .17762
/estimated_length=unknown
gap 18955. .19054
/estimated_length=unknown
gap 20332. .20431
/estimated_length=unknown
gap 21843. .21942
/estimated_length=unknown
gap 23882. .23981
/estimated_length=unknown
gap 25748. .25847
/estimated_length=unknown
gap 28496. .28595
/estimated_length=unknown
gap 32088. .32187
/estimated_length=unknown
gap 35365. .35464
/estimated_length=unknown
gap 38971. .39070
/estimated_length=unknown
gap 54857. .54956
/estimated_length=unknown
gap 65433. .65532
/estimated_length=unknown
gap 83372. .83471
/estimated_length=unknown
gap 98005. .98104
/estimated_length=unknown
gap 124316. .124415
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 162264;
Best Local Similarity 97.6%; Pred. No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
|||||
Db 82722 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 82762

RESULT 29
AC138888
LOCUS AC138888 167184 bp DNA linear HTG 21-JAN-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-380E24, WORKING DRAFT
SEQUENCE, 16 unordered pieces.

ACCESSION AC138888
VERSION AC138888.1 GI:27805300
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 167184)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
2 (bases 1 to 167184)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 552405
Center clone name: RPCI-11_380E24

Summary Statistics
Consensus quality: 161117 bases at least Q40
Consensus quality: 162076 bases at least Q30
Consensus quality: 162990 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 165684; sum-of-contigs estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation
Quality coverage: 11.18 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1454: contig of 1454 bp in length
* 1455 1554: gap of unknown length
* 1555 2744: contig of 1190 bp in length
* 2745 2844: gap of unknown length
* 2845 4464: contig of 1620 bp in length
* 4465 4564: gap of unknown length
* 4565 6074: contig of 1510 bp in length
* 6075 6174: gap of unknown length
* 6175 7741: contig of 1567 bp in length
* 7742 7841: gap of unknown length
* 7842 8865: contig of 1024 bp in length
* 8866 8965: gap of unknown length
* 8966 10250: contig of 1285 bp in length
* 10251 10350: gap of unknown length
* 10351 11528: contig of 1178 bp in length
* 11529 11628: gap of unknown length
* 11629 14061: contig of 2433 bp in length
* 14062 14161: gap of unknown length
* 14162 17282: contig of 3121 bp in length
* 17283 17382: gap of unknown length
* 17383 26902: contig of 9520 bp in length
* 26903 27002: gap of unknown length
* 27003 42762: contig of 15760 bp in length
* 42763 42862: gap of unknown length
* 42863 64561: contig of 21699 bp in length
* 64562 64661: gap of unknown length
* 64662 89820: contig of 25159 bp in length
* 89821 89920: gap of unknown length
* 89921 110575: contig of 20655 bp in length
* 110576 110675: gap of unknown length
* 110676 167184: contig of 56509 bp in length.

FEATURES
source

1. .167184
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-380E24"
/clone_lib="RPCI human BAC library 11"
1455. .1554
/estimated_length=unknown
2745. .2844

gap
gap


```

/estimated_length=unknown
4465. .4564
/estimated_length=unknown
6075. .6174
/estimated_length=unknown
7742. .7841
/estimated_length=unknown
8866. .8965
/estimated_length=unknown
10251. .10350
/estimated_length=unknown
11529. .11628
/estimated_length=unknown
14062. .14161
/estimated_length=unknown
17283. .17382
/estimated_length=unknown
26903. .27002
/estimated_length=unknown
42763. .42862
/estimated_length=unknown
64562. .64661
/estimated_length=unknown
89821. .89920
/estimated_length=unknown
110576. .110675
/estimated_length=unknown

ORIGIN
Query Match          100.0%;   Score 41;   DB 14;   Length 167184;
Best Local Similarity 97.6%;   Pred. No. 0.013;
Matches 40;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 89670 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 89710

RESULT 30
AC138901
LOCUS
DEFINITION
Homo sapiens chromosome 16 clone RP11-53114, *** SEQUENCING IN
PROGRESS ***, 5 ordered pieces.
AC138901
AC138901.3 GI:29336209
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 168230)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE
Direct Submission
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 168230)
DOE Joint Genome Institute.
TITLE
Direct Submission
JOURNAL
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 168230)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE
Direct Submission
JOURNAL
Submitted (28-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT
On Mar 28, 2003 this sequence version replaced gi:28008527.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
```

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* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 53269: contig of 53269 bp in length
* 53270 53369: gap of unknown length
* 53370 69791: contig of 16422 bp in length
* 69792 69891: gap of unknown length
* 69892 70664: contig of 773 bp in length
* 70665 70764: gap of unknown length
* 70765 160499: contig of 89735 bp in length
* 160500 160599: gap of unknown length
* 160600 168230: contig of 7631 bp in length.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 610465
Center clone name: RP11-53114
-----
Summary Statistics
Consensus quality: 166501 bases at least Q40
Consensus quality: 166789 bases at least Q30
Consensus quality: 166959 bases at least Q20
Estimated insert size: 167825; agarose-fp estimation
Estimated insert size: 167130; sum-of-contigs

estimation
Quality coverage: 0.99 in Q20 bases; agarose-fp
estimation
Quality coverage: 1 in Q20 bases; sum-of-contigs
estimation.
FEATURES
source
Location/Qualifiers
1. .168230
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-53114"
53270. .53369
/estimated_length=unknown
69792. .69891
/estimated_length=unknown
70665. .70764
/estimated_length=unknown
160500. .160599
/estimated_length=unknown

ORIGIN
Query Match          100.0%;   Score 41;   DB 14;   Length 168230;
Best Local Similarity 97.6%;   Pred. No. 0.013;
Matches 40;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 52969 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 53009

RESULT 31
AC139265
LOCUS
DEFINITION
Homo sapiens chromosome 16 clone RP11-1428P22, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
AC139265
AC139265.1 GI:28009381
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 168408)
```

AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 168408)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2768368
Center clone name: RPCI-11_1428P22

Summary Statistics
Consensus quality: 164984 bases at least Q40
Consensus quality: 165330 bases at least Q30
Consensus quality: 165596 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 167808; agarose-fp estimation
Quality coverage: 13.12 in Q20 bases; agarose-fp estimation
Quality coverage: 13.68 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1051: contig of 1051 bp in length
* 1052 1151: gap of unknown length
* 1152 2903: contig of 1752 bp in length
* 2904 3003: gap of unknown length
* 3004 5134: contig of 2131 bp in length
* 5135 5234: gap of unknown length
* 5235 21508: contig of 16274 bp in length
* 21509 21608: gap of unknown length
* 21609 39653: contig of 18045 bp in length
* 39654 39753: gap of unknown length
* 39754 78533: contig of 38780 bp in length
* 78534 78633: gap of unknown length
* 78634 168408: contig of 89775 bp in length.
FEATURES
source
1. .168408
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1428P22"
/clone_lib="RPCI human BAC library 11"
1052. .1151
/estimated_length=unknown
2904. .3003
/estimated_length=unknown
5135. .5234
/estimated_length=unknown
21509. .21608
/estimated_length=unknown
39654. .39753
/estimated_length=unknown
78534. .78633
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 168408;
Best Local Similarity 97.6%; Pred. No. 0.013;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCTCCGATGCCAGTCCCTCATCGTGGCCCGGCG 41

Db 38926 AAGCTCCGATGCCAGTCCCTCATCGTGGCCCGGCG 38966
|||||
RESULT 32
AC142081/c 172474 bp DNA linear HTG 21-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-1321D20, WORKING DRAFT
DEFINITION SEQUENCE, 9 unordered pieces.
AC142081
AC142081.1 GI:29135556
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 172474)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 172474)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2726990
Center clone name: RPCI-11_1321D20

Summary Statistics
Consensus quality: 169588 bases at least Q40
Consensus quality: 170176 bases at least Q30
Consensus quality: 170569 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 171674; sum-of-contigs estimation
Quality coverage: 13.27 in Q20 bases; agarose-fp estimation
Quality coverage: 13.61 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1068: contig of 1068 bp in length
* 1069 1168: gap of unknown length
* 1169 6747: contig of 5579 bp in length
* 6748 6847: gap of unknown length
* 6848 13485: contig of 6638 bp in length
* 13486 13585: gap of unknown length
* 13586 22941: contig of 9356 bp in length
* 22942 23041: gap of unknown length
* 23042 35439: contig of 12398 bp in length
* 35440 35539: gap of unknown length
* 35540 46853: contig of 11314 bp in length
* 46854 46953: gap of unknown length
* 46954 66628: contig of 19675 bp in length
* 66629 66728: gap of unknown length
* 66729 101269: contig of 34541 bp in length
* 101270 101369: gap of unknown length
* 101370 172474: contig of 71105 bp in length.
FEATURES
Location/Qualifiers
1. .172474
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

/chromosome="16"
/clone="RP11-1321D20"
/clone_lib="RPCI human BAC library 11"
1069. .1168
/estimated_length=unknown
6748. .6847
/estimated_length=unknown
13486. .13585
/estimated_length=unknown
22942. .23041
/estimated_length=unknown
35440. .35539
/estimated_length=unknown
46854. .46953
/estimated_length=unknown
66629. .66728
/estimated_length=unknown
101270. .101369
/estimated_length=unknown

ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 172474;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGNCGCG 41
|||||
Db 67062 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGTCGCG 67022
|||||

RESULT 33
AC141410/c
LOCUS AC141410 173775 bp DNA linear HTG 14-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-891N17, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC141410
VERSION AC141410.1 GI:28951156
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 173775)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173775)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1636977
Center clone name: RPCI-11_891N17

Summary Statistics
Consensus quality: 172677 bases at least Q40
Consensus quality: 172933 bases at least Q30
Consensus quality: 173141 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 173575; sum-of-contigs estimation
Quality coverage: 16.15 in Q20 bases; agarose-fp estimation
Quality coverage: 16.74 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1237: contig of 1237 bp in length
* 1238 1337: gap of unknown length
* 1338 78991: contig of 77654 bp in length
* 78992 79091: gap of unknown length
* 79092 173775: contig of 94684 bp in length.
FEATURES
location/Qualifiers
source
1. .173775
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-891N17"
/clone_lib="RPCI human BAC library 11"
1238. .1337
/estimated_length=unknown
78992. .79091
/estimated_length=unknown

ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 173775;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 95387 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCGCG 95347
|||||

RESULT 34
AC137806/c
LOCUS AC137806 177920 bp DNA linear HTG 03-DEC-2002
DEFINITION Homo sapiens chromosome 16 clone RP11-876J15, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
ACCESSION AC137806
VERSION AC137806.1 GI:26006548
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 177920)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 177920)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1631119
Center clone name: RPCI-11_876J15

Summary Statistics
Consensus quality: 173780 bases at least Q40
Consensus quality: 174683 bases at least Q30
Consensus quality: 175248 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 176820; sum-of-contigs estimation
Quality coverage: 11.17 in Q20 bases; agarose-fp estimation
Quality coverage: 10.1 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1526: contig of 1526 bp in length
1527 1626: gap of unknown length
1627 2737: contig of 1111 bp in length
2738 2837: gap of unknown length
2838 4892: contig of 2055 bp in length
4893 4992: gap of unknown length
4993 7232: contig of 2240 bp in length
7233 7332: gap of unknown length
7333 9840: contig of 2508 bp in length
9841 9940: gap of unknown length
9941 16612: contig of 6672 bp in length
16613 16712: gap of unknown length
16713 24572: contig of 7860 bp in length
24573 24672: gap of unknown length
24673 31339: contig of 6667 bp in length
31340 31439: gap of unknown length
31440 42416: contig of 10977 bp in length
42417 42516: gap of unknown length
42517 76996: contig of 34480 bp in length
76997 77096: gap of unknown length
77097 119504: contig of 42408 bp in length
119505 119604: gap of unknown length
119605 177920: contig of 58316 bp in length.

FEATURES

source
1. .177920
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-876J15"
/clone_lib="RPCI human BAC library 11"
1527. .1626
/estimated_length=unknown
2738. .2837
/estimated_length=unknown
4893. .4992
/estimated_length=unknown
7233. .7332
/estimated_length=unknown
9841. .9940
/estimated_length=unknown
16613. .16712
/estimated_length=unknown
24573. .24672
/estimated_length=unknown
31340. .31439
/estimated_length=unknown
42417. .42516
/estimated_length=unknown
76997. .77096
/estimated_length=unknown
119505. .119604
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 177920;
Best Local Similarity 97.6%; Pred. NO. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
|||||
Db 42775 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 42735
|||||

RESULT 35
AC141465
LOCUS AC141465 179399 bp DNA linear HTG 27-MAR-2003

DEFINITION

Homo sapiens chromosome 16 clone RP11-847E10, WORKING DRAFT
SEQUENCE, 4 ordered pieces.
AC141465
VERSION AC141465.3 GI:29294006
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 179399)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 179399)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 179399)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Mar 27, 2003 this sequence version replaced gi:29171368.
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 19943: contig of 19943 bp in length
* 19944 20043: gap of unknown length
* 20044 41569: contig of 21526 bp in length
* 41570 41669: gap of unknown length
* 41670 47815: contig of 6146 bp in length
* 47816 47915: gap of unknown length
* 47916 179399: contig of 131484 bp in length.

FEATURES

Location/Qualifiers
source
1. .179399
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-847E10"
19944. .20043
/estimated_length=unknown
41570. .41569
/estimated_length=unknown
47816. .47915
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 179399;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
|||||
Db 3639 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 3679
|||||

RESULT 36
AC141465/c
LOCUS
DEFINITION
AC141465 179399 bp DNA linear HTG 27-MAR-2003
Homo sapiens chromosome 16 clone RP11-847E10, WORKING DRAFT
SEQUENCE, 4 ordered pieces.
AC141465
AC141465.3 GI:29294006
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 179399)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 179399)
DOE Joint Genome Institute.
Direct Submission
Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 179399)
DOE Joint Genome Institute.
Direct Submission
Submitted (27-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 27, 2003 this sequence version replaced gi:29171368.
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 19944 20043: contig of 19943 bp in length
* 20044 41569: contig of 21526 bp in length
* 41570 41669: gap of unknown length
* 41670 47815: contig of 6146 bp in length
* 47816 47915: gap of unknown length
* 47916 179399: contig of 131484 bp in length.
Location/Qualifiers
1. .179399
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-847E10"
19944. .20043
/estimated_length=unknown
41570. .41669
/estimated_length=unknown
47816. .47915
/estimated_length=unknown

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATGCTGGCCCGNCGCG 41
|||||
Db 126482 AAGCCTCCGGATGCCAGTCCCTCATGCTGGCCCGTCCG 126442
|||||
RESULT 37
AC141616/c
LOCUS
DEFINITION
AC141616 179754 bp DNA linear HTG 18-MAR-2003
Homo sapiens chromosome 16 clone RP11-958M13, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
AC141616
AC141616.1 GI:29029201
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 179754)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 179754)
DOE Joint Genome Institute.
Direct Submission
Submitted (18-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1662677
Center clone name: RPCI-11_958M13

Summary Statistics
Consensus quality: 175245 bases at least Q40
Consensus quality: 176826 bases at least Q30
Consensus quality: 177518 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 179054; sum-of-contigs estimation
Quality coverage: 10.49 in Q20 bases; agarose-fp estimation
Quality coverage: 10.25 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 6779: contig of 6779 bp in length
* 6780 6879: gap of unknown length
* 6880 14927: contig of 8048 bp in length
* 14928 15027: gap of unknown length
* 15028 31236: contig of 16209 bp in length
* 31237 31336: gap of unknown length
* 31337 45749: contig of 14413 bp in length
* 45750 45849: gap of unknown length
* 45850 64995: contig of 19146 bp in length
* 64996 65095: gap of unknown length
* 65096 99462: contig of 34367 bp in length
* 99463 99562: gap of unknown length
* 99563 134459: contig of 34897 bp in length
* 134460 134559: gap of unknown length
* 134560 179754: contig of 45195 bp in length.
Location/Qualifiers
1. .179754
/organism="Homo sapiens"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 179399;
Best Local Similarity 97.6%; Pred. No. 0.012;

FEATURES
source
1. .179399
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-847E10"
19944. .20043
/estimated_length=unknown
41570. .41669
/estimated_length=unknown
47816. .47915
/estimated_length=unknown

FEATURES
source
1. .179754
/organism="Homo sapiens"
/mol_type="genomic DNA"

db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-958M13"
/clone_lib="RPCI human BAC library 11"
6780. .6879
/estimated_length=unknown
14928. .15027
/estimated_length=unknown
31237. .31336
/estimated_length=unknown
45750. .45849
/estimated_length=unknown
64996. .65095
/estimated_length=unknown
99463. .99562
/estimated_length=unknown
134460. .134559
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 179754;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 65147 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTGCGG 65107

RESULT 38
AC138932/c
LOCUS AC138932 180798 bp DNA linear PRI 07-APR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-680G24, complete sequence.
ACCESSION AC138932
VERSION AC138932.4 GI:29570376
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 180798)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Unpublished
2 (bases 1 to 180798)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 180798)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Submitted (28-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 180798)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Apr 7, 2003 this sequence version replaced gi:29336210.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of sequence;
Estimated Total Number of Errors is 0.1.
NOTE: Unresolved dinucleotide repeat region 111025-111533. Unsure
number of repeat copies 111025-111533. Forced join 111355.

FEATURES
Source Location/Qualifiers
1. .180798
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-680G24"
111025. .111533
/note="NOTE: Unresolved dinucleotide repeat region
111025-111533. Unsure number of repeat copies
111025-111533. Forced join 111355."

misc_feature
Query Match 100.0%; Score 41; DB 8; Length 180798;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 127830 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTGCGG 127790

RESULT 39
AC138903/c
LOCUS AC138903 181231 bp DNA linear HTG 22-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-566I3, WORKING DRAFT
SEQUENCE, 2 ordered pieces.
ACCESSION AC138903
VERSION AC138903.2 GI:29150348
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 181231)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 181231)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 181231)
DOE Joint Genome Institute.
Direct Submission
Submitted (22-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 22, 2003 this sequence version replaced gi:27805315.
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 41176: contig of 41176 bp in length
* 41177 41276: gap of unknown length
* 41277 181231: contig of 139955 bp in length.
Location/Qualifiers
1. .181231
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-566I3"
41177. .41276
/estimated_length=unknown
gap
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 181231;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41
|||||
Db 57793 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGTCCGG 57753
|||||
RESULT 40
AC142195/c
LOCUS AC142195 183215 bp DNA linear HTG 25-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1006H4, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
AC142195
AC142195.1 GI:29171371
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 183215)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
DOE Joint Genome Institute.
2 (bases 1 to 183215)
Direct Submission
DOE Joint Genome Institute.
Submitted (25-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1680980
Center clone name: RPCI-11_1006H4

Summary Statistics
Consensus quality: 181858 bases at least Q40
Consensus quality: 182021 bases at least Q30
Consensus quality: 182181 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 182915; sum-of-contigs estimation
Quality coverage: 15.08 in Q20 bases; agarose-fp estimation
Quality coverage: 14.84 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 16451: contig of 16451 bp in length
* 16452 16551: gap of unknown length
* 16552 51103: contig of 34552 bp in length
* 51104 51203: gap of unknown length
* 51204 107468: contig of 56265 bp in length
* 107469 107568: gap of unknown length
* 107569 183215: contig of 75647 bp in length.
Location/Qualifiers
1. .183215
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1006H4"
/clone_lib="RPCI human BAC library 11"
16452. .16551
/estimated_length=unknown
51104. .51203
/estimated_length=unknown
107469. .107568
/estimated_length=unknown
gap
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 183215;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41
|||||
Db 16793 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGTCCGG 16753
|||||
RESULT 41
AC141266/c
LOCUS AC141266 183537 bp DNA linear HTG 11-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1357B21, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
AC141266
AC141266.1 GI:28913046
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 183537)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
DOE Joint Genome Institute.
2 (bases 1 to 183537)
Direct Submission
DOE Joint Genome Institute.
Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 2740767
Center clone name: RPCI-11_1357B21

Summary Statistics
Consensus quality: 178517 bases at least Q40
Consensus quality: 179942 bases at least Q30
Consensus quality: 180696 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 182837; sum-of-contigs estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation

Quality coverage: 9.9 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1161: contig of 1161 bp in length
1162 1261: gap of unknown length
1262 2521: contig of 1260 bp in length
2522 2621: gap of unknown length
2622 5829: contig of 3208 bp in length
5830 5929: gap of unknown length
5930 9996: contig of 4067 bp in length
9997 10096: gap of unknown length
10097 15804: contig of 5708 bp in length
15805 15904: gap of unknown length
15905 27778: contig of 11874 bp in length
27779 27878: gap of unknown length
27879 70728: contig of 42850 bp in length
70729 70828: gap of unknown length
70829 183537: contig of 112709 bp in length.

Location/Qualifiers
1. 183537
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1357B21"
/clone_lib="RPCI human BAC library 11"

1162: .1261
/estimated_length=unknown
2522: .2621
/estimated_length=unknown
5830: .5929
/estimated_length=unknown
9997: .10096
/estimated_length=unknown
15805: .15904
/estimated_length=unknown
27779: .27878
/estimated_length=unknown
70729: .70828
/estimated_length=unknown

ORIGIN
source
Query Match 100.0%; Score 41; DB 14; Length 183537;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 71080 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 71040
|||||

RESULT 42
AC139258/c
LOCUS AC139258 187226 bp DNA linear HTG 21-FEB-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1228E2, WORKING DRAFT
SEQUENCE, 3 ordered pieces.
ACCESSION AC139258
VERSION AC139258.2 GI:28460744
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 187226)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
2 (bases 1 to 187226)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 187226)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-FEB-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 21, 2003 this sequence version replaced gi:28009167.
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 4513: contig of 4513 bp in length
4514 4613: gap of unknown length
4614 94503: contig of 89890 bp in length
94504 94603: gap of unknown length
94604 187226: contig of 92623 bp in length.

FEATURES
source
1. 187226
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1228E2"
4514: .4613
/estimated_length=unknown
94504: .94603
/estimated_length=unknown

Query Match 100.0%; Score 41; DB 14; Length 187226;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 111119 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 111079
|||||

RESULT 43
AC141304
LOCUS AC141304 188734 bp DNA linear HTG 11-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-800P6, WORKING DRAFT
SEQUENCE, 12 unordered pieces.

AC141304
AC141304.1 GI:28913084
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 188734)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 188734)
DOE Joint Genome Institute.
Direct Submission
Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1602070
Center clone name: RPCI-11_800P6

Summary Statistics
Consensus quality: 179991 bases at least Q40
Consensus quality: 182288 bases at least Q30
Consensus quality: 183598 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 187634; sum-of-contigs estimation
Quality coverage: 10.73 in Q20 bases; agarose-fp estimation
Quality coverage: 10.07 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1144: contig of 1144 bp in length
* 1145 1244: gap of unknown length
* 1245 2328: contig of 1084 bp in length
* 2329 2428: gap of unknown length
* 2429 3544: contig of 1116 bp in length
* 3545 3644: gap of unknown length
* 3645 4797: contig of 1153 bp in length
* 4798 4897: gap of unknown length
* 4898 6155: contig of 1258 bp in length
* 6156 6256: gap of unknown length
* 6256 7347: contig of 1091 bp in length
* 7347 7447: gap of unknown length
* 7447 8755: contig of 1308 bp in length
* 8755 8855: gap of unknown length
* 8855 9987: contig of 1132 bp in length
* 9987 10087: gap of unknown length
* 10087 25546: contig of 15460 bp in length
* 25547 25647: gap of unknown length
* 25647 43663: contig of 18016 bp in length
* 43663 43763: gap of unknown length
* 43763 106057: contig of 62294 bp in length
* 106057 106156: gap of unknown length
* 106157 188734: contig of 82578 bp in length.
Location/Qualifiers
1. .188734
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-800P6"
/clone_lib="RPCI human BAC library 11"

gap 1145. .1244
/estimated_length=unknown
gap 2329. .2428
/estimated_length=unknown
gap 3545. .3644
/estimated_length=unknown
gap 4798. .4897
/estimated_length=unknown
gap 6156. .6255
/estimated_length=unknown
gap 7347. .7446
/estimated_length=unknown
gap 8755. .8854
/estimated_length=unknown
gap 9987. .10086
/estimated_length=unknown
gap 25547. .25646
/estimated_length=unknown
gap 43663. .43762
/estimated_length=unknown
gap 106057. .106156
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 188734;
Best Local Similarity 97.6%; Pred.No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 105107 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 105147
|||||
RESULT 44
AC141613/c
LOCUS AC141613 194670 bp DNA linear HTG 18-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-837F19, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
AC141613
VERSION AC141613.1 GI:29029198
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 194670)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 194670)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1616051
Center clone name: RPCI-11_837F19

Summary Statistics
Consensus quality: 191315 bases at least Q40
Consensus quality: 191814 bases at least Q30
Consensus quality: 192245 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 194070; sum-of-contigs estimation
Quality coverage: 13.92 in Q20 bases; agarose-fp estimation
Quality coverage: 12.63 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1051: contig of 1051 bp in length
1052 1151: gap of unknown length
1152 10992: contig of 9841 bp in length
10993 11092: gap of unknown length
11093 18333: contig of 7241 bp in length
18334 18433: gap of unknown length
18434 31888: contig of 13455 bp in length
31889 31988: gap of unknown length
31989 55558: contig of 23570 bp in length
55559 55658: gap of unknown length
55659 121024: contig of 65366 bp in length
121025 121124: gap of unknown length
121125 194670: contig of 73546 bp in length.

FEATURES

source
1. .194670
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-837F19"
/clone_lib="RPCI human BAC library 11"
1052. .1151
/estimated_length=unknown
10993. .11092
/estimated_length=unknown
18334. .18433
/estimated_length=unknown
31889. .31988
/estimated_length=unknown
55559. .55658
/estimated_length=unknown
121025. .121124
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 194670;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|||||
Db 48312 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGTCCG 48272

RESULT 45

AC009065 AC009065 199759 bp DNA linear PRI 15-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-304L19, complete sequence.
DEFINITION AC009065
ACCESSION AC009065
VERSION AC009065.8 GI:28973803
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 199759)

REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.

TITLE Direct Submission
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 199759)

AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE

3 (bases 1 to 199759)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.

TITLE Direct Submission

JOURNAL Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA

COMMENT On Mar 15, 2003 this sequence version replaced gi:13786295.
Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.1.

NOTE: Unsure number of dinucleotide repeat copies from
172446-172529. Forced join at 172492.

FEATURES

Location/Qualifiers
source
1. .199759
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-304L19"
172446. .172529
misc_feature
/note="NOTE: Unsure number of dinucleotide repeat copies
from 172446-172529. Forced join at 172492."

ORIGIN

Query Match 100.0%; Score 41; DB 8; Length 199759;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|||||

Db 141374 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGTCCG 141414

RESULT 46

AC141468/c AC141468 202656 bp DNA linear HTG 16-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-954C1, WORKING DRAFT
DEFINITION AC141468
ACCESSION AC141468
VERSION AC141468.1 GI:28975021
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 202656)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 16

Unpublished

2 (bases 1 to 202656)

DOE Joint Genome Institute.

Direct Submission

Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1660889
Center clone name: RPCI-11_954C1

Summary Statistics
Consensus quality: 194148 bases at least Q40
Consensus quality: 196921 bases at least Q30
Consensus quality: 198190 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation

Estimated insert size: 201356; sum-of-contigs estimation
Quality coverage: 9.93 in Q20 bases; agarose-fp estimation
Quality coverage: 8.68 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1000: contig of 1000 bp in length
* 1001 1100: gap of unknown length
* 1101 2460: contig of 1360 bp in length
* 2461 2560: gap of unknown length
* 2561 4920: contig of 2360 bp in length
* 4921 5020: gap of unknown length
* 5021 9609: contig of 4589 bp in length
* 9610 9709: gap of unknown length
* 9710 14495: contig of 4786 bp in length
* 14496 14595: gap of unknown length
* 14596 21832: contig of 7237 bp in length
* 21833 21932: gap of unknown length
* 21933 32172: contig of 10240 bp in length
* 32173 32272: gap of unknown length
* 32273 49575: contig of 17303 bp in length
* 49576 49675: gap of unknown length
* 49676 64516: contig of 14841 bp in length
* 64517 64617: gap of unknown length
* 64617 85275: contig of 20659 bp in length
* 85276 85375: gap of unknown length
* 85376 106615: contig of 21240 bp in length
* 106616 106715: gap of unknown length
* 106716 126404: contig of 19689 bp in length
* 126405 126504: gap of unknown length
* 126505 152876: contig of 26372 bp in length
* 152877 152976: gap of unknown length
* 152977 202656: contig of 49680 bp in length.

FEATURES

source

1. .202656
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone_lib="RPCI human BAC library 11"
1001. .1100
/estimated_length=unknown
2461. .2560
/estimated_length=unknown
4921. .5020
/estimated_length=unknown
9610. .9709
/estimated_length=unknown
14496. .14595
/estimated_length=unknown
21833. .21932
/estimated_length=unknown
32173. .32272
/estimated_length=unknown
49576. .49675
/estimated_length=unknown
64517. .64616
/estimated_length=unknown
85276. .85375
/estimated_length=unknown
106616. .106715
/estimated_length=unknown
126405. .126504
/estimated_length=unknown
152877. .152976
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 202656;
Best Local Similarity 97.6%; Pred.No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 106967 AAGCCTCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGC 106927
|||||

RESULT 47

AC141411/c
LOCUS AC141411 202882 bp DNA linear HTG 14-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-908J13, WORKING DRAFT
SEQUENCE, 6 unordered pieces.
AC141411
AC141411.1 GI:28951157
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 202882)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 202882)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1643405
Center clone name: RPCI-11_908J13

Summary Statistics
Consensus quality: 200623 bases at least Q40
Consensus quality: 200957 bases at least Q30
Consensus quality: 201268 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 202382; sum-of-contigs estimation
Quality coverage: 10.09 in Q20 bases; agarose-fp estimation
Quality coverage: 8.98 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 3071: contig of 3071 bp in length
* 3072 3171: gap of unknown length
* 3172 16126: contig of 12955 bp in length
* 16127 16226: gap of unknown length
* 16227 38564: contig of 22338 bp in length
* 38565 38664: gap of unknown length
* 38665 73667: contig of 35003 bp in length
* 73668 73767: gap of unknown length
* 73768 138424: contig of 64657 bp in length
* 138425 138524: gap of unknown length
* 138525 202882: contig of 64358 bp in length.

FEATURES

source

1. .202882
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

gap /chromosome="16"
gap /clone="RP11-908J13"
gap /clone_lib="RPCI human BAC library 11"
gap 3072. .3171
gap /estimated_length=unknown
gap 16127. .16226
gap /estimated_length=unknown
gap 38565. .38664
gap /estimated_length=unknown
gap 73668. .73767
gap /estimated_length=unknown
gap 138425. .138524
gap /estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 202882;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 38970 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 38930
|||||

RESULT 48
AC141267 204500 bp DNA linear HTG 11-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-1381A15, WORKING DRAFT
DEFINITION SEQUENCE, 13 unordered pieces.
ACCESSION AC141267
VERSION AC141267.1 GI:28913047
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 204500)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204500)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2749953
Center clone name: RPCI-11_1381A15

Summary Statistics
Consensus quality: 192455 bases at least Q40
Consensus quality: 197383 bases at least Q30
Consensus quality: 199302 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 203300; sum-of-contigs estimation
Quality coverage: 7.7 in Q20 bases; agarose-fp estimation
Quality coverage: 6.66 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1079: contig of 1079 bp in length
* 1080 1179: gap of unknown length

1180 2333: contig of 1154 bp in length
2334 2433: gap of unknown length
2434 4475: contig of 2042 bp in length
4476 4575: gap of unknown length
4576 7754: contig of 3179 bp in length
7755 7854: gap of unknown length
7855 14689: contig of 6835 bp in length
14690 14789: gap of unknown length
14790 20823: contig of 6034 bp in length
20824 20923: gap of unknown length
20924 25585: contig of 4662 bp in length
25586 25685: gap of unknown length
25686 31075: contig of 5390 bp in length
31076 31175: gap of unknown length
31176 41943: contig of 10768 bp in length
41944 42043: gap of unknown length
42044 61500: contig of 19457 bp in length
61501 61600: gap of unknown length
61601 101721: contig of 40121 bp in length
101722 101821: gap of unknown length
101822 132225: contig of 30404 bp in length
132226 132325: gap of unknown length
132326 204500: contig of 72175 bp in length.

FEATURES
Location/Qualifiers
1..204500
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1381A15"
/clone_lib="RPCI human BAC library 11"
1080..1179
/estimated_length=unknown
2334..2433
/estimated_length=unknown
4476..4575
/estimated_length=unknown
7755..7854
/estimated_length=unknown
14690..14789
/estimated_length=unknown
20824..20923
/estimated_length=unknown
25586..25685
/estimated_length=unknown
31076..31175
/estimated_length=unknown
41944..42043
/estimated_length=unknown
61501..61600
/estimated_length=unknown
101722..101821
/estimated_length=unknown
132226..132325
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 204500;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 101600 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 101640
|||||

RESULT 49
AC141253/c
LOCUS AC141253
DEFINITION Homo sapiens chromosome 16 clone RP11-126903, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
ACCESSION AC141253
VERSION AC141253.1 GI:28913033


```
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 204638)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204638)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 2707269
Center clone name: RPCI-11_126903
-----
Summary Statistics
Consensus quality: 199061 bases at least Q40
Consensus quality: 200424 bases at least Q30
Consensus quality: 201383 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 203438; sum-of-contigs estimation
Quality coverage: 11.16 in Q20 bases; agarose-fp estimation
Quality coverage: 9.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1075: contig of 1075 bp in length
* 1076 1175: gap of unknown length
* 1176 2298: contig of 1123 bp in length
* 2299 2398: gap of unknown length
* 2399 4411: contig of 2013 bp in length
* 4412 4511: gap of unknown length
* 4512 6238: contig of 1727 bp in length
* 6239 6339: gap of unknown length
* 6339 10193: contig of 3855 bp in length
* 10194 10293: gap of unknown length
* 10294 17059: contig of 6766 bp in length
* 17060 17159: gap of unknown length
* 17160 24203: contig of 7044 bp in length
* 24204 24303: gap of unknown length
* 24304 29859: contig of 5556 bp in length
* 29860 29959: gap of unknown length
* 29960 35329: contig of 5370 bp in length
* 35330 35429: gap of unknown length
* 35430 46589: contig of 11160 bp in length
* 46590 46689: gap of unknown length
* 46690 59464: contig of 12775 bp in length
* 59465 59564: gap of unknown length
* 59565 93991: contig of 34427 bp in length
* 93992 94091: gap of unknown length
* 94092 204638: contig of 110547 bp in length.
Location/Qualifiers
1. .204638
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-126903"
/clone_lib="RPCI human BAC library 11"
```

```
gap 1076. .1175
/estimated_length=unknown
gap 2299. .2398
/estimated_length=unknown
gap 4412. .4511
/estimated_length=unknown
gap 6239. .6338
/estimated_length=unknown
gap 10194. .10293
/estimated_length=unknown
gap 17060. .17159
/estimated_length=unknown
gap 24204. .24303
/estimated_length=unknown
gap 29860. .29959
/estimated_length=unknown
gap 35330. .35429
/estimated_length=unknown
gap 46590. .46689
/estimated_length=unknown
gap 59465. .59564
/estimated_length=unknown
gap 93992. .94091
/estimated_length=unknown
ORIGIN
Query Match 100.0%; Score 41; DB 14; Length 204638;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 59769 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGTCCGCG 59729
|||||
RESULT 50
AC141607 AC141607 215974 bp DNA linear HTG 18-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-644A22, WORKING DRAFT
DEFINITION SEQUENCE, 12 unordered pieces.
ACCESSION AC141607
VERSION AC141607.1 GI:29029192
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 215974)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 215974)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1541822
Center clone name: RPCI-11_644A22
-----
Summary Statistics
Consensus quality: 210022 bases at least Q40
Consensus quality: 211176 bases at least Q30
Consensus quality: 212214 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 214874; sum-of-contigs estimation
Quality coverage: 7.64 in Q20 bases; agarose-fp estimation
```

Quality coverage: 6.26 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

- * 1 1006: contig of 1006 bp in length
- * 1007 1106: gap of unknown length
- * 1107 2415: contig of 1309 bp in length
- * 2416 2515: gap of unknown length
- * 2516 7493: contig of 4978 bp in length
- * 7494 7593: gap of unknown length
- * 7594 14882: contig of 7289 bp in length
- * 14883 14982: gap of unknown length
- * 14983 25966: contig of 10984 bp in length
- * 25967 26066: gap of unknown length
- * 26067 37589: contig of 11523 bp in length
- * 37590 37689: gap of unknown length
- * 37690 52557: contig of 14868 bp in length
- * 52558 52657: gap of unknown length
- * 52658 70474: contig of 17817 bp in length
- * 70475 70574: gap of unknown length
- * 70575 86827: contig of 16253 bp in length
- * 86828 86927: gap of unknown length
- * 86928 123298: contig of 36371 bp in length
- * 123299 123398: gap of unknown length
- * 123399 159741: contig of 36343 bp in length
- * 159742 159841: gap of unknown length
- * 159842 215974: contig of 56133 bp in length.

FEATURES

source

- 1. .215974
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-644A22"
/clone_lib="RPCI human BAC library 11"
1007. .1106
/estimated_length=unknown
2416. .2515
/estimated_length=unknown
7494. .7593
/estimated_length=unknown
14883. .14982
/estimated_length=unknown
25967. .26066
/estimated_length=unknown
37590. .37689
/estimated_length=unknown
52558. .52657
/estimated_length=unknown
70475. .70574
/estimated_length=unknown
86828. .86927
/estimated_length=unknown
123299. .123398
/estimated_length=unknown
159742. .159841
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 41; DB 14; Length 215974;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|||||

Db 86666 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGTCCGCG 86706
|||||

RESULT 51

AC138969/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC138969 216759 bp DNA linear PRI 07-APR-2003
Homo sapiens chromosome 16 clone RP11-958N24, complete sequence.
AC138969
AC138969.2 GI:29570377
HTG.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 216759)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Unpublished
2 (bases 1 to 216759)
DOE Joint Genome Institute.
Direct Submission
Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 216759)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Apr 7, 2003 this sequence version replaced gi:27805381.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.sbgc.stanford.edu

Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 241kb). It is clipped at the overlap with AC136624. The
number of bases overlapped is 130609. Large tandem repeat 1 to
75000. Unsure number of dinucleotide repeats from 18586-18838.
Force join at 18810. Unsure number of dinucleotide repeats from
62780-62985. Force join at 62870.
Location/Qualifiers
1. .216759
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-958N24"
1. .75000
/note="Large tandem repeat 1 to 75000."
18586. .18838
/note="Unsure number of dinucleotide repeats from
18586-18838. Force join at 18810."
62780. .62985
/note="Unsure number of dinucleotide repeats from
62780-62985. Force join at 62870."

FEATURES

source

- 1. .216759
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-958N24"
1. .75000
/note="Large tandem repeat 1 to 75000."
18586. .18838
/note="Unsure number of dinucleotide repeats from
18586-18838. Force join at 18810."
62780. .62985
/note="Unsure number of dinucleotide repeats from
62780-62985. Force join at 62870."

misc_feature

misc_feature

misc_feature

ORIGIN

Query Match 100.0%; Score 41; DB 8; Length 216759;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|||||

Db 79414 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGTCCGCG 79374
|||||

RESULT 52

AC126755

LOCUS

DEFINITION

ACCESSION

AC126755 223432 bp DNA linear PRI 07-APR-2003
Homo sapiens chromosome 16 clone RP11-1212A22, complete sequence.
AC126755

VERSION AC126755.3 GI:29570366
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 223432)
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
AUTHORS DOE Joint Genome Institute.
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
REFERENCE Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
AUTHORS 3 (bases 1 to 223432)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
REFERENCE Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
AUTHORS 4 (bases 1 to 223432)
TITLE DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
JOURNAL Direct Submission
COMMENT Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Apr 7, 2003 this sequence version replaced gi:22857527.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 1.1.
NOTE: Large tandem repeat 31000 to 120000. Unsure number of
dinucleotide repeats from 55000-55100. Force join at 55065. Unsure
number of dinucleotide repeats from 94330-94487. Force join at
94368.
misc_feature 31000..120000
misc_feature 55000..55100
misc_feature 94330..94487
ORIGIN
Query Match 100.0%; Score 41; DB 8; Length 223432;
Best Local Similarity 97.6%; Pred. No. 0.012;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41
Db 34333 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGTCCGC 34373
RESULT 53
HSA323057/c
LOCUS HSA323057 865 bp DNA linear PRI 18-JUL-2002
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
NR5-118R.
ACCESSION AJ323057
VERSION AJ323057.1 GI:15867436

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,
Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
PUBMED 12136098
REFERENCE 2 (bases 1 to 865)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
source Location/Qualifiers
1..865
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NR5-118R"
ORIGIN
Query Match 96.1%; Score 39.4; DB 8; Length 865;
Best Local Similarity 95.1%; Pred. No. 0.1;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41
Db 235 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCTGGTCGCG 195
RESULT 54
AC141236/c
LOCUS AC141236 38848 bp DNA linear HTG 11-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-350G9, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
ACCESSION AC141236
VERSION AC141236.1 GI:28913016
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 38848)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 38848)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1220753
Center clone name: LANL-16c_350G9

Summary Statistics
Consensus quality: 35738 bases at least Q40
Consensus quality: 36543 bases at least Q30
Consensus quality: 37150 bases at least Q20

Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 38448; sum-of-contigs estimation
Quality coverage: 14.51 in Q20 bases; agarose-fp estimation
Quality coverage: 15.1 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1051: contig of 1051 bp in length
* 1052 1151: gap of unknown length
* 1152 2351: contig of 1200 bp in length
* 2352 2451: gap of unknown length
* 2452 9815: contig of 7364 bp in length
* 9816 9915: gap of unknown length
* 9916 16604: contig of 6689 bp in length
* 16605 16704: gap of unknown length
* 16705 38848: contig of 22144 bp in length.

FEATURES

source

1. .38848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16c-350G9"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
1052: .1151
/estimated_length=unknown
2352: .2451
/estimated_length=unknown
9816: .9915
/estimated_length=unknown
16605: .16704
/estimated_length=unknown

ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 38848;
Best Local Similarity 95.1%; Pred. No. 0.049;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGTCGCCGNCGCG 41
|||||
Db 10119 AAGCCTCCGGATGCCAGTCCCTCATCGTCGCCCTGGTCGCG 10079
|||||

RESULT 55

AC040158

LOCUS

DEFINITION Homo sapiens chromosome 16 clone CTA-133B4, WORKING DRAFT SEQUENCE,
14 unordered pieces.

ACCESSION AC040158

VERSION AC040158.3 GI:9965546

KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 129473)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 16

Unpublished

2 (bases 1 to 129473)

DOE Joint Genome Institute.

Direct Submission

Submitted (11-APR-2000) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Sep 3, 2000 this sequence version replaced gi:9090652.

-----Genome Center

Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information

Center Project Name: 0
Center clone name: CIT978SKA_133B4

Summary Statistics

Consensus quality: 90046 bases at least Q40
Consensus quality: 99266 bases at least Q30
Consensus quality: 104098 bases at least Q20
Estimated insert size: 125000; agarose-fp estimation
Estimated insert size: 128173; sum-of-contigs estimation
Quality coverage: 4.51 in Q20 bases; agarose-fp estimation
Quality coverage: 4.4 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1718: contig of 1718 bp in length
* 1719 1818: gap of unknown length
* 1819 3832: contig of 2014 bp in length
* 3833 3932: gap of unknown length
* 3933 5567: contig of 1635 bp in length
* 5568 5667: gap of unknown length
* 5668 7520: contig of 1853 bp in length
* 7521 7620: gap of unknown length
* 7621 9146: contig of 1526 bp in length
* 9147 9246: gap of unknown length
* 9247 11144: contig of 1898 bp in length
* 11145 11244: gap of unknown length
* 11245 12746: contig of 1502 bp in length
* 12747 12846: gap of unknown length
* 12847 14568: contig of 1722 bp in length
* 14569 14668: gap of unknown length
* 14669 19396: contig of 4728 bp in length
* 19397 19496: gap of unknown length
* 19497 25634: contig of 6138 bp in length
* 25635 25734: gap of unknown length
* 25735 36780: contig of 11046 bp in length
* 36781 36880: gap of unknown length
* 36881 50223: contig of 13343 bp in length
* 50224 50323: gap of unknown length
* 50324 71312: contig of 20989 bp in length
* 71313 71412: gap of unknown length
* 71413 129473: contig of 58061 bp in length.

FEATURES

source

1. .129473
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="CTA-133B4"
/clone_lib="CalTech human BAC library A"
1719: .1818
/estimated_length=unknown
3833: .3932
/estimated_length=unknown
5568: .5667
/estimated_length=unknown
7521: .7620
/estimated_length=unknown
9147: .9246
/estimated_length=unknown
11145: .11244
/estimated_length=unknown
12747: .12846
/estimated_length=unknown

gap

gap

gap

gap

gap

gap

gap


```
gap      14569. .14668
/estimated_length=unknown
gap      19397. .19496
/estimated_length=unknown
gap      25635. .25734
/estimated_length=unknown
gap      36781. .36880
/estimated_length=unknown
gap      50224. .50323
/estimated_length=unknown
gap      71313. .71412
/estimated_length=unknown

ORIGIN
Query Match      96.1%; Score 39.4; DB 14; Length 129473;
Best Local Similarity 95.1%; Pred. No. 0.039;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db      47443 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCTGGTCGCG 47483
|||||

RESULT 56
AC141602
LOCUS      AC141602      144161 bp      DNA      linear      HTG 18-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1381B13, WORKING DRAFT
ACCESSION      AC141602
VERSION      AC141602.1 GI:29029187
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 144161)
AUTHORS      DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 16
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 144161)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (18-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 2749975
Center clone name: RPCI-11_1381B13
-----
Summary Statistics
Consensus quality: 140581 bases at least Q40
Consensus quality: 141190 bases at least Q30
Consensus quality: 141648 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 143061; sum-of-contigs estimation
Quality coverage: 7.62 in Q20 bases; agarose-fp estimation
Quality coverage: 9.38 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*      1      1363: contig of 1363 bp in length
*      1364      1463: gap of unknown length
*      1464      4438: contig of 2975 bp in length
```

```
*      4439      4538: gap of unknown length
*      4539      8092: contig of 3554 bp in length
*      8093      8192: gap of unknown length
*      8193      13626: contig of 5434 bp in length
*      13627      13726: gap of unknown length
*      13727      21117: contig of 7391 bp in length
*      21118      21217: gap of unknown length
*      21218      31407: contig of 10190 bp in length
*      31408      31507: gap of unknown length
*      31508      42598: contig of 11091 bp in length
*      42599      42698: gap of unknown length
*      42699      55092: contig of 12394 bp in length
*      55093      55192: gap of unknown length
*      55193      72553: contig of 17361 bp in length
*      72554      72653: gap of unknown length
*      72654      88814: contig of 16161 bp in length
*      88815      88914: gap of unknown length
*      88915      123281: contig of 34367 bp in length
*      123282      123381: gap of unknown length
*      123382      144161: contig of 20780 bp in length.

FEATURES
          Location/Qualifiers
            1..144161
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
              /chromosome="16"
              /clone="RP11-1381B13"
              /clone_lib="RPCI human BAC library 11"
              1364..1463
                /estimated_length=unknown
                4439..4538
                  /estimated_length=unknown
                  8093..8192
                    /estimated_length=unknown
                    13627..13726
                      /estimated_length=unknown
                      21118..21217
                        /estimated_length=unknown
                        31408..31507
                          /estimated_length=unknown
                          42599..42698
                            /estimated_length=unknown
                            55093..55192
                              /estimated_length=unknown
                              72554..72653
                                /estimated_length=unknown
                                88815..88914
                                  /estimated_length=unknown
                                  123282..123381
                                    /estimated_length=unknown

ORIGIN
Query Match      96.1%; Score 39.4; DB 14; Length 144161;
Best Local Similarity 95.1%; Pred. No. 0.039;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db      123042 AAGCCTCTGATGCCAGTCCCTCATCGCTGGCCCGTGGCG 123082
|||||

RESULT 57
AC154112
LOCUS      AC154112      183396 bp      DNA      linear      HTG 30-JUN-2005
DEFINITION Pan troglodytes clone RP43-11J15, WORKING DRAFT SEQUENCE, 13
ordered pieces.
ACCESSION      AC154112
VERSION      AC154112.3 GI:68342116
KEYWORDS      HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

REFERENCE
AUTHORS

Hominidae; Pan.
1 (bases 1 to 183396)
Eichler,E., Johnson,M., Antonellis,A., Ayele,K., Bass,D.,
Benjamin,B., Bera,J., Blakesley,R.W., Bouffard,G.G., Brinkley,C.,
Brooks,S., Chu,G., Coleman,H., Engle,J., Fuksenko,T., Gestole,M.,
Greene,A., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N.,
Ho,S.-L., Hu,P., Hunter,G., Hurle,B., Idol,J.R., Kwong,P.,
Laric,P., Larson,S., Lee-Lin,S.-Q., Legaspi,R., Madden,M.,
Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,
McDowell,J., Mojidi,H.A., Mullikin,J.C., Oestreicher,J.S., Park,M.,
Portnoy,M.E., Prasad,A., Puri,O., Reddix-Dugue,N., Sante,A.,
Schandler,K., Schueler,M.G., Sison,C., Stantripop,S., Stephen,E.,
Taye,A., Thomas,J.W., Thomas,P.J., Tsipouri,V., Ung,L., Vogt,J.L.,
Wetherby,K.D., Withers,T.R., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 183396)
Green,E.D.
Direct Submission
Submitted (23-DEC-2004) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
3 (bases 1 to 183396)
Green,E.D.
Direct Submission
Submitted (30-JUN-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Jun 30, 2005 this sequence version replaced gi:58219703.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

43148: contig of 15775 bp in length
43248: gap of unknown length
45468: contig of 2220 bp in length
45568: gap of unknown length
62655: contig of 17087 bp in length
62755: gap of unknown length
85032: contig of 22277 bp in length
85132: gap of unknown length
99815: contig of 14683 bp in length
99915: gap of unknown length
122872: contig of 22957 bp in length
122972: gap of unknown length
134501: contig of 11529 bp in length
134601: gap of unknown length
140529: contig of 5928 bp in length
140629: gap of unknown length
160723: contig of 20094 bp in length
160823: gap of unknown length
173513: contig of 12690 bp in length
173613: gap of unknown length
183396: contig of 9783 bp in length.
FEATURES
 source
 1..183396
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-11J15"
 /clone_lib="RP43"
 /note="BAC resource: http://bacpac.chori.org/"
 1..2055
 /note="assembly_fragment"
 clone end:SP6
 vector_side:left
 2056..2155
 /estimated_length=unknown
 2156..27273
 /note="assembly_fragment"
 27274..27373
 /estimated_length=unknown
 27374..43148
 /note="assembly_fragment"
 43149..43248
 /estimated_length=unknown
 43249..45468
 /note="assembly_fragment"
 45469..45568
 /estimated_length=unknown
 45569..62655
 /note="assembly_fragment"
 62656..62755
 /estimated_length=unknown
 62756..85032
 /note="assembly_fragment"
 85033..85132
 /estimated_length=unknown
 85133..99815
 /note="assembly_fragment"
 99816..99915
 /estimated_length=unknown
 99916..122872
 /note="assembly_fragment"
 122873..122972
 /estimated_length=unknown
 122973..134501
 /note="assembly_fragment"
 134502..134601
 /estimated_length=unknown
 134602..140529
 /note="assembly_fragment"
 140530..140629
 /estimated_length=unknown
 140630..160723
 /note="assembly_fragment"
misc_feature
 1..2055
 clone end:SP6
 vector_side:left
 2056..2155
 /estimated_length=unknown
misc_feature
 2156..27273
 /note="assembly_fragment"
 27274..27373
 /estimated_length=unknown
misc_feature
 27374..43148
 /note="assembly_fragment"
 43149..43248
 /estimated_length=unknown
 43249..45468
 /note="assembly_fragment"
 45469..45568
 /estimated_length=unknown
 45569..62655
 /note="assembly_fragment"
 62656..62755
 /estimated_length=unknown
 62756..85032
 /note="assembly_fragment"
 85033..85132
 /estimated_length=unknown
 85133..99815
 /note="assembly_fragment"
 99816..99915
 /estimated_length=unknown
 99916..122872
 /note="assembly_fragment"
 122873..122972
 /estimated_length=unknown
 122973..134501
 /note="assembly_fragment"
 134502..134601
 /estimated_length=unknown
 134602..140529
 /note="assembly_fragment"
 140530..140629
 /estimated_length=unknown
 140630..160723
 /note="assembly_fragment"

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gap          160724. .160823
misc_feature /estimated length=unknown
             160824. .173513
             /note="assembly_fragment"
gap          173514. .173613
misc_feature /estimated length=unknown
             173614. .183396
             /note="assembly_fragment
clone_end:T7
vector_side:right"

ORIGIN
Query Match          96.1%; Score 39.4; DB 14; Length 183396;
Best Local Similarity 95.1%; Pred. No. 0.037;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
    |||||||
Db 62806 AAGCCTCCGGATGCCAGTCACTCATCGCTGGCCCGTCCGCG 62846

RESULT 58
AC092137/c
LOCUS          AC092137          184891 bp          DNA          linear          PRI 07-APR-2003
DEFINITION    Homo sapiens chromosome 16 clone RP11-344H15, complete sequence.
ACCESSION     AC092137
VERSION       AC092137.3 GI:28973806
KEYWORDS      HTG.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominiidae; Homo.
REFERENCE     1 (bases 1 to 184891)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
               Alamos National Laboratory.
TITLE         Direct Submission
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 184891)
AUTHORS      DOE Joint Genome Institute.
TITLE         Direct Submission
JOURNAL       Submitted (22-JUN-2001) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE     3 (bases 1 to 184891)
AUTHORS      DOE Joint Genome Institute.
TITLE         Direct Submission
JOURNAL       Submitted (24-NOV-2002) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE     4 (bases 1 to 184891)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
               Alamos National Laboratory.
TITLE         Direct Submission
JOURNAL       Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
               Drive, Walnut Creek, CA 94598, USA
REFERENCE     5 (bases 1 to 184891)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
               Alamos National Laboratory.
TITLE         Direct Submission
JOURNAL       Submitted (07-APR-2003) DOE Joint Genome Institute, 2800 Mitchell
               Drive, Walnut Creek, CA 94598, USA
COMMENT       On Mar 15, 2003 this sequence version replaced gi:25229204.
               Draft Sequence Produced by DOE Joint Genome Institute
               www.jgi.doe.gov
               Finishing Completed at Stanford Human Genome Center and Los Alamos
               National Laboratory
               www-shgc.stanford.edu
               Quality: Phrap Quality >=40 99.9% of Sequence;
               Estimated Total Number of Errors is 0.1.
               NOTE: Unsure number of dinucleotide repeats from 93650-94165.
               Forced join at 94008. The number of missing bases by PCR is 100.
               Location/Qualifiers
                 1. .184891
                   /organism="Homo sapiens"

FEATURES             source
    source            1. .184891
                       /organism="Homo sapiens"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-344H15"
93650. .94165
/note="NOTE: Unsure number of dinucleotide repeats from
93650-94165. Forced join at 94008. The number of missing
bases by PCR is 100."

misc_feature

ORIGIN
Query Match          96.1%; Score 39.4; DB 8; Length 184891;
Best Local Similarity 95.1%; Pred. No. 0.037;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
    |||||||
Db 116614 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCTGGTCGCG 116574

RESULT 59
AC126763
LOCUS          AC126763          187721 bp          DNA          linear          PRI 18-MAR-2003
DEFINITION    Homo sapiens chromosome 16 clone RP11-1390J18, complete sequence.
ACCESSION     AC126763
VERSION       AC126763.4 GI:29029241
KEYWORDS      HTG.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominiidae; Homo.
REFERENCE     1 (bases 1 to 187721)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
               Alamos National Laboratory.
TITLE         Direct Submission
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 187721)
AUTHORS      DOE Joint Genome Institute.
TITLE         Direct Submission
JOURNAL       Submitted (09-JUL-2002) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE     3 (bases 1 to 187721)
AUTHORS      DOE Joint Genome Institute.
TITLE         Direct Submission
JOURNAL       Submitted (14-SEP-2002) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE     4 (bases 1 to 187721)
AUTHORS      DOE Joint Genome Institute.
TITLE         Direct Submission
JOURNAL       Submitted (23-OCT-2002) Production Sequencing Facility, DOE Joint
               Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE     5 (bases 1 to 187721)
AUTHORS      DOE Joint Genome Institute, Stanford Human Genome Center and Los
               Alamos National Laboratory.
TITLE         Direct Submission
JOURNAL       Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
               Drive, Walnut Creek, CA 94598, USA
COMMENT       On Mar 18, 2003 this sequence version replaced gi:24270685.
               Draft Sequence Produced by DOE Joint Genome Institute
               www.jgi.doe.gov
               Finishing Completed at Stanford Human Genome Center and Los Alamos
               National Laboratory
               www-shgc.stanford.edu
               Quality: Phrap Quality >=40 99.9% of Sequence;
               Estimated Total Number of Errors is 0.1.
               Location/Qualifiers
                 1. .187721
                   /organism="Homo sapiens"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9606"
                   /chromosome="16"
                   /clone="RP11-1390J18"

FEATURES             source
    source            1. .187721
                       /organism="Homo sapiens"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:9606"
                       /chromosome="16"
                       /clone="RP11-1390J18"

ORIGIN
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Query Match 96.1%; Score 39.4; DB 8; Length 187721;
Best Local Similarity 95.1%; Pred. No. 0.037;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 184518 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCTGGTCGCG 184558
|||||

RESULT 60
AC139281/c
LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-79C9, WORKING DRAFT SEQUENCE,
9 unordered pieces.
AC139281
AC139281.1 GI:28009876
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 189770)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 189770)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 436758
Center clone name: RPCI-11_79C9

Summary Statistics
Consensus quality: 186019 bases at least Q40
Consensus quality: 186858 bases at least Q30
Consensus quality: 187442 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 188970; sum-of-contigs estimation
Quality coverage: 12.88 in Q20 bases; agarose-fp estimation
Quality coverage: 11.92 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1112: contig of 1112 bp in length
* 1113 1212: gap of unknown length
* 1213 2537: contig of 1325 bp in length
* 2538 2637: gap of unknown length
* 2638 5280: contig of 2643 bp in length
* 5281 5380: gap of unknown length
* 5381 12999: contig of 7619 bp in length
* 13000 13099: gap of unknown length
* 13100 34114: contig of 21015 bp in length
* 34115 34214: gap of unknown length
* 34215 70477: contig of 36263 bp in length
* 70478 70577: gap of unknown length
* 70578 98195: contig of 27618 bp in length
* 98196 98295: gap of unknown length
* 98296 132998: contig of 34703 bp in length
* 132999 133098: gap of unknown length

* 133099 189770: contig of 56672 bp in length.
FEATURES
source
1. 189770
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-79C9"
/clone_lib="RPCI human BAC library 11"
1113. 1212
/estimated_length=unknown
2538. 2637
/estimated_length=unknown
5281. 5380
/estimated_length=unknown
13000. 13099
/estimated_length=unknown
34115. 34214
/estimated_length=unknown
70478. 70577
/estimated_length=unknown
98196. 98295
/estimated_length=unknown
132999. 133098
/estimated_length=unknown
ORIGIN
Query Match 96.1%; Score 39.4; DB 14; Length 189770;
Best Local Similarity 95.1%; Pred. No. 0.037;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 99396 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCTGGTCGCG 99356
|||||

RESULT 61
AC136442
LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-470K5, *** SEQUENCING IN
PROGRESS ***, 5 ordered pieces.
AC136442
AC136442.2 GI:29336204
KEYWORDS HTG; HTGS PHASE2; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 196687)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Unpublished
2 (bases 1 to 196687)
DOE Joint Genome Institute.
Direct Submission
Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 196687)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
Submitted (28-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 28, 2003 this sequence version replaced gi:24462332.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced

* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 83902: contig of 83902 bp in length
* 83903 84002: gap of unknown length
* 84003 94898: contig of 10896 bp in length
* 94899 94998: gap of unknown length
* 94999 120178: contig of 25180 bp in length
* 120179 120278: gap of unknown length
* 120279 142935: contig of 22657 bp in length
* 142936 143035: gap of unknown length
* 143036 196687: contig of 53652 bp in length.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 587090
Center clone name: RP11-470K5

Summary Statistics
Consensus quality: 194751 bases at least Q40
Consensus quality: 195030 bases at least Q30
Consensus quality: 195153 bases at least Q20
Estimated insert size: 197000; agarose-fp estimation
Estimated insert size: 195279; sum-of-contigs
estimation
Quality coverage: 0.99 in Q20 bases; agarose-fp
estimation
Quality coverage: 1 in Q20 bases; sum-of-contigs
estimation.
Location/Qualifiers
1. 196687
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-470K5"
83903. .84002
/estimated_length=unknown
94899. .94998
/estimated_length=unknown
120179. .120278
/estimated_length=unknown
142936. .143035
/estimated_length=unknown
ORIGIN
Query Match 96.1%; Score 39.4; DB 14; Length 196687;
Best Local Similarity 95.1%; Pred. No. 0.036;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCGCG 41
|||||
Db 120055 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCTGGTCGCG 120095
AC141467 215222 bp DNA linear HTG 16-MAR-2003
Homo sapiens chromosome 16 clone RP11-927M3, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC141467
AC141467.1 GI:28975020
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 215222)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 215222)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1650763
Center clone name: RPCI-11_927M3

Summary Statistics
Consensus quality: 207729 bases at least Q40
Consensus quality: 209189 bases at least Q30
Consensus quality: 210079 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 214122; sum-of-contigs estimation
Quality coverage: 6.85 in Q20 bases; agarose-fp estimation
Quality coverage: 5.63 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1037: contig of 1037 bp in length
* 1038 1137: gap of unknown length
* 1138 5338: contig of 4201 bp in length
* 5339 5438: gap of unknown length
* 5439 9722: contig of 4284 bp in length
* 9723 9822: gap of unknown length
* 9823 15226: contig of 5404 bp in length
* 15227 15326: gap of unknown length
* 15327 21907: contig of 6581 bp in length
* 21908 22007: gap of unknown length
* 22008 28900: contig of 6893 bp in length
* 28901 29000: gap of unknown length
* 29001 41504: contig of 12504 bp in length
* 41505 41604: gap of unknown length
* 41605 56820: contig of 15216 bp in length
* 56821 56920: gap of unknown length
* 56921 80192: contig of 23272 bp in length
* 80193 80292: gap of unknown length
* 80293 117096: contig of 36804 bp in length
* 117097 117196: gap of unknown length
* 117197 156379: contig of 39183 bp in length
* 156380 156479: gap of unknown length
* 156480 215222: contig of 58743 bp in length.
FEATURES
Location/Qualifiers
1. 215222
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-927M3"
/clone_lib="RPCI human BAC library 11"
1038. .1137
/estimated_length=unknown
5339. .5438
/estimated_length=unknown
9723. .9822
/estimated_length=unknown
15227. .15326
/estimated_length=unknown
21908. .22007
/estimated_length=unknown
28901. .29000
gap
gap
gap
gap
gap
gap

gap /estimated_length=unknown
41505. .41604
gap /estimated_length=unknown
56821. .56920
gap /estimated_length=unknown
80193. .80292
gap /estimated_length=unknown
117097. .117196
gap /estimated_length=unknown
156380. .156479
gap /estimated_length=unknown

ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 215222;
Best Local Similarity 95.1%; Pred. No. 0.036;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCTCCGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 28672 AAGCTCCGATGCCAGTCCCTCATCGCTGGCTGGTCGCG 28712

RESULT 63

AC144881/c

LOCUS

AC144881 215960 bp DNA linear HTG 18-JUL-2003
Gorilla gorilla gorilla clone CH255-120J14, WORKING DRAFT SEQUENCE,
19 unordered pieces.

ACCESSION

AC144881

VERSION

AC144881.2 GI:32964875

KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE

Gorilla gorilla gorilla (lowland gorilla)

ORGANISM

Gorilla gorilla gorilla

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Gorilla.

1 (bases 1 to 215960)

Eichler,E.E., Johnson,M.E., Antonellis,A., Ayele,K.,

Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,

Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Chu,G.,

Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J.,

Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B.,

Idol,J.R., Karlins,E., Kwong,P., Laric,P., Lee-Lin,S.-Q.,

Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C.,

Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E.,

Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,

Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V.,

Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.

NISC Comparative Sequencing Initiative

Unpublished

2 (bases 1 to 215960)

Green,E.D.

Direct Submission

Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717

Grovemont Circle, Gaithersburg, MD 20877, USA

On Jul 18, 2003 this sequence version replaced gi:31044296.

----- Genome Center

Center: NIH Intramural Sequencing Center

Center code: NISC

Web site: <http://www.nisc.nih.gov>

Contact: nisc_zoo@nhgri.nih.gov

----- Project Information

Center project name: eni

Center clone name: 120J14

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 209508 bases at least Q40

Consensus quality: 210752 bases at least Q30
Consensus quality: 211509 bases at least Q20
Insert size: 22000; agarose-fp
Insert size: 214160; sum-of-contigs
Quality coverage: 11.70x in Q20 bases; agarose-fp
Quality coverage: 12.02x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2293: contig of 2293 bp in length
* 2294 2393: gap of unknown length
* 2394 4498: contig of 2105 bp in length
* 4499 4598: gap of unknown length
* 4599 7155: contig of 2557 bp in length
* 7156 7255: gap of unknown length
* 7256 10105: contig of 2850 bp in length
* 10106 10205: gap of unknown length
* 10206 13671: contig of 3466 bp in length
* 13672 13771: gap of unknown length
* 13772 15857: contig of 2086 bp in length
* 15858 15957: gap of unknown length
* 15958 20009: contig of 4052 bp in length
* 20010 20109: gap of unknown length
* 20110 24472: contig of 4363 bp in length
* 24473 24572: gap of unknown length
* 24573 27197: contig of 2625 bp in length
* 27198 27297: gap of unknown length
* 27298 33250: contig of 5953 bp in length
* 33251 33350: gap of unknown length
* 33351 39952: contig of 6602 bp in length
* 39953 40052: gap of unknown length
* 40053 52004: contig of 11952 bp in length
* 52005 52104: gap of unknown length
* 52105 67492: contig of 15388 bp in length
* 67493 67592: gap of unknown length
* 67593 85255: contig of 17663 bp in length
* 85256 85355: gap of unknown length
* 85356 107738: contig of 22383 bp in length
* 107739 126829: contig of 18991 bp in length
* 126830 126929: gap of unknown length
* 126930 146098: contig of 19169 bp in length
* 146099 146198: gap of unknown length
* 146199 183617: contig of 37419 bp in length
* 183618 183717: gap of unknown length
* 183718 215960: contig of 32243 bp in length.

FEATURES

source

1..215960
/organism="Gorilla gorilla gorilla"
/mol_type="genomic DNA"
/sub_species="gorilla"
/db_xref="taxon:9595"
/clone="CH255-120J14"
/clone_lib="CH255"

misc_feature

1..2293
/note="assembly_fragment"
2294..2393
/estimated_length=unknown
2394..4498
/note="assembly_fragment"
4499..4598
/estimated_length=unknown
4599..7155
/note="assembly_fragment"
7156..7255
/estimated_length=unknown
7256..10105

gap

misc_feature

gap

misc_feature

gap

misc_feature

gap /note="assembly_fragment"
10106. .10205
/estimated_length=unknown
misc_feature 10206. .13671
/note="assembly_fragment"
gap 13672. .13771
/estimated_length=unknown
misc_feature 13772. .15857
/note="assembly_fragment"
gap 15858. .15957
/estimated_length=unknown
misc_feature 15958. .20009
/note="assembly_fragment"
gap 20010. .20109
/estimated_length=unknown
misc_feature 20110. .24472
/note="assembly_fragment"
gap 24473. .24572
/estimated_length=unknown
misc_feature 24573. .27197
/note="assembly_fragment"
gap 27198. .27297
/estimated_length=unknown
misc_feature 27298. .33250
/note="assembly_fragment"
gap 33251. .33350
/estimated_length=unknown
misc_feature 33351. .39952
/note="assembly_fragment"
gap 39953. .40052
/estimated_length=unknown
misc_feature 40053. .52004
/note="assembly_fragment"
gap 52005. .52104
/estimated_length=unknown
misc_feature 52105. .67492
/note="assembly_fragment"
gap 67493. .67592
/estimated_length=unknown
misc_feature 67593. .85255
/note="assembly_fragment"
gap 85256. .85355
/estimated_length=unknown
misc_feature 85356. .107738
/note="assembly_fragment"
gap 107739. .107838
/estimated_length=unknown
misc_feature 107839. .126829
/note="assembly_fragment"
gap 126830. .126929
/estimated_length=unknown
misc_feature 126930. .146098
/note="assembly_fragment"
clone_end:SP6
vector_side:right"
gap 146099. .146198
/estimated_length=unknown
misc_feature 146199. .183617
/note="assembly_fragment"
gap 183618. .183717
/estimated_length=unknown
misc_feature 183718. .215960
/note="assembly_fragment"
clone_end:T7
vector_side:right"

ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 215960;
Best Local Similarity 95.1%; Pred.No. 0.036;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNCGG 41
{|||||}|||||}|||||}|||||}|||||}|||||}|||||}

Db 41238 AAGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 41198

RESULT 64
AC141303/c
LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-795L17, WORKING DRAFT
SEQUENCE, 15 unordered pieces.
ACCESSION AC141303
VERSION AC141303.1 GI:28913083
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 218593)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 218593)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1600065
Center clone name: RPCI-11_795L17

Summary Statistics
Consensus quality: 206479 bases at least Q40
Consensus quality: 210696 bases at least Q30
Consensus quality: 212699 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 217193; sum-of-contigs estimation
Quality coverage: 6.63 in Q20 bases; agarose-fp estimation
Quality coverage: 5.37 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1100: contig of 1100 bp in length
* 1101 1200: gap of unknown length
* 1201 2911: contig of 1711 bp in length
* 2912 3011: gap of unknown length
* 3012 6661: contig of 3650 bp in length
* 6662 6761: gap of unknown length
* 6762 11364: contig of 4603 bp in length
* 11365 11464: gap of unknown length
* 11465 17383: contig of 5919 bp in length
* 17384 17483: gap of unknown length
* 17484 24477: contig of 6994 bp in length
* 24478 24577: gap of unknown length
* 24578 30168: contig of 5591 bp in length
* 30169 30269: gap of unknown length
* 30269 39963: contig of 9695 bp in length
* 39964 40063: gap of unknown length
* 40064 53361: contig of 13298 bp in length
* 53362 53461: gap of unknown length
* 53462 67963: contig of 14502 bp in length
* 67964 68063: gap of unknown length
* 68064 84693: contig of 16630 bp in length
* 84694 84793: gap of unknown length
* 84794 102881: contig of 18088 bp in length

* 102882 102981: gap of unknown length
* 102982 123663: contig of 20682 bp in length
* 123664 123763: gap of unknown length
* 123764 166750: contig of 42987 bp in length
* 166751 166850: gap of unknown length
* 166851 218593: contig of 51743 bp in length.

FEATURES

source

1. .218593
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-795L17"
/clone_lib="RPCI human BAC library 11"
1101. .1200
/estimated_length=unknown
2912. .3011
/estimated_length=unknown
6662. .6761
/estimated_length=unknown
11365. .11464
/estimated_length=unknown
17384. .17483
/estimated_length=unknown
24478. .24577
/estimated_length=unknown
30169. .30268
/estimated_length=unknown
39964. .40063
/estimated_length=unknown
53362. .53461
/estimated_length=unknown
67964. .68063
/estimated_length=unknown
84694. .84793
/estimated_length=unknown
102882. .102981
/estimated_length=unknown
123664. .123763
/estimated_length=unknown
166751. .166850
/estimated_length=unknown

ORIGIN

Query Match 96.1%; Score 39.4; DB 14; Length 218593;
Best Local Similarity 95.1%; Pred. No. 0.036;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTCGCGGCCGCG 41
|||||
Db 7733 AAGCCTCCGATGCCAGTCCCTCATCGTCGCGGCCGCG 7693
|||||

RESULT 65
AC141401

LOCUS AC141401 192549 bp DNA linear HTG 14-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1000N11, WORKING DRAFT
SEQUENCE, 14 unordered pieces.

ACCESSION AC141401
VERSION AC141401.1 GI:289511147
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 192549)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192549)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission

JOURNAL

COMMENT

Submitted (14-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information

Center Project Name: 1678827
Center clone name: RPCI-11_1000N11

Summary Statistics

Consensus quality: 186509 bases at least Q40
Consensus quality: 188167 bases at least Q30
Consensus quality: 189310 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 191249; sum-of-contigs estimation
Quality coverage: 4.93 in Q20 bases; agarose-fp estimation
Quality coverage: 4.54 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2751: contig of 2751 bp in length
* 2752 2851: gap of unknown length
* 2852 5567: contig of 2716 bp in length
* 5568 5667: gap of unknown length
* 5668 9517: contig of 3850 bp in length
* 9518 9617: gap of unknown length
* 9618 14758: contig of 5141 bp in length
* 14759 14858: gap of unknown length
* 14859 21951: contig of 7093 bp in length
* 21952 22051: gap of unknown length
* 22052 34179: contig of 12128 bp in length
* 34180 34279: gap of unknown length
* 34280 43482: contig of 9203 bp in length
* 43483 43582: gap of unknown length
* 43583 53114: contig of 9532 bp in length
* 53115 53214: gap of unknown length
* 53215 66390: contig of 13176 bp in length
* 66391 66490: gap of unknown length
* 66491 83717: contig of 17227 bp in length
* 83718 83817: gap of unknown length
* 83818 109611: contig of 25794 bp in length
* 109612 109711: gap of unknown length
* 109712 140463: contig of 30752 bp in length
* 140464 140563: gap of unknown length
* 140564 164642: contig of 24079 bp in length
* 164643 164742: gap of unknown length
* 164743 192549: contig of 27807 bp in length.

FEATURES

source

1. .192549
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1000N11"
/clone_lib="RPCI human BAC library 11"
2752. .2851
/estimated_length=unknown
5568. .5667
/estimated_length=unknown
9518. .9617
/estimated_length=unknown
14759. .14858
/estimated_length=unknown
21952. .22051
/estimated_length=unknown
34180. .34279

gap

gap

gap

gap

gap

gap

gap /estimated_length=unknown
43483. .43582
gap /estimated_length=unknown
53115. .53214
gap /estimated_length=unknown
66391. .66490
gap /estimated_length=unknown
83718. .83817
gap /estimated_length=unknown
109612. .109711
gap /estimated_length=unknown
140464. .140563
gap /estimated_length=unknown
164643. .164742
gap /estimated_length=unknown

ORIGIN

Query Match 92.2%; Score 37.8; DB 14; Length 192549;
Best Local Similarity 92.7%; Pred. No. 0.11;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
|||||
Db 109263 AAGCTCCGGATGCCAGTCCATCATCGCTGGCCCGGTCTCG 109303
|||||

RESULT 66
AC138872

LOCUS AC138872 131818 bp DNA linear HTG 21-JAN-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-16405, WORKING DRAFT
SEQUENCE, 13 unordered pieces.

ACCESSION AC138872
VERSION AC138872.1 GI:27805284
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 131818)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 131818)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 469682
Center clone name: RPCI-11_16405

Summary Statistics
Consensus quality: 127808 bases at least Q40
Consensus quality: 128485 bases at least Q30
Consensus quality: 129118 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 130618; sum-of-contigs estimation
Quality coverage: 9.99 in Q20 bases; agarose-fp estimation
Quality coverage: 13.77 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1275: contig of 1275 bp in length
* 1276: gap of unknown length
* 1376: contig of 1208 bp in length
* 2584: gap of unknown length
* 2684: contig of 1310 bp in length
* 3994: gap of unknown length
* 4094: contig of 2051 bp in length
* 6145: gap of unknown length
* 6245: contig of 1836 bp in length
* 8081: gap of unknown length
* 8181: contig of 2041 bp in length
* 10222: gap of unknown length
* 10322: contig of 3053 bp in length
* 13375: gap of unknown length
* 13475: contig of 4244 bp in length
* 17719: gap of unknown length
* 17819: contig of 5537 bp in length
* 23356: gap of unknown length
* 23456: contig of 15793 bp in length
* 39249: gap of unknown length
* 39349: contig of 17361 bp in length
* 56710: gap of unknown length
* 56810: contig of 18249 bp in length
* 75059: gap of unknown length
* 75159: contig of 56660 bp in length.

FEATURES
Location/Qualifiers
1. .131818
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone_lib="RPCI human BAC library 11"
1276. .1375
/estimated_length=unknown
2584. .2683
/estimated_length=unknown
3994. .4093
/estimated_length=unknown
6145. .6244
/estimated_length=unknown
8081. .8180
/estimated_length=unknown
10222. .10321
/estimated_length=unknown
13375. .13474
/estimated_length=unknown
17719. .17818
/estimated_length=unknown
23356. .23455
/estimated_length=unknown
39249. .39348
/estimated_length=unknown
56710. .56809
/estimated_length=unknown
75059. .75158
/estimated_length=unknown

ORIGIN

Query Match 88.8%; Score 36.4; DB 14; Length 131818;
Best Local Similarity 94.7%; Pred. No. 0.31;
Matches 36; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
|||||
Db 56520 AAGCTCCGGATGACAGTCCCTCATCGCTGGCCCGGTC 56557
|||||

RESULT 67
AC140805

LOCUS AC140805 51437 bp DNA linear HTG 03-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone LA16c-374G11, WORKING DRAFT
SEQUENCE, 11 unordered pieces.

AC140805
AC140805.1 GI:28631186
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 51437)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 51437)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1223059
Center clone name: LANL-16c_374G11

Summary Statistics
Consensus quality: 44663 bases at least Q40
Consensus quality: 46358 bases at least Q30
Consensus quality: 47357 bases at least Q20
Estimated insert size: 40000; agarose-fp estimation
Estimated insert size: 50437; sum-of-contigs estimation
Quality coverage: 14.38 in Q20 bases; agarose-fp estimation
Quality coverage: 11.4 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1000: contig of 1000 bp in length
* 1001 1100: gap of unknown length
* 1101 2330: contig of 1230 bp in length
* 2331 2430: gap of unknown length
* 2431 3461: contig of 1031 bp in length
* 3462 3561: gap of unknown length
* 3562 4768: contig of 1207 bp in length
* 4769 4868: gap of unknown length
* 4869 5890: contig of 1022 bp in length
* 5891 5990: gap of unknown length
* 5991 7171: contig of 1181 bp in length
* 7172 7271: gap of unknown length
* 7272 8793: contig of 1522 bp in length
* 8794 8893: gap of unknown length
* 8894 14430: contig of 5537 bp in length
* 14431 14530: gap of unknown length
* 14531 29913: contig of 15383 bp in length
* 29914 30013: gap of unknown length
* 30014 32595: contig of 2582 bp in length
* 32596 32696: gap of unknown length
* 32696 51437: contig of 18742 bp in length.
Location/Qualifiers
1. .51437
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="LA16c-374G11"
/clone_lib="Los Alamos human chromosome 16 cosmid
libraries; LA16NC01 and LA16NC02"
1001. .1100
gap

/estimated_length=unknown
2331. .2430
/estimated_length=unknown
3462. .3561
/estimated_length=unknown
4769. .4868
/estimated_length=unknown
5891. .5990
/estimated_length=unknown
7172. .7271
/estimated_length=unknown
8794. .8893
/estimated_length=unknown
14431. .14530
/estimated_length=unknown
29914. .30013
/estimated_length=unknown
32596. .32695
/estimated_length=unknown

ORIGIN

Query Match 88.3%; Score 36.2; DB 14; Length 51437;
Best Local Similarity 90.2%; Pred. No. 0.42;
Matches 37; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGGCGCG 41
|||||
Db 14351 AAGCCTCCGATGCCAGTCCCTCATCGTGGCGGTCGCG 14391
|||||

RESULT 68
AC148537
LOCUS
DEFINITION
AC148537 162696 bp DNA linear HTG 26-MAY-2004
Pan troglodytes clone CH251-160D4, WORKING DRAFT SEQUENCE, 8
ordered pieces.
AC148537
VERSION AC148537.3 GI:47679103
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1 (bases 1 to 162696)
AUTHORS
Eichler,E., Johnson,M., Antonellis,A., Ayele,K., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G.,
Coleman,B., Coleman,H., Daki,N., Engle,J., Guan,X., Gupta,J.,
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B.,
Idol,J.R., Jones,C., Karlins,E., Kim,H., Kwong,P., Laric,P.,
Larson,S., Lee-Lin,S.-Q., Legaspi,R., Madden,M., Maduro,Q.L.,
Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J.,
Mullikin,J.C., Paguirigan,C., Park,M., Portnoy,M.E., Prasad,A.,
Puri,O., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V.,
Vogt,J.L., Wetherby,K.D., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
REFERENCE 2 (bases 1 to 162696)
AUTHORS
Green,E.D.
TITLE
Direct Submission
JOURNAL
Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
REFERENCE 3 (bases 1 to 162696)
AUTHORS
Green,E.D.
TITLE
Direct Submission
JOURNAL
Submitted (26-MAY-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT
On May 26, 2004 this sequence version replaced gi:46849620.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@nhgri.nih.gov

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1053: contig of 1053 bp in length
* 1054 1153: gap of unknown length
* 1154 17390: contig of 16237 bp in length
* 17391 17490: gap of unknown length
* 17491 36178: contig of 18688 bp in length
* 36179 36278: gap of unknown length
* 36279 166278: contig of 130000 bp in length.

FEATURES

source

1. .166278
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-232G22"
/clone_lib="RPCI human BAC library 11"
1054. .1153
/estimated_length=unknown
17391. .17490
/estimated_length=unknown
36179. .36278
/estimated_length=unknown

ORIGIN

Query Match 88.3%; Score 36.2; DB 14; Length 166278;
Best Local Similarity 90.2%; Pred. No. 0.34;
Matches 37; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCGGNCGCG 41
|||||
Db 36623 AAGCTCCGGATGCCCTTCCCTCATCTAGCCCGGTCGCG 36583

RESULT 70

AC141080

LOCUS AC141080 198295 bp DNA linear HTG 07-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-902P10, WORKING DRAFT
SEQUENCE, 4 unordered pieces.

ACCESSION

VERSION

AC141080.1 GI:28875940

KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

JOURNAL

COMMENT

1 (bases 1 to 198295)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 198295)
DOE Joint Genome Institute.
Direct Submission
Submitted (07-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1641242
Center clone name: RPCI-11_902P10

Summary Statistics
Consensus quality: 195612 bases at least Q40
Consensus quality: 196104 bases at least Q30
Consensus quality: 196475 bases at least Q20

Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 197995; sum-of-contigs estimation
Quality coverage: 9.57 in Q20 bases; agarose-fp estimation
Quality coverage: 8.51 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2067: contig of 2067 bp in length
* 2068 2167: gap of unknown length
* 2168 16911: contig of 14744 bp in length
* 16912 17011: gap of unknown length
* 17012 36673: contig of 19662 bp in length
* 36674 36773: gap of unknown length
* 36774 198295: contig of 161522 bp in length.

FEATURES

source

1. .198295
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-902P10"
/clone_lib="RPCI human BAC library 11"
2068. .2167
/estimated_length=unknown
16912. .17011
/estimated_length=unknown
36674. .36773
/estimated_length=unknown

ORIGIN

Query Match 86.3%; Score 35.4; DB 14; Length 198295;
Best Local Similarity 94.6%; Pred. No. 0.57;
Matches 35; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
|||||

Db 197694 CTTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGC 197730

RESULT 71

AC141270/c

LOCUS

AC141270 202023 bp DNA linear HTG 11-MAR-2003
DEFINITION Homo sapiens chromosome 16 clone RP11-1403C5, WORKING DRAFT
SEQUENCE, 16 unordered pieces.

ACCESSION

VERSION

AC141270.1 GI:28913050

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 202023)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
2 (bases 1 to 202023)
DOE Joint Genome Institute.
Direct Submission
Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 2758439

Center clone name: RPCI-11_1403C5

Summary Statistics
Consensus quality: 188196 bases at least Q40
Consensus quality: 193761 bases at least Q30
Consensus quality: 196373 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 200523; sum-of-contigs estimation
Quality coverage: 6.9 in Q20 bases; agarose-fp estimation
Quality coverage: 6.05 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1163: contig of 1163 bp in length
* 1164 1263: gap of unknown length
* 1264 2683: contig of 1420 bp in length
* 2684 2783: gap of unknown length
* 2784 3977: contig of 1194 bp in length
* 3978 4077: gap of unknown length
* 4078 6061: contig of 1984 bp in length
* 6062 6161: gap of unknown length
* 6162 8287: contig of 2126 bp in length
* 8288 8387: gap of unknown length
* 8388 11347: contig of 2960 bp in length
* 11348 11447: gap of unknown length
* 11448 14935: contig of 3488 bp in length
* 14936 15035: gap of unknown length
* 15036 18719: contig of 3684 bp in length
* 18720 18819: gap of unknown length
* 18820 23842: contig of 5023 bp in length
* 23843 23942: gap of unknown length
* 23943 28674: contig of 4732 bp in length
* 28675 28774: gap of unknown length
* 28775 37698: contig of 8924 bp in length
* 37699 37798: gap of unknown length
* 37799 49026: contig of 11228 bp in length
* 49027 49126: gap of unknown length
* 49127 69390: contig of 20264 bp in length
* 69391 69490: gap of unknown length
* 69491 98117: contig of 28627 bp in length
* 98118 98217: gap of unknown length
* 98218 123984: contig of 25767 bp in length
* 123985 124084: gap of unknown length
* 124085 202023: contig of 77939 bp in length.

FEATURES

source

1. .202023
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1403C5"
/clone_lib="RPCI human BAC library 11"
1164. .1263
/estimated_length=unknown
2684. .2783
/estimated_length=unknown
3978. .4077
/estimated_length=unknown
6062. .6161
/estimated_length=unknown
8288. .8387
/estimated_length=unknown
11348. .11447
/estimated_length=unknown
14936. .15035
/estimated_length=unknown
18720. .18819
/estimated_length=unknown

gap 23843. .23942
/estimated_length=unknown
gap 28675. .28774
/estimated_length=unknown
gap 37699. .37798
/estimated_length=unknown
gap 49027. .49126
/estimated_length=unknown
gap 69391. .69490
/estimated_length=unknown
gap 98118. .98217
/estimated_length=unknown
gap 123985. .124084
/estimated_length=unknown

ORIGIN

Query Match 84.4%; Score 34.6; DB 14; Length 202023;
Best Local Similarity 87.8%; Pred. No. 0.98;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
|||||
Db 124133 AAGCTCCGGATAGCAGTCCCTCATCGCTGGCCCGGAGCG 124093

RESULT 72

AC140888/c 159468 bp DNA linear HTG 05-MAR-2003
LOCUS Homo sapiens chromosome 16 clone RP11-1374G10, WORKING DRAFT
DEFINITION SEQUENCE, 12 unordered pieces.

ACCESSION AC140888
VERSION AC140888.1 GI:28849999
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 159468)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159468)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2747404
Center clone name: RPCI-11_1374G10

Summary Statistics
Consensus quality: 154250 bases at least Q40
Consensus quality: 155068 bases at least Q30
Consensus quality: 155682 bases at least Q20
Estimated insert size: 176000; agarose-fp estimation
Estimated insert size: 158368; sum-of-contigs estimation
Quality coverage: 7.76 in Q20 bases; agarose-fp estimation
Quality coverage: 8.62 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1068: contig of 1068 bp in length

* 1069 1168: gap of unknown length
* 1169 2349: contig of 1181 bp in length
* 2350 2449: gap of unknown length
* 2450 3954: contig of 1505 bp in length
* 3955 4054: gap of unknown length
* 4055 6271: contig of 2217 bp in length
* 6272 6371: gap of unknown length
* 6372 15136: contig of 8765 bp in length
* 15137 15236: gap of unknown length
* 15237 21442: contig of 6206 bp in length
* 21443 21542: gap of unknown length
* 21543 29526: contig of 7984 bp in length
* 29527 29626: gap of unknown length
* 29627 37049: contig of 7423 bp in length
* 37050 37149: gap of unknown length
* 37150 48202: contig of 11053 bp in length
* 48203 48302: gap of unknown length
* 48303 60861: contig of 12559 bp in length
* 60862 60961: gap of unknown length
* 60962 106290: contig of 45329 bp in length
* 106291 106390: gap of unknown length
* 106391 159468: contig of 53078 bp in length.

FEATURES
source

Location/Qualifiers
1. .159468
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1374G10"
/clone_lib="RPCI human BAC library 11"
1069. .1168
/estimated_length=unknown
2350. .2449
/estimated_length=unknown
3955. .4054
/estimated_length=unknown
6272. .6371
/estimated_length=unknown
15137. .15236
/estimated_length=unknown
21443. .21542
/estimated_length=unknown
29527. .29626
/estimated_length=unknown
37050. .37149
/estimated_length=unknown
48203. .48302
/estimated_length=unknown
60862. .60961
/estimated_length=unknown
106291. .106390
/estimated_length=unknown

ORIGIN

Query Match 74.1%; Score 30.4; DB 14; Length 159468;
Best Local Similarity 82.5%; Pred. No. 18;
Matches 33; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
||||| ||||||||| ||||| |||||||: ||
Db 61271 AAGCCTACGGATGCCAGTCCATCATCTTTGGCCCTGTAGC 61232

RESULT 73
AX281458/c
LOCUS AX281458 6423 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 122 from Patent WO0177376.
ACCESSION AX281458
VERSION AX281458.1 GI:16608713
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with metastasis
JOURNAL Patent: WO 0177376-A 122 18-OCT-2001;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
source 1. .6423
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 72.7%; Score 29.8; DB 6; Length 6423;
Best Local Similarity 80.5%; Pred. No. 51;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
|| ||||| || || ||||||||| ||||: ||||
Db 1563 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 1523

RESULT 74
AX348742/c

LOCUS AX348742 6423 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 200 from Patent WO0202807.
ACCESSION AX348742
VERSION AX348742.1 GI:18614777
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with cell signalling
JOURNAL Patent: WO 0202807-A 200 10-JAN-2002;
Epigenomics AG (DE)

FEATURES
source

Location/Qualifiers
1. .6423
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 72.7%; Score 29.8; DB 6; Length 6423;
Best Local Similarity 80.5%; Pred. No. 51;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
|| ||||| || || ||||||||| ||||: ||||
Db 1563 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 1523

RESULT 75
AC150732

LOCUS AC150732 187328 bp DNA linear HTG 17-DEC-2004
DEFINITION Papio anubis clone RP41-22E4, WORKING DRAFT SEQUENCE, 12 ordered pieces.
ACCESSION AC150732
VERSION AC150732.2 GI:56693405
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE Papio anubis (olive baboon)
ORGANISM Papio anubis

REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
1 (bases 1 to 187328)
Eichler,E., Johnson,M., Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A., Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H., Engle,J., Gestole,M., Guan,X., Gupta,J., Gutierrez,P., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G., Hurle,B., Idol,J.R., Jones,C., Kwong,P., Laric,P.,

Larson, S., Lee-Lin, S.-Q., Legaspi, R., Madden, M., Maduro, Q.L.,
Maduro, V.B., Margulies, E.H., Masiello, C., Maakeri, B., McDowell, J.,
Mullikin, J.C., Oestreicher, J.S., Park, M., Portnoy, M.E., Prasad, A.,
Puri, O., Reddix-Dugue, N., Rosas, B., Schandler, K., Schueler, M.G.,
Sison, C., Stantripop, S., Stephen, E., Taye, A., Thomas, J.W.,
Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and
Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 187328)
Green, E.D.
Direct Submission
Submitted (04-AUG-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 187328)
Green, E.D.
Direct Submission
Submitted (17-DEC-2004) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Dec 17, 2004 this sequence version replaced gi:50950307.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
Center project name: hdd
Center clone name: 022E04

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is generally based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182980 bases at least Q40
Consensus quality: 184487 bases at least Q30
Consensus quality: 185588 bases at least Q20
Insert size: 205000; agarose-fp
Insert size: 186228; sum-of-contigs
Quality coverage: 8.35x in Q20 bases; agarose-fp
Quality coverage: 9.19x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 680: contig of 680 bp in length
* 681 780: gap of unknown length
* 781 13903: contig of 13123 bp in length
* 13904 14003: gap of unknown length
* 14004 23574: contig of 9571 bp in length
* 23575 23674: gap of unknown length
* 23675 26625: contig of 2951 bp in length
* 26626 26725: gap of unknown length
* 26726 33344: contig of 6619 bp in length
* 33345 33444: gap of unknown length
* 33445 39599: contig of 6155 bp in length

* 39600 39699: gap of unknown length
* 39700 79220: contig of 39521 bp in length
* 79221 79320: gap of unknown length
* 79321 110884: contig of 31564 bp in length
* 110885 110984: gap of unknown length
* 110985 139631: contig of 28647 bp in length
* 139632 139731: gap of unknown length
* 139732 158383: contig of 18652 bp in length
* 158384 158483: gap of unknown length
* 158484 160485: contig of 2002 bp in length
* 160486 160585: gap of unknown length
* 160586 187328: contig of 26743 bp in length.
FEATURES
source
1.187328
/organism="Papio anubis"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
/clone="RP41-22E4"
/clone_lib="RP41"
/note="BAC resource: <http://bacpac.chori.org/>"
1.680
misc_feature
/note="assembly_fragment
clone_end:T7
vector_side:left"
681..780
/estimated_length=unknown
781..13903
/note="assembly_fragment"
13904..14003
/estimated_length=unknown
14004..23574
/note="assembly_fragment"
23575..23674
/estimated_length=unknown
23675..26625
/note="assembly_fragment"
26626..26725
/estimated_length=unknown
26726..33344
/note="assembly_fragment"
33345..33444
/estimated_length=unknown
33445..39599
/note="assembly_fragment"
39600..39699
/estimated_length=unknown
39700..79220
/note="assembly_fragment"
79221..79320
/estimated_length=unknown
79321..110884
/note="assembly_fragment"
110885..110984
/estimated_length=unknown
110985..139631
/note="assembly_fragment"
139632..139731
/estimated_length=unknown
139732..158383
/note="assembly_fragment"
158384..158483
/estimated_length=unknown
158484..160485
/note="assembly_fragment"
160486..160585
/estimated_length=unknown
160586..187328
/note="assembly_fragment
clone_end:SP6
vector_side:right"

ORIGIN

Query Match 70.7%; Score 29; DB 14; Length 187328;

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GUDE
Center clone name: CH230-372F11
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 164395 bases at least Q40
Consensus quality: 165606 bases at least Q30
Consensus quality: 166400 bases at least Q20
Estimated insert size: 167474; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 172229: contig of 172229 bp in length
* 172230 172329: gap of unknown length
* 172330 173370: contig of 1041 bp in length.
FEATURES
 source
 Location/Qualifiers
 1..173370
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-372F11"
 1..2547
 /note="wgs_end_extension
 clone_end:T7"
 3694..4596
 /note="clone_boundary
 clone_end:T7"
 site:
 end_sequence:BZ220031"
 complement(164094..165012)
 /note="clone_boundary
 clone_end:Sp6
 site:
 end_sequence:BZ220033"
 17121..172229
 /note="wgs_end_extension
 clone_end:Sp6"
 172230..172329
 /estimated_length=unknown
ORIGIN
Query Match 61.5%; Score 25.2; DB 14; Length 173370;
Best Local Similarity 76.3%; Pred. No. 6.4e+02;
Matches 29; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
 ||||| ||||| ||||| ||||| ||||| ||: ||
Db 149617 CCTCAGATGCCAGTTCCTCATCTCTGCAGGAAGG 149654

RESULT 78
AC126160
LOCUS AC126160 192405 bp DNA linear HTG 19-NOV-2002
DEFINITION Rattus norvegicus clone CH230-513K6, WORKING DRAFT SEQUENCE.
ACCESSION AC126160
VERSION AC126160.3 GI:25074406
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 192405)
REFERENCE
AUTHORS
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jollivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokeme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 192405)
Worley,K.C.
Direct Submission
Submitted (04-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 192405)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:22855903.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: KAGX
Center clone name: CH230-513K6

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 172657 bases at least Q40
Consensus quality: 174253 bases at least Q30
Consensus quality: 175360 bases at least Q20
Estimated insert size: 178085; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 192405: contig of 192405 bp in length.

FEATURES
source

Location/Qualifiers
1. .192405
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-513K6"

misc_feature

1. .2212
/note="wgs_contig"

misc_feature

6017. .7570
/note="wgs_contig"

misc_feature

complement(179873..180733)
/note="clone boundary
clone_end:Sp6
site:
end sequence:RXBVJ63TV"

misc_feature

181620..183234
/note="wgs_end_extension
clone_end:Sp6"

misc_feature

191336..192405
/note="wgs_end_extension
clone_end:Sp6"

ORIGIN

Query Match 61.5%; Score 25.2; DB 14; Length 192405;
Best Local Similarity 76.3%; Pred. No. 6.3e+02;
Matches 29; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 8518 CCTCAGATGCCAGTTCCTCATCTCTGCGAGGGAAGG 8555

RESULT 79
AY574424/c

LOCUS AY574424 371 bp DNA linear ENV 11-APR-2004
DEFINITION Uncultured bacterium isolate DGGE gel band 8-e-2 16S ribosomal RNA
gene, partial sequence.
ACCESSION AY574424

VERSION
KEYWORDS

AY574424.1 GI:46242060
ENV.

SOURCE
ORGANISM

uncultured bacterium
uncultured bacterium
Bacteria; environmental samples.

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 371)
Holben,W.E., Feris,K.P., Kettunen,A. and Apajalahti,J.H.
GC Fractionation Enhances Microbial Community Diversity Assessment
and Detection of Minority Populations of Bacteria by Denaturing
Gradient Gel Electrophoresis
Appl. Environ. Microbiol. 70 (4), 2263-2270 (2004)
15066821

JOURNAL
PUBMED

2 (bases 1 to 371)

REFERENCE
AUTHORS
TITLE

Holben,W.E., Feris,K.P., Kettunen,A. and Apajalahti,J.H.A.
Direct Submission
Submitted (17-MAR-2004) Microbial Ecology Program, The University
of Montana, Division of Biological Sciences, HS 104, Missoula, MT
59812, USA

JOURNAL

FEATURES
source

Location/Qualifiers
1. .371
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolate="DGGE gel band 8-e-2"
/isolation_source="chicken gastrointestinal tract"
/specific_host="chicken"
/db_xref="taxon:77133"
/environmental_sample
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/product="16S ribosomal RNA"

rrna

ORIGIN

Query Match 61.0%; Score 25; DB 3; Length 371;
Best Local Similarity 73.2%; Pred. No. 2.3e+03;
Matches 30; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 84 AAGCCCCGGATTTCACCTCCCACTGCGCGGCCCGCTGCG 44

RESULT 80
AR621724/c

LOCUS
DEFINITION

AR621724 1424 bp DNA linear PAT 14-FEB-2005
Sequence 3125 from patent US 6833447.

ACCESSION
VERSION

AR621724
AR621724.1 GI:59726206

KEYWORDS
SOURCE

Unknown.
Unknown.

ORGANISM

Unclassified.

REFERENCE
AUTHORS

1 (bases 1 to 1424)
Goldman,B.S., Hinkle,G.J., Slater,S.C. and Wiegand,R.C.

TITLE
JOURNAL

Myxococcus xanthus genome sequences and uses thereof
Patent: US 6833447-A 3125 21-DEC-2004;
Monsanto Technology, LLC; St. Louis, MO

FEATURES
source

Location/Qualifiers
1. .1424
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 60.0%; Score 24.6; DB 6; Length 1424;
Best Local Similarity 74.4%; Pred. No. 2.4e+03;
Matches 29; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 606 GCGCGCGGGGCCAGGCCCTCGATGCTGGCCCGGTAGCG 568

RESULT 81

AR619747/c
LOCUS

AR619747 15268 bp DNA linear PAT 14-FEB-2005

FEATURES source	Brazil	Location/Qualifiers	
		1. .12393	
		/organism="Xanthomonas campestris pv. campestris str. ATCC 33913"	
		/mol_type="genomic DNA"	
		/strain="ATCC 33913"	
		/db_xref="ATCC:33913"	
		/db_xref="taxon:190485"	
		/note="pathovar: campestris"	
gene		88. .291	
CDS		/gene="XCC2999"	
		88. .291	
		/gene="XCC2999"	
		/note="putative; ORF located using Glimmer/Genemark"	
		/codon_start=1	
		/transl_table=11	
		/product="hypothetical protein"	
		/protein_id="AAM42271.1"	
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		/translation="MYVCNPFVCGASYTGHTELTGLCSPSGMPHAHSDLPPTPGYLRA MALKAYREVANAQMDDLDAAP"	
gene		470. .595	
CDS		/gene="XCC3000"	
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		/gene="XCC3000"	
		/note="putative; ORF located using Glimmer/Genemark"	
		/codon_start=1	
		/transl_table=11	
		/product="hypothetical protein"	
		/protein_id="AAM42272.1"	
		/db_xref="GI:21114212"	
		/translation="MAQLMLRGLLMSRTHSMHALATDAAMELLLDYGSVAREISA"	
gene		592. .831	
CDS		/gene="XCC3001"	
		592. .831	
		/gene="XCC3001"	
		/note="putative; ORF located using Glimmer/Genemark"	
		/codon_start=1	
		/transl_table=11	
		/product="hypothetical protein"	
		/protein_id="AAM42273.1"	
		/db_xref="GI:21114213"	
		/translation="MSQSNGWATAQAPRFVDAPSQSQYVAPHKKREQADVLRQVE AHLASGGAYEVITTPRPIGKSLAALALRSTVRKG"	
gene		859. .3522	
CDS		/gene="orf37"	
		/note="synonym: XCC3002"	
		859. .3522	
		/gene="orf37"	
		/note="identified by sequence similarity; putative; ORF located using Blastx/Glimmer/Genemark"	
		/codon_start=1	
		/transl_table=11	
		/product="phage-related protein"	
		/protein_id="AAM42274.1"	
		/db_xref="GI:21114214"	
		/translation="MLQLRDYGLKHSRGSYMRGGVCPACSKKELYTFEPKPPWIK CGREAKCGHELHVKDLYDDLFDWSKRFPMTQASPTASADAYLESSRGFALAPRLGY TQESYYDIKVKEGTATRFALDKGQWVERLIDRPHRFGQKARFAPGKSYAGAWWCAP AAAEMLRTATEWIVEGIFDAIALLQHGVCAMVSCNAFPDESRLQLAKLRAGNLPT LVWGLDNEPGARDYTHKHARRADALGFNSRAALIAQPVTKKIDWNDLHLRAQAGDS QKQWDAALTEARYQGDLLMARSAIEKGLLMYDHNQASDFWLEYRSRLYWFEDTVRFE KLRLDVEPEEDSEIDPDKLIRRAACSVNKIANCYPEALYFQRQVTDSEWYFRID FPHDANSVKGFTTGGHISASEFFKKRLISLAAGAMFTGSGHQLDRLIEEQTEAIKTVE AIDFVGYSKEHRAYLLGDIVRDGEVVTANEEDYFSFKLRLKSTQKSIRLEIQRDPE AFRMDWLPWLWQCFGTHGMVAMTFWFGSLFAEQIRAGHKSFPFLEATGEAGAGKTTLL TFLWKLGRSDYEGFDPKASKAGARAMQISGMPVVLLEADRSEPDKAHAKTFEWD ELKDFGGGTLATRGVRNGGNDTYEPPFRGTIVISQNAAVDASEAILRIIVKLHPKRP QVTTESRIAADNLNALQVEELSHFLIKAVRCEGAILEKFAERVKFYEARLREKFDLRL ERVINKHAQMLALLDCLRMVITIPEEMIKATRDALLEMAFERQKAISADHAQVNEFWE VVEYLEATGNKPKPVNHSRDASRIAINLNQFAKAAQFSQVVPDLKVLRLGLLADSRRH KLVSANTAVNSAVLTNGFGAGTTVKCWVFSK"	

gene	4103. .4327	
CDS	/gene="XCC3003"	
	4103. .4327	
	/gene="XCC3003"	
		/note="putative; ORF located using Glimmer/Genemark"
		/codon_start=1
		/transl_table=11
		/product="hypothetical protein"
		/protein_id="AAM42275.1"
		/db_xref="GI:21114215"
		/translation="MMQGYVLAMLHSDAQHDVAPVLIACEATGFDVLLGGDAHSVVL GRLHVCMRVDLAVDVLTLWLQKQARANGAAR"
gene	4324. .4587	
CDS	/gene="XCC3004"	
	4324. .4587	
	/gene="XCC3004"	
		/note="putative; ORF located using Glimmer/Genemark"
		/codon_start=1
		/transl_table=11
		/product="hypothetical protein"
		/protein_id="AAM42276.1"
		/db_xref="GI:21114216"
		/translation="MNSVRATAYPEDADYTISEEEHDLRWVQQAASLLATLNHDIAT RAGISHDGIAAVADFMRELLDIACNARHVREPTKPTGADLI"
gene	4666. .5076	
CDS	/gene="XCC3005"	
	4666. .5076	
	/gene="XCC3005"	
		/note="putative; ORF located using Glimmer/Genemark"
		/codon_start=1
		/transl_table=11
		/product="hypothetical protein"
		/protein_id="AAM42277.1"
		/db_xref="GI:21114217"
		/translation="MQOHAVTRSQISSAGPGQEATTPVEAAFDLAVGKDCSAIATLYI THDAVVVVAALTMGQSSAAQRWERRRPGKGKWLISGPRFLTSEAHRI SNALAKFMD DLDPFPDLANMLPRRPPTAAAEAAIAAAAREVAHA"
gene	5090. .5245	
CDS	/gene="XCC3006"	
	5090. .5245	
	/gene="XCC3006"	
		/note="putative; ORF located using Glimmer/Genemark"
		/codon_start=1
		/transl_table=11
		/product="conserved hypothetical protein"
		/protein_id="AAM42278.1"
		/db_xref="GI:21114218"
		/translation="MIAPTIGGALLYRLWISRPTTAHIGLAVGQIPQRLRRRRAMAV RRMVAHG"
gene	5238. .5513	
CDS	/gene="XCC3007"	
	5238. .5513	
	/gene="XCC3007"	
		/note="putative; ORF located using Glimmer/Genemark"
		/codon_start=1
		/transl_table=11
		/product="conserved hypothetical protein"
		/protein_id="AAM42279.1"
		/db_xref="GI:21114219"
		/translation="MAESIVVYGPMAKSGKSLNAEATCQAYGLKRVVVELDERLQKGD WQLSQNDVVMLTNDQALAEARTQMRVKTVAITEARLRVGAARALR"
gene	5606. .5755	
CDS	/gene="XCC3008"	
	5606. .5755	
	/gene="XCC3008"	
		/note="putative; ORF located using Glimmer/Genemark"
		/codon_start=1
		/transl_table=11
		/product="conserved hypothetical protein"
		/protein_id="AAM42280.1"
		/db_xref="GI:21114220"
		/translation="MLNRHDWLADMDYTTIAQALDRIDEDTTAHLRQAERAIRNGAGAA BENTA"

gene	5932. .6024				
CDS	/gene="XCC3009"				
	5932. .6024				
	/gene="XCC3009"				
/note="putative; ORF located using Glimmer/Genemark"					
Query Match	59.0%; Score 24.2; DB 1; Length 12393;				
Best Local Similarity	75.7%; Pred. No. 2.1e+03;				
Matches	28; Conservative	1; Mismatches	8; Indels	0; Gaps	0;
QY	5	CTCGGATGCCAGTCCCTCATCGCTGGCCGCGCG	41		
Db	11465	CGCGGATGCCGTCGCTTGCGCGTGGCCCTGTGCGG	11429		
RESULT 85					
AC020333					
LOCUS	AC020333	33483 bp	DNA	linear	HTG 03-JAN-2000
DEFINITION	Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.				
ACCESSION	AC020333				
VERSION	AC020333.1 GI:6664564				
KEYWORDS	HTG; HTGS_PHASE2.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 33483)				
AUTHORS	Adams,M. and Venter,J.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA				
COMMENT	This sequence was identified as CDM:10212803 by the submitter. For more information on this record e-mail to fly@celera.com.				
FEATURES	* NOTE: This is a 'working draft' sequence.				
	* This sequence will be replaced				
	* by the finished sequence as soon as it is available and				
	* the accession number will be preserved.				
	Location/Qualifiers				
source	1. .33483				
ORIGIN	/organism="Drosophila melanogaster"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:7227"				
Query Match	59.0%; Score 24.2; DB 14; Length 33483;				
Best Local Similarity	75.7%; Pred. No. 1.7e+03;				
Matches	28; Conservative	1; Mismatches	8; Indels	0; Gaps	0;
QY	3	GCCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGCG	39		
Db	28360	GTCTCCGGATGCCACACCCACAGCGCTGGAGTGGCGG	28396		
RESULT 86					
BA000040_71					
WPCOMMENT					
Sequence split into 91 fragments LOCUS BA000040 Accession BA000040					
Fragment Name Begin End					
BA000040_00 1 110000					
BA000040_01 100001 210000					
BA000040_02 200001 310000					
BA000040_03 300001 410000					
BA000040_04 400001 510000					
BA000040_05 500001 610000					
BA000040_06 600001 710000					
BA000040_07 700001 810000					
BA000040_08 800001 910000					
BA000040_09 900001 1010000					
BA000040_10 1000001 1110000					
BA000040_11 1100001 1210000					
BA000040_12 1200001 1310000					
BA000040_13 1300001 1410000					

1400001	1510000
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1600001	1710000
1700001	1810000
1800001	1910000
1900001	2010000
2000001	2110000
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8500001	8610000
8600001	8710000

BA000040_87 8700001 8810000
BA000040_88 8910000
BA000040_89 9010000
BA000040_90 9105828
Continuation (72 of 91) of BA000040 from base 7100001 (BA000040 Bradyrhizobium japonicum)

Query Match 59.0%; Score 24.2; DB 1; Length 110000;
Best Local Similarity 75.7%; Pred. No. 1.4e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
||||| ||||||| ||| ||| |||||:||||
Db 62568 CCTCCTGGTGCCAGTCCAGCAGCGAGCGCCCGTGCGC 62604

RESULT 87
CP000050_13
WPCOMMENT

Sequence split into 52 fragments LOCUS CP000050 Accession CP000050

Fragment Name	Begin	End
CP000050_00	1	110000
CP000050_01	100001	210000
CP000050_02	200001	310000
CP000050_03	300001	410000
CP000050_04	400001	510000
CP000050_05	500001	610000
CP000050_06	600001	710000
CP000050_07	700001	810000
CP000050_08	800001	910000
CP000050_09	900001	1010000
CP000050_10	1000001	1110000
CP000050_11	1100001	1210000
CP000050_12	1200001	1310000
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CP000050_15	1500001	1610000
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CP000050_40	4000001	4110000
CP000050_41	4100001	4210000
CP000050_42	4200001	4310000
CP000050_43	4300001	4410000
CP000050_44	4400001	4510000
CP000050_45	4500001	4610000
CP000050_46	4600001	4710000
CP000050_47	4700001	4810000
CP000050_48	4800001	4910000
CP000050_49	4900001	5010000
CP000050_50	5000001	5110000
CP000050_51	5100001	5148708

Continuation (14 of 52) of CP000050 from base 1300001 (CP000050 Xanthomonas campestris p

Query Match 59.0%; Score 24.2; DB 1; Length 110000;
Best Local Similarity 75.7%; Pred. No. 1.4e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||||||| ||| ||| |||||:||||
Db 84070 CGCCGGATGGCGCTGCTGGCGCTGGCCCTGTGCGG 84106

RESULT 88
AC093438/c

LOCUS
DEFINITION

ACCESSION
AC093438

VERSION
AC093438.2 GI:21397245

KEYWORDS
HTG.

SOURCE
ORGANISM

REFERENCE
AUTHORS

REFERENCE
AUTHORS

REFERENCE
AUTHORS

REFERENCE
AUTHORS

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Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

Unpublished

3 (bases 1 to 167344)

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Tansey, J., Taylor, C., Taylor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission

Submitted (24-AUG-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 167344)

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,

Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (29-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

5 (bases 1 to 167344)

Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (03-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Query Match 59.0%; Score 24.2; DB 2; Length 167344;

Best Local Similarity 75.7%; Pred. No. 1.3e+03;

Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCTCATCGTGGCCCGNCG 39

| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

VERSION	AC108990.4	GI:23101240	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.		
REFERENCE	1	(bases 1 to 254095)	
AUTHORS	Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lourenshewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokeleneh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.		
	Direct Submission		
JOURNAL	Unpublished		
REFERENCE	2	(bases 1 to 254095)	
AUTHORS	Worley,K.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		
	3	(bases 1 to 254095)	
REFERENCE	Rat Genome Sequencing Consortium.		
AUTHORS	Direct Submission		
TITLE	Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		
JOURNAL	On Sep 18, 2002 this sequence version replaced gi:21737656.		
COMMENT	The sequence in this assembly is a combination of BAC based reads		
	and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.		
	----- Genome Center		
	Center: Baylor College of Medicine		
	Center code: BCM		
	Web site: http://www.hgsc.bcm.tmc.edu/		
	Contact: hgsc-help@bcm.tmc.edu		
	----- Project Information		
	Center project name: GPNF		
	Center clone name: CH230-239N24		
	----- Summary Statistics		
	Assembly program: Phrap; version 0.990329		
	Consensus quality: 221155 bases at least Q40		
	Consensus quality: 223317 bases at least Q30		
	Consensus quality: 224925 bases at least Q20		
	Estimated insert size: 242501; sum-of-contigs estimation		
	Quality coverage: 4x in Q20 bases; sum-of-contigs estimation		

	* NOTE: Estimated insert size may differ from sequence length		
	* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).		
	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 3 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
	* 1 234792: contig of 234792 bp in length		
	* 234793 234892: gap of unknown length		
	* 234893 252933: contig of 18041 bp in length		
	* 252934 253033: gap of unknown length		
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	Best Local Similarity 75.7%; Pred. No. 1.2e+03;		
	Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;		
QY	2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38		
Db	209977 ACCCTCCAGATCCAGTCCCTCTCTCACTGCAGGGCC 209941		
RESULT 91			
AE003541/c			
LOCUS	AE003541 265524 bp DNA linear INV 09-AUG-2005		
DEFINITION	Drosophila melanogaster chromosome 3L, section 44 of 83 of the complete sequence.		
ACCESSION	AE003541 AE002602 AE014296		


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/db_xref="FLYBASE:FBgn0036278"
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31348..31531,36114..36887))
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/old_locus_tag="CG10698"
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YSLMFHLSIADVLVTWFCITGEAAWCYTVQWLANELTCKLVKLFQMFSLYSTYVLVL
IGVDRWIAVKYPMKSLNMAKCHRLLGTYILSLVLSLPQFFIFHVARGPFFVEEFYC
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AVTQVDGTGGSSRQMRAFRQOSYRSSSNGTAGPGAAPFKEQVGLLHVGPNGTPGGS
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Query Match          59.0%; Score 24.2; DB 2; Length 265524;
Best Local Similarity 75.7%; Pred. No. 1.2e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGNCG 39
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Db 166930 GTCTCCGGATGCCACACCCACAGCGCTGGAGTGGCG 166894
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WPCOMMENT
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BA000030_02       200001    310000
BA000030_03       300001    410000
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BA000030_05       500001    610000
BA000030_06       600001    710000
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BA000030_90 900001 9025608

Continuation (6 of 91) of BA000030 from base 500001 (BA000030 Streptomyces avermitilis M

Query Match 58.5%; Score 24; DB 1; Length 110000;
Best Local Similarity 72.5%; Pred. No. 1.6e+03;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGC 40
Db 96716 ACGTCTCCGACGCCAGGCCACCTCGCAGGCCCGGCTGGC 96755

RESULT 93
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WPCOMMENT

Sequence split into 360 fragments LOCUS AP008208 Accession AP008208

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Query Match 58.5%; Score 24; DB 14; Length 132830;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;

Matches 26; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 9 GGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
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Db 106172 GGATGTGAGTCCCCAACGCTGGCCCGGTAGC 106141

RESULT 95

AP005055

LOCUS

DEFINITION

AP005055

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AP005055 137841 bp DNA linear PLN 16-NOV-2004

Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,

PAC clone:P0684A08.

AP005055

AP005055.2 GI:46309311

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC

clone:P0684A08

Published Only in Database (2002)

2 (bases 1 to 137841)

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Submitted (03-APR-2002) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannonдай

2-1-2, Tsukuba, Ibaraki, 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

On Apr 8, 2004 this sequence version replaced gi:19919065.

Genes were predicted from the integrated results of the following:

GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH

(http://www.softberry.com/), GeneMark.hmm

(http://opal.biology.gatech.edu/GeneMark/), GlimmerM

(http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM

(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor

(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4

(http://globin.cse.psu.edu/html/docs/sim4.html), gap2

(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The

genomic sequence was searched against NCBI NonRedundant protein

database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA

sequence database at RGP or DBJ. Protein homologies of the coding

regions were searched against NCBI NonRedundant Protein database

with BLASTP. ESTs represent the identified cDNA sequences using

Full-length cDNAs represent the identified cDNA sequences using

BLASTN with the corresponding DBJ accession no. and RGP clone ID.

BLASTN with the corresponding DBJ accession no.

A gene with identity or significant homology to a protein is

classified based on the protein name to indicate the homology level

such as same name, 'putative-' and '-like protein'. A gene without

significant homology to any protein but with full-length cDNA or

EST homology (covering almost the entire length of partial

sequence) is classified as an 'unknown' protein. A gene predicted

by two or more gene prediction programs is classified as a

'hypothetical' protein according to IRGSP standard. A gene

predicted by a single gene prediction program is also classified as

a probable 'hypothetical' protein and is included as a

miscellaneous feature of the sequence.

The orientation of the sequence is from T7 to SP6 of the PAC clone.

This sequence of P0684A08 clone has an overlap with OJ1725_H08

(DDBJ: AP004858) clone at 5' end and with OJ1493_H11 (DDBJ:

AP004188) at 3' end. Detailed information on overlap and assembly

quality together with annotation of this entry is available at

http://rgp.dna.affrc.go.jp/GenomeSeq.html.

FEATURES

source

1. .137841

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complement (<1599..>1817)

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/note="start and end point are not identified"

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/translation="MAHLTPGLVAVNVFPRRHHLASTGCSLGSNGTVFAQASSKSG

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EKCDVQLSGGTLCSEAVPASNETVCPILNSDNTNSDSDVDPSFVAEKKGSJETVV

TEDGKKQAMDVTEDEKKQDVDEGSSLEEMPLRSAFSYTHEVKERNILKKYVGTH

NFNFTTRTKAEDPAAKRFIISFAADRVVNLGDIDFIRCEVVGQSFMHLQIRKMIGLA

VAVMRNCAPESIYDVAFRKDVNLNVPTAPEVGLYLDECMFTSYNKKWKDSHEAVSMEP

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complement (6394..7421)

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/note="supported by full-length cDNA(s): AK060958"

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TNHSVCAALRFVGEALVFTTVVSLEFWILOAVREAEVHEQARVPVGAREQGGDGGPGM

RAPA"

misc_feature /gene="OJ1725_H08.1" complement(join(1970..2000,2094..2344,3414..3458,4888..4942,5289..5341)) /gene="OJ1725_H08.1" /note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard" gene complement(7201..7629) /gene="OJ1725_H08.2" complement(<7201..>7629) /gene="OJ1725_H08.2" /note="start and end point are not identified" CDS complement(7201..7629) /gene="OJ1725_H08.2" /note="predicted by FGENESH etc." /codon_start=1 /product="hypothetical protein" /protein_id="BAD28122.1" /db_xref="GI:50252126" /translation="MASRCFFPREAEAGGRHHHQSKAABEALEQLHHGGRVLSREDV GGAVRVKIVSKRELKHMVAALGSGTGGGAVAAAAVTAAGERHRQRAAGGAGGPGA EQLQSLRRRSMRRAEAARMQANGEWEPGLQSIPEEYV" join(9896..9962,10064..10203) /gene="OJ1725_H08.3" join(9896..9962,10064..10203) /gene="OJ1725_H08.3" /note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard" gene complement(10949..11196) /gene="OJ1725_H08.4" complement(join(<10949..11031,11127..>11196)) /gene="OJ1725_H08.4" /note="start and end point are not identified" CDS complement(join(10949..11031,11127..11196)) /gene="OJ1725_H08.4" /note="predicted by GeneMark.hmm etc." /codon_start=1 /product="hypothetical protein" /protein_id="BAD28123.1" /db_xref="GI:50252127" /translation="MPCRDCGDAAIPRCVDVRELRADARADLTPSIGWAARRSPRAG GDRDS" complement(12736..13504) /gene="OJ1725_H08.5" complement(12736..13504) /gene="OJ1725_H08.5" /note="supported by full-length cDNA(s): AK058228" complement(12739..13489) /gene="OJ1725_H08.5" /note="supported by full-length cDNA(s): AK099066" complement(13017..13409) /gene="OJ1725_H08.5" /note="contains EST(s): AU174095(S15891),D49183(S15891) contains full-length cDNA(s): AK058228,AK099066" /codon_start=1 /product="unknown protein" /protein_id="BAD28124.1" /db_xref="GI:50252128" /translation="MEMEAATPVPRSDGRKLARCPRLQMDAKTVTAIEQSTGAATADA AAAGAEGAGGMRVKIVLSKQQLKQVAAAAGGAFALPPALEQLVSVLKRQHAKQV AAAADVVGRRRCRWSPALQSIPEECFS" complement(join(13784..13891,14436..14523,15371..15483)) /gene="OJ1725_H08.6" complement(join(13784..13891,14436..14523,15371..15483)) /gene="OJ1725_H08.6" /note="hypothetical ORF predicted by GENSCAN this category is not included in IRGSP standard" join(18408..18828,18964..19039,19131..19217,19334..19414,19509..19541,19784..19837,19931..19972,20098..20176,20262..20332,20407..20828) /gene="OJ1725_H08.7-1"

mrna join(18408..18828,18964..19039,19131..19217,19334..19414,19509..19541,19784..19837,19931..19972,20098..20176,20262..20332,20407..20828) /gene="OJ1725_H08.7-1" /note="supported by full-length cDNA(s): AK059662" 18444..20821 /gene="OJ1725_H08.7-2" join(<18444..19217,19334..19414,19509..19837,19931..19972,20098..20176,20262..20332,20407..>20821) /gene="OJ1725_H08.7-2" /note="supported by full-length cDNA(s): AK072754" 18444..20821 /gene="OJ1725_H08.7-2" /note="contains full-length cDNA(s): AK072754 non-coding transcript probably inactive due to including stop codon(s) in CDS" join(18806..18828,18964..19039,19131..19217,19334..19414,19509..19541,19784..19837,19931..19972,20098..20176,20262..20332,20407..20496) /gene="OJ1725_H08.7-1" /note="contains full-length cDNA(s): AK059662" /codon_start=1 /product="tetracycline transporter protein-like" /protein_id="BAD28125.1" /db_xref="GI:50252129" /translation="MVSLLTGSLTLSGAAIVTFYSLGEHGLQTALLYLYLKAQFGYSK DEFANLLLIAGAAGMLSQLTMPVLARFVGEDILLIIGLGGTHVFLYGIAWSYWP YLSAVFIILSAFVPSIRTNVSKSVGSNEQIGIAQSGICISSFASILAPLIFTPLTAW VLSETAPFKFKGFSIMCAGFCTLIAFIISMRRAGQSGASEMLAIVQHEQA" complement(join(20818..21313,24190..24375,25021..25594)) /gene="OJ1725_H08.8-1" complement(join(20818..21313,24190..24375,25021..25594)) /gene="OJ1725_H08.8-1" /note="supported by full-length cDNA(s): AK073500" complement(join(21008..21313,24190..24375,25021..25542)) /gene="OJ1725_H08.8-1" /note="contains full-length cDNA(s): AK073500 similar to Oryza sativa chromosome 4, OSJNBa0039K24.20" /codon_start=1 /product="unknown protein" /protein_id="BAD28126.1" /db_xref="GI:50252130" /translation="MARHAKTDSVTS LAPSSPPRSPRRSAYVLS PAASHPDVVVAS GGAGGGGGVAAAEKMSFAGSTPAESPLHYHYHSGAAVHHSRESSTGRLLFSQDLRS GAAAGVPWRRLLAQSGAGSVGDDDDDEGLLAGAASQWRCYALGAFVAVFAFLLVL WGASKSYKPHVVVKSVPFETYHIQGGTDRGTGPTXMSVNA TVLRFNRNRTFFSLHV TSTPFHLFYDDLTVATGHMAEFYQPRRSGRVTVSVVGKQVP LYGAGAE LHSKPNNGR LGPAVVPVRMAFVLRARAHILGLLVRSKFYRRVRLCLRDREASLGKPVHGVAAADCEYH DGR" join(21444..21478,21966..22509) /gene="OJ1725_H08.9" join(<21444..21478,21966..>22509) /gene="OJ1725_H08.9" /note="start and end point are not identified" join(21444..21478,21966..22509) /gene="OJ1725_H08.9" Query Match 58.5%; Score 24; DB 15; Length 155431; Best Local Similarity 72.5%; Pred. No. 1.5e+03; Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0; Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| Db 87762 AAGCCGCGGCTGCCGCGCCCTCCGTGCTGCCGCGCCTC 87801 RESULT 97 AC160739 AC160739 236171 bp DNA linear HTG 01-JUL-2005 LOCUS Bos taurus clone CH240-82C7, *** SEQUENCING IN PROGRESS ***, 32 DEFINITION unordered pieces. AC160739 AC160739.2 GI:68303054 ACCESSION VERSION

KEYWORDS
SOURCE
ORGANISM

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Bos taurus (cow)
Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 236171)

REFERENCE
AUTHORS

Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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Mangum,B., Mapua,P., Martin,K., McNeill,T.Z., Meenen,E.,
Mawhiney,S., McLeod,M.P., Morris,G., Minja,E., Montemayor,J., Moore,S.,
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Morgan,M., Morris,K., Morris,S., Newton,N., Nguyen,N., Norris,S.,
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Nwaakelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
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Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
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Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished
2 (bases 1 to 236171)

Worley,K.C.

Direct Submission

Submitted (30-APR-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 236171)

Cow Genome Sequencing Consortium.

Direct Submission

Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jun 29, 2005 this sequence version replaced gi:62988449.

The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: FFXF

Center clone name: CH240-82C7

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 222350 bases at least Q40

Consensus quality: 224708 bases at least Q30

Consensus quality: 226874 bases at least Q20

Estimated insert size: 225772; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 32 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1647: contig of 1647 bp in length

* 1648 1697: gap of 50 bp

* 1698 4756: contig of 3059 bp in length

* 4757 4806: gap of 50 bp

* 4807 27812: contig of 23006 bp in length

* 27813 27862: gap of 50 bp

* 27863 35577: contig of 7715 bp in length

* 35578 35627: gap of 50 bp

* 35628 77799: contig of 42172 bp in length

* 77800 77849: gap of 50 bp

* 77850 81497: contig of 3648 bp in length

* 81498 81547: gap of 50 bp

* 81548 83829: contig of 2282 bp in length

* 83830 83879: gap of 50 bp

* 83880 86633: contig of 2754 bp in length

* 86634 86683: gap of 50 bp

* 86684 91473: contig of 4790 bp in length

* 91474 91601: gap of 128 bp

* 91602 95198: contig of 3597 bp in length

* 95199 95248: gap of 50 bp

* 95249 105003: contig of 9755 bp in length

* 105004 105053: gap of 50 bp

* 105054 111222: contig of 6169 bp in length

* 111223 111272: gap of 50 bp

* 111273 112437: contig of 1165 bp in length

* 112438 115590: gap of 3153 bp

* 115591 122531: contig of 6941 bp in length

* 122532 122581: gap of 50 bp

* 122582 125026: contig of 2445 bp in length

* 125027 125115: gap of 89 bp

* 125116 128652: contig of 3537 bp in length

* 128653 128752: gap of unknown length

* 128753 130219: contig of 1467 bp in length

* 130220 130269: gap of 50 bp

* 130270 134001: contig of 3732 bp in length

* 134002 134051: gap of 50 bp

* 134052 142565: contig of 8514 bp in length

* 142566 142615: gap of 50 bp
* 142616 146534: contig of 3919 bp in length
* 146535 146584: gap of 50 bp
* 146585 159314: contig of 12730 bp in length
* 159315 159364: gap of 50 bp
* 159365 161847: contig of 2483 bp in length
* 161848 161947: gap of unknown length
* 161948 177733: contig of 15786 bp in length
* 177734 178000: gap of 267 bp
* 178001 188762: contig of 10762 bp in length
* 188763 188812: gap of 50 bp
* 188813 211713: contig of 22901 bp in length
* 211714 212063: gap of 350 bp
* 212064 227032: contig of 14969 bp in length
* 227033 227584: gap of 552 bp
* 227585 229483: contig of 1899 bp in length
* 229484 229583: gap of unknown length
* 229584 230628: contig of 1045 bp in length
* 230629 230728: gap of unknown length
* 230729 231738: contig of 1010 bp in length
* 231739 231838: gap of unknown length
* 231839 233118: contig of 1280 bp in length
* 233119 233218: gap of unknown length
* 233219 234568: contig of 1350 bp in length
* 234569 234668: gap of unknown length
* 234669 236171: contig of 1503 bp in length.

FEATURES

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Query Match 58.5%; Score 24; DB 14; Length 236171;
Best Local Similarity 72.5%; Pred. No. 1.4e+03;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGCCCGNCGC 40
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Db 20751 AAGACTCCCTGCCAGTCCATCATGGAGGCCCTGCC 20790

RESULT 98
AC012890/c

LOCUS AC012890 95614 bp DNA linear HTG 03-NOV-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
ACCESSION AC012890
VERSION AC012890.1 GI:6223432
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 95614)
AUTHORS Adams,M. and Venter,J.C.

TITLE
JOURNAL

COMMENT

Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10211172 by the submitter.
For further information on this sequence you may e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES

source
1. .95614
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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ORIGIN

Query Match 58.0%; Score 23.8; DB 14; Length 95614;
Best Local Similarity 77.1%; Pred. No. 1.9e+03;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCCCGNC 38
||||||| ||| ||||| ||||| :|

Db 4714 CCTCGGATTTCAGATCCTCATAGCTGGCCTATC 4680

RESULT 99

AC005889

LOCUS

AC005889 108924 bp DNA linear INV 30-OCT-1998
Drosophila melanogaster, chromosome 2L, region 30A3- 30A6, P1 clones DS06958 and DS03097, complete sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

1 (bases 1 to 108924)
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E., Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.
Sequencing of Drosophila chromosome 2L, region 30A3- 30A6 Unpublished (1998)
2 (bases 1 to 108924)
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E., Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (30-OCT-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121 Berkeley, CA 94720

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (<http://www.fruitfly.org/sequence/>) or send email to bdgp@fruitfly.berkeley.edu.

P1 library locations: 73-46, 33-25.
Location/Qualifiers
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/clone_lib="P1 library, partial Sau3A in pNS582tet14Ad10"
/note="DS03097 (D336) and DS06958 (D292) were completed
as a project. DS03097 extends from P1 end at bp 1 to P1
end at bp 48731. DS06958 extends from P1 end at bp 27620
to P1 end at bp 108,924."

ORIGIN

Query Match 58.0%; Score 23.8; DB 2; Length 108924;
Best Local Similarity 77.1%; Pred. No. 1.8e+03;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
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RESULT 100
CP000076_54
WPCOMMENT

Sequence split into 71 fragments LOCUS CP0000076 Accession CP0000076

Fragment Name	Begin	End
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CP000076_08	800001	910000
CP000076_09	900001	1010000
CP000076_10	1000001	1110000
CP000076_11	1100001	1210000
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CP000076_14	1400001	1510000
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CP000076_66 6600001 6710000
CP000076_67 6700001 6810000
CP000076_68 6800001 6910000
CP000076_69 6900001 7010000
CP000076_70 7000001 7074893
Continuation (55 of 71) of CP000076 from base 5400001 (CP000076 Pseudomonas fluorescens

Query Match 58.0%; Score 23.8; DB 1; Length 110000;
Best Local Similarity 77.1%; Pred. No. 1.8e+03;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
|| ||||| ||||| ||||| ||||| ||||| :|
Db 66305 CCACCGGCTGCAAGTCCACAGCGCTTGACGGCC 66339

Search completed: May 9, 2006, 22:56:49
Job time : 2213 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model
Run on: May 9, 2006, 22:09:39 ; Search time 270 Seconds
(without alignments)
1012.046 Million cell updates/sec

Title: US-09-904-968A-1_N3336_COPY_3300_3340
Perfect score: 41
Sequence: 1 aagcctccgagtcagctcc.....tcatcgctggcccgncgcg 41

Scoring table: IDENTITY_NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : N_Geneseq_21.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*
- 14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	53522	6	AAD30228 Human PKD
2	41	100.0	53522	13	ADU03973 Human pol
3	41	100.0	53522	14	AEB35216 Human Gef
4	41	100.0	53526	2	AAT94101 Human PKD
5	41	100.0	53577	2	AAT18551 Human pol
6	41	100.0	53577	2	AAT94108 Human PKD
7	29.8	72.7	623	6	ABQ16060 Oligonucl
8	29.8	72.7	623	6	ABQ16061 Oligonucl
9	29.8	72.7	6423	6	ABL34569 Human met
10	29.8	72.7	6423	6	ABL70310 Chemicall
11	29.8	72.7	6423	7	ADS99830 Complemen
12	24.6	60.0	1424	14	ACL66662
13	24.6	60.0	15268	14	ACL64679 M. xanthu
14	24.2	59.0	2202	4	ABL30357 Drosophil
15	24.2	59.0	5083	4	ABL30356 Drosophil
16	23	56.1	413	8	ABX51214 Bovine ES
17	23	56.1	3750	12	ADQ59193
18	22.6	55.1	768	13	ADT43870 Bacterial
19	22.6	55.1	2213	13	ADR07671 Full leng

20	22.6	55.1	22715	9	ADA02852
21	22.6	55.1	22715	10	ADB72590 Human CBX
22	22.6	55.1	22715	10	ADC85331 Mouse Cbx
23	22.6	55.1	22715	12	ADM74447 Human car
24	22.4	54.6	622	10	ADK57630 Plant DNA
25	22.4	54.6	1269	11	ABD04866 Pseudomon
26	22.4	54.6	2940	10	ADF28721 Guanylate
27	22.4	54.6	3568	10	ADF28719 Human SAP
28	22.4	54.6	3568	13	ADS09784 Human the
29	22.4	54.6	3705	10	ADC51948 Human pos
30	22.4	54.6	3723	6	ABS67754 Human int
31	22.4	54.6	243390	13	ABD33366 Human can
32	22.4	54.6	243934	14	ADZ13446 Human can
33	22.2	54.1	8301	4	AAF90035 Nucleotid
34	22.2	54.1	34071	4	AAF90033 Nucleotid
35	22.2	54.1	42717	4	AAF90032 Nucleotid
36	22	53.7	918	6	ABN98657 Arabidops
37	22	53.7	1281	14	ACL70733 M. xanthu
38	22	53.7	1441	5	ABA20206 Human ner
39	22	53.7	2145	8	ACA43467 Prokaryot
40	22	53.7	2423	11	ADR42106 Human can
41	22	53.7	2423	11	ADR42064 Human can
42	22	53.7	2979	6	ABZ12243 Arabidops
43	22	53.7	4257	13	ADS45922 Bacterial
44	22	53.7	6052	4	AAK84334 Human imm
45	22	53.7	6430	14	ACL64206 M. xanthu
46	22	53.7	43039	14	ADZ13665_4
47	22	53.7	75252	11	ACN44450_4
48	22	53.7	90597	10	ADJ72363 Streptomy
49	22	53.7	90600	6	ABQ78872 S. roseos
50	21.8	53.2	289	10	ABX86165 Corn ear-
51	21.8	53.2	623	6	ABQ16058 Oligonucl
52	21.8	53.2	623	6	ABQ16059 Oligonucl
53	21.8	53.2	687	14	ACL72417 M. xanthu
54	21.8	53.2	963	13	ADX65687 Plant ful
55	21.8	53.2	1057	14	AEB66674 Rice geno
56	21.8	53.2	6423	6	ABL34568 Human met
57	21.8	53.2	6423	6	ABL70309 Chemicall
58	21.8	53.2	6423	7	ADS99829 Bisulphit
59	21.8	53.2	6492	4	ABL02587 Drosophil
60	21.8	53.2	9941	3	AAA81461 N. mening
61	21.8	53.2	10528	14	ACL64482 M. xanthu
62	21.8	53.2	16105	4	ABL02586 Drosophil
63	21.8	53.2	110000	3	AAA81490_03
64	21.8	53.2	349980	3	AAF21607_
65	21.6	52.7	230	3	ABQ62923 Mycobacte
66	21.6	52.7	562	13	ADQ54664 Novel can
67	21.6	52.7	1689	14	ACL66884 M. xanthu
68	21.6	52.7	18537	14	ACL64694 M. xanthu
69	21.6	52.7	24883	13	ABD33069 Murine ca
70	21.6	52.7	349980	6	ABQ81846 Bifidobac
71	21.4	52.2	234	11	ABD06358 Pseudomon
72	21.4	52.2	292	6	ABQ99123 Human ORF
73	21.4	52.2	381	8	ABX51176 Bovine ES
74	21.4	52.2	381	8	ABX51132 Bovine ES
75	21.4	52.2	381	8	ABX50790 Bovine ES
76	21.4	52.2	395	8	ABX50908 Bovine ES
77	21.4	52.2	409	14	ACL68775 M. xanthu
78	21.4	52.2	419	8	ABX50923 Bovine ES
79	21.4	52.2	444	11	ABD12724 Pseudomon
80	21.4	52.2	501	11	ABD12690 Pseudomon
81	21.4	52.2	526	12	ACH78213 Human gen
82	21.4	52.2	572	4	ABA31177 Probe #96
83	21.4	52.2	572	4	AAK12507 Human bra
84	21.4	52.2	597	10	ADD68671 Murine DN
85	21.4	52.2	630	2	AAK1396 Polynucle
86	21.4	52.2	654	11	ABD14505 Pseudomon
87	21.4	52.2	738	11	ABD14229 Pseudomon
88	21.4	52.2	816	11	ABD11508 Pseudomon
89	21.4	52.2	834	11	ABD11440 Pseudomon
90	21.4	52.2	909	11	ABD11189 Pseudomon
91	21.4	52.2	966	11	ABD14344 Pseudomon
92	21.4	52.2	1236	13	ADT47081 Bacterial

c 93	21.4	52.2	1305	9	ADA48031	Ada48031 Rice gene
c 94	21.4	52.2	1329	10	ADE07095	Ade07095 Novel cod
c 95	21.4	52.2	1329	14	ADU40252	Adu40252 Novel hum
c 96	21.4	52.2	1356	11	ABD06331	Abd06331 Pseudomon
c 97	21.4	52.2	1440	12	ADL94139	Adl94139 Human Rap
c 98	21.4	52.2	1470	6	ABQ91417	Abq91417 M. capsul
99	21.4	52.2	1861	4	ABL19573	Ab119573 Drosophil
100	21.4	52.2	2000	11	ACL36154	Acl36154 Rice stre
c 101	21.4	52.2	2046	11	ABD06378	Abd06378 Pseudomon
102	21.4	52.2	2266	4	ABL02533	Ab102533 Drosophil
c 103	21.4	52.2	2751	13	ADS58538	Ads58538 Bacterial
104	21.4	52.2	2886	13	ADT16481	Adt16481 Plant cdn
105	21.4	52.2	3274	14	ADW43466	Adw43466 Nemadicti
c 106	21.4	52.2	3548	8	ABT19245	Abt19245 Aspergill
c 107	21.4	52.2	3642	8	ABT21065	Abt21065 Aspergill
c 108	21.4	52.2	3880	8	ABT18651	Abt18651 Aspergill
c 109	21.4	52.2	3880	8	ABT20467	Abt20467 Aspergill
c 110	21.4	52.2	4236	14	ACL68904	Acl68904 M. xanthu
c 111	21.4	52.2	4579	8	ABT18057	Abt18057 Aspergill
c 112	21.4	52.2	5880	8	ABT19871	Abt19871 Aspergill
113	21.4	52.2	6037	4	ABL02532	Ab102532 Drosophil
114	21.4	52.2	6233	4	AAS33449	Aas33449 DNA encod
115	21.4	52.2	6233	4	ABL19572	Ab119572 Drosophil
c 116	21.4	52.2	6683	10	ADB53086	Adb53086 Primary r
c 117	21.4	52.2	6683	13	ADV41291	Adv41291 Rat cardi
c 118	21.4	52.2	11854	14	ACL64574	Acl64574 M. xanthu
c 119	21.4	52.2	18871	4	ABK42430	Abk42430 Genomic s
c 120	21.4	52.2	18871	9	ADB60586	Adb60586 Connectiv
121	21.4	52.2	34662	14	ACL64798	Acl64798 M. xanthu
c 122	21.4	52.2	44567	8	AAD56117	Aad56117 Human BAT
c 123	21.4	52.2	44567	9	ADA02479	Ada02479 Human BAT
c 124	21.4	52.2	44567	10	ADB72218	Adb72218 Human BAT
125	21.4	52.2	98546	11	ACN44790	Acn44790 Human gen
126	21.2	51.7	477	13	ADT46232	Adt46232 Bacterial
127	21.2	51.7	1029	10	ADE07634	Ade07634 Novel cod
c 128	21.2	51.7	3288	5	AAS85789	Aas85789 DNA encod
129	21.2	51.7	3288	5	AAS87346	Aas87346 DNA encod
130	21.2	51.7	3288	5	AAS77395	Aas77395 DNA encod
131	21.2	51.7	3288	5	AAS88746	Aas88746 DNA encod
c 132	21.2	51.7	3288	5	AAS86010	Aas86010 DNA encod
133	21.2	51.7	3575	10	ADE63964	Ade63964 Rat gene
c 134	21.2	51.7	9154	10	ADE56030	Ade56030 Rat gene
c 135	21.2	51.7	9154	10	ADE56034	Ade56034 Rat gene
136	21.2	51.7	110000	4	AAI99682_20	Continuation (21 o
137	21.2	51.7	110000	4	AAI99683_20	Continuation (21 o
c 138	21	51.2	420	11	ABD14686	Abd14686 Pseudomon
c 139	21	51.2	583	10	ADB57230	Adb57230 Toxicity-
c 140	21	51.2	583	10	ADB51782	Abd51782 Primary r
141	21	51.2	624	11	ABD14070	Abd14070 Pseudomon
142	21	51.2	693	14	AEA43179	Aea43179 Perhydrol
143	21	51.2	826	12	ADI16417	Adi16417 Human pro
144	21	51.2	893	4	ABA77068	Aba77068 Prolifera
145	21	51.2	929	3	AAF15097	Aaf15097 Trichoder
146	21	51.2	929	13	ADU59138	Adu59138 Trichoder
147	21	51.2	929	14	ADZ97141	Adz97141 Trichoder
c 148	21	51.2	946	13	ADR21640	Adr21640 Human enz
149	21	51.2	972	9	ACD26650	Acd26650 Rat corpu
150	21	51.2	972	9	ADA06988	Ada06988 Rat eukar
151	21	51.2	972	10	ADI00806	Adi00806 Rat apopt
152	21	51.2	972	12	ADM74631_3'	Adm74631 3' end of
153	21	51.2	972	13	ADR70244	Adr70244 Rat apopt
154	21	51.2	972	14	ADW69319	Adw69319 Rat DNA s
155	21	51.2	972	14	ADW48051	Adw48051 Rat apopt
156	21	51.2	972	14	ADY78115	Ady78115 Rat eukar
157	21	51.2	1024	14	ADW15641	Adw15641 Novel Euc
158	21	51.2	1053	4	AAH44045	Aah44045 Streptomy
159	21	51.2	1065	5	AAH78255	Aah78255 Nucleotid
160	21	51.2	1065	6	ABL41306	Ab141306 Streptomy
161	21	51.2	1139	9	ACD26642	Acd26642 cDNA enco
162	21	51.2	1139	9	ADA06968	Ada06968 Rat eukar
163	21	51.2	1139	10	ADI00796	Adi00796 Rat apopt
164	21	51.2	1139	12	ADM74635	Adm74635 Rat apopt
165	21	51.2	1139	13	ADR70234	Adr70234 Rat corpu

166	21	51.2	1139	14	ADM69309	Adw69309 Deoxyhypu
167	21	51.2	1139	14	ADW48041	Adw48041 Rat apopt
168	21	51.2	1139	14	ADY78105	Ady78105 Rat eukar
169	21	51.2	1146	11	ABD14214	Abd14214 Pseudomon
170	21	51.2	1236	3	AAC36186	Aac36186 Arabidops
171	21	51.2	1302	6	AAI70852	Aai70852 Wheat glu
c 172	21	51.2	1302	8	ACA37686	Aca37686 Prokaryot
c 173	21	51.2	1362	14	ACL71897	Acl71897 M. xanthu
174	21	51.2	1373	13	ADT15055	Adt15055 Plant cdn
175	21	51.2	1737	14	ACL69099	Acl69099 M. xanthu
176	21	51.2	1815	13	ADT44783	Adt44783 Bacterial
c 177	21	51.2	1845	11	ABD14520	Abd14520 Pseudomon
c 178	21	51.2	1887	13	ADS58861	Ads58861 Bacterial
c 179	21	51.2	2185	10	ADB62402	Adb62402 Human cdn
180	21	51.2	2256	13	ADW78707	Adw78707 Jjiefie wh
c 181	21	51.2	2421	14	ACL68693	Acl68693 M. xanthu
182	21	51.2	3174	11	ADM03469	Adm03469 Human cdn
c 183	21	51.2	3672	8	ACA43496	Aca43496 Prokaryot
c 184	21	51.2	3921	8	ACA40351	Aca40351 Prokaryot
c 185	21	51.2	3921	14	AEB91813	Aeb91813 DNA encod
186	21	51.2	3975	8	ADA69835	Ada69835 Rice gene
187	21	51.2	3975	11	ACL26811	Acl26811 Rice abio
188	21	51.2	6798	4	AAH44043	Aah44043 Streptomy
189	21	51.2	6798	5	AAH78258	Aah78258 Nucleotid
190	21	51.2	6798	6	AAD31022	Aad31022 Streptomy
191	21	51.2	6798	12	ADP90610	Adp90610 Streptomy
192	21	51.2	6798	13	ADR16784	Adr16784 Streptomy
193	21	51.2	7628	14	ACL64412	Acl64412 M. xanthu
194	21	51.2	8077	6	AAD31028	Aad31028 Operon F
195	21	51.2	8719	12	ADP90614	Adp90614 Streptomy
196	21	51.2	8719	13	ADR16788	Adr16788 Streptomy
c 197	21	51.2	8974	4	ABK42191	Abk42191 Genomic s
c 198	21	51.2	8974	9	ADB60347	Adb60347 Connectiv
c 199	21	51.2	10923	4	ABK42192	Abk42192 Genomic s
c 200	21	51.2	10923	9	ADB60348	Adb60348 Connectiv
c 201	21	51.2	23673	6	ABZ75344	Abz75344 Human R11
c 202	21	51.2	29559	14	ACL64791	Acl64791 M. xanthu
203	21	51.2	39892	11	ACN44150_4	Continuation (5 of
c 204	21	51.2	41170	14	ACL64804	Acl64804 M. xanthu
c 205	21	51.2	109519	5	AAS08693	Aas08693 Micromono
206	21	51.2	110000	4	AAI99682_06	Continuation (7 of
207	21	51.2	110000	4	AAI99683_06	Continuation (7 of
c 208	21	51.2	143306	6	ABK49586	Abk49586 Human tra
209	20.8	50.7	100	8	ADA72678	Ada72678 Rice gene
210	20.8	50.7	270	10	ADF57793	Adf57793 Human pol
c 211	20.8	50.7	352	4	AAK65757	Aak65757 Human imm
c 212	20.8	50.7	352	4	AAK65758	Aak65758 Human imm
c 213	20.8	50.7	368	4	AAK55348	Aak55348 Human imm
c 214	20.8	50.7	372	8	ABZ54330	Abz54330 Aspergill
215	20.8	50.7	451	9	ACH23802	Ach23802 Human adu
c 216	20.8	50.7	462	4	AAD16510	Aad16510 Human ABC
c 217	20.8	50.7	462	5	AAS29559	Aas29559 Human end
c 218	20.8	50.7	462	9	ADA27257	Ada27257 cDNA enco
c 219	20.8	50.7	462	10	ADA12860	Ada12860 Human ABC
c 220	20.8	50.7	478	12	ADN12937	Adn12937 Human pro
c 221	20.8	50.7	496	13	ACF89534	Acf89534 Human SIR
222	20.8	50.7	497	9	ACH27203	Ach27203 Human adu
223	20.8	50.7	525	12	ACH69280	Ach69280 Human gen
224	20.8	50.7	570	14	ACL69478	Acl69478 M. xanthu
c 225	20.8	50.7	682	3	AAA62589	Aaa62589 Mycobacte
c 226	20.8	50.7	682	9	ADA26951	Ada26951 DNA encod
c 227	20.8	50.7	717	8	ACA43744	Aca43744 Prokaryot
c 228	20.8	50.7	800	8	ACF64391	Acf64391 Human MPO
c 229	20.8	50.7	810	4	AAF60766	Aaf60766 Pseudomona
c 230	20.8	50.7	834	11	ACL29778	Acl29778 Rice abio
231	20.8	50.7	891	12	ADI57634	Adi57634 Human bre
c 232	20.8	50.7	958	14	ACL63731	Acl63731 M. xanthu
233	20.8	50.7	1134	6	ABL51021	Ab151021 Mouse Tab
234	20.8	50.7	1134	9	ACD07907	Acd07907 DNA encod
235	20.8	50.7	1253	12	ADI57635	Adi57635 Human bre
236	20.8	50.7	1424	13	ADX31585	Adx31585 Plant ful
237	20.8	50.7	1661	6	ABL51010	Ab151010 Mouse Tab
238	20.8	50.7	1661	9	ACD07896	Acd07896 cDNA enco

C 239	20.8	50.7	1875	12	ADQ62872	Adg62872 Novel hum
C 240	20.8	50.7	1887	8	ACA27178	Aca27178 Prokaryot
C 241	20.8	50.7	2166	8	ACA43742	Aca43742 Prokaryot
C 242	20.8	50.7	7000	8	ABZ74421	Abz74421 Secreted
C 243	20.8	50.7	7000	10	ADC20884	Adc20884 Human sec
C 244	20.8	50.7	7000	10	ABZ67978	Abz67978 Human sec
C 245	20.8	50.7	10813	6	ABQ88640	Abq88640 Human cof
C 246	20.8	50.7	21635	11	ACN44628	Acn44628 Mouse gen
C 247	20.8	50.7	27756	9	ADA02570	Ada02570 Human Gat
C 248	20.8	50.7	27756	10	ADB72308	Adb72308 Human GAT
C 249	20.8	50.7	27756	10	ADE95818	Ade95818 Human GAT
C 250	20.8	50.7	113193	8	AAD54645	Aad54645 Streptomy
C 251	20.8	50.7	241748	14	ADZ13116	Adz13116 Murine ca
C 252	20.6	50.2	93	2	AAQ63782	Aaq63782 Bovine tr
C 253	20.6	50.2	514	7	ADJ78648	Adj78648 Different
C 254	20.6	50.2	683	2	AAQ63794	Aaq63794 Bovine tr
C 255	20.6	50.2	699	3	AAA08526	Aaa08526 DNA encod
C 256	20.6	50.2	699	4	AAF81479	Aaf81479 Bovine me
C 257	20.6	50.2	701	2	AAQ63795	Aaq63795 Bovine tr
C 258	20.6	50.2	702	3	AAA08525	Aaa08525 DNA encod
C 259	20.6	50.2	744	14	ACL69981	AcL69981 M. xanthu
C 260	20.6	50.2	777	14	ACL66904	AcL66904 M. xanthu
C 261	20.6	50.2	824	4	AAI94462	Aai94462 Human neu
C 262	20.6	50.2	891	4	AAI94329	Aai94329 Human neu
C 263	20.6	50.2	930	10	ABZ66791	Abz66791 Orthosomy
C 264	20.6	50.2	1019	10	ADI60268	Adi60268 Secreted
C 265	20.6	50.2	1026	13	ADU06864	Adu06864 Cell adhe
C 266	20.6	50.2	1128	13	ADU06879	Adu06879 Cell adhe
C 267	20.6	50.2	1206	14	AEB91740	Aeb91740 DNA encod
C 268	20.6	50.2	1209	12	ADK13720	Adk13720 E. coli i
C 269	20.6	50.2	1209	14	AEB91857	Aeb91857 DNA encod
C 270	20.6	50.2	1319	12	ADM80854	Adm80854 Human CAD
C 271	20.6	50.2	1347	8	ABX56047	Abx56047 M. echino
C 272	20.6	50.2	1398	5	AAS88418	Aas88418 DNA encod
C 273	20.6	50.2	1437	8	ACA27324	Aca27324 Prokaryot
C 274	20.6	50.2	1565	5	AAS80911	Aas80911 DNA encod
C 275	20.6	50.2	1610	10	ADI60463	Adi60463 Secreted
C 276	20.6	50.2	1912	5	AAS88896	Aas88896 DNA encod
C 277	20.6	50.2	2218	12	ADQ67316	Adq67316 Novel hum
C 278	20.6	50.2	2280	13	ADU06882	Adu06882 Cell adhe
C 279	20.6	50.2	3002	4	ABL21972	AbL21972 Drosophil
C 280	20.6	50.2	3060	8	ADA69629	Ada69629 Rice gene
C 281	20.6	50.2	3233	4	AAS21284	Aas21284 Human cDN
C 282	20.6	50.2	3233	8	ACA03643	Aca03643 cDNA encd
C 283	20.6	50.2	3233	8	ABX89181	Abx89181 DNA encd
C 284	20.6	50.2	3233	8	ACD41835	AcD41835 Human sec
C 285	20.6	50.2	3233	8	ACA04064	Aca04064 Human cDN
C 286	20.6	50.2	3233	9	ADA45600	Ada45600 Novel hum
C 287	20.6	50.2	3233	9	ADA76031	Ada76031 Human PRO
C 288	20.6	50.2	3233	9	ADA18681	Ada18681 Human PRO
C 289	20.6	50.2	3233	9	ADA61304	Ada61304 Homo sapi
C 290	20.6	50.2	3233	9	ADB19089	Adb19089 Novel hum
C 291	20.6	50.2	3233	9	ADB27630	Adb27630 cDNA enco
C 292	20.6	50.2	3233	9	ADA86109	Ada86109 Novel hum
C 293	20.6	50.2	3233	9	ADB15673	Adb15673 Human PRO
C 294	20.6	50.2	3233	9	ADA47459	Ada47459 Human PRO
C 295	20.6	50.2	3233	9	ADA67254	Ada67254 Human PRO
C 296	20.6	50.2	3233	9	ADB30261	Adb30261 cDNA enco
C 297	20.6	50.2	3233	9	ADA85557	Ada85557 Novel hum
C 298	20.6	50.2	3233	9	ADA96769	Ada96769 Human PRO
C 299	20.6	50.2	3233	9	ADA79073	Ada79073 Human PRO
C 300	20.6	50.2	3233	9	ADA87212	Ada87212 Novel hum
C 301	20.6	50.2	3233	9	ADB16414	Adb16414 Human PRO
C 302	20.6	50.2	3233	9	ADA91506	Ada91506 Novel hum
C 303	20.6	50.2	3233	9	ADB14569	Adb14569 Human PRO
C 304	20.6	50.2	3233	9	ADB18530	Adb18530 Novel hum
C 305	20.6	50.2	3233	9	ADA93745	Ada93745 Human PRO
C 306	20.6	50.2	3233	9	ADB19641	Adb19641 Novel hum
C 307	20.6	50.2	3233	9	ADB12953	Adb12953 Human PRO
C 308	20.6	50.2	3233	9	ACD98464	Acd98464 Novel hum
C 309	20.6	50.2	3233	9	ADA74207	Ada74207 Human PRO
C 310	20.6	50.2	3233	9	ADB24440	Adb24440 Human PRO
C 311	20.6	50.2	3233	9	ADA81964	Ada81964 Human PRO

312	20.6	50.2	3233	9	ADA74927	Ada74927 Human PRO
313	20.6	50.2	3233	9	ADA85005	Ada85005 Novel hum
314	20.6	50.2	3233	9	ADAB8453	Ada84453 Novel hum
315	20.6	50.2	3233	9	ADB29709	Adb29709 cDNA enco
316	20.6	50.2	3233	9	ADA80237	Ada80237 Human PRO
317	20.6	50.2	3233	9	ADA75479	Ada75479 Human PRO
318	20.6	50.2	3233	9	ADA46704	Ada46704 Human PRO
319	20.6	50.2	3233	9	ADB25000	Adb25000 Human PRO
320	20.6	50.2	3233	9	ADA93176	Ada93176 Human PRO
321	20.6	50.2	3233	9	ADB26526	Adb26526 cDNA enco
322	20.6	50.2	3233	9	ADB30813	Adb30813 cDNA enco
323	20.6	50.2	3233	9	ADA60741	Ada60741 Homo sapi
324	20.6	50.2	3233	9	ADB23888	Ada23888 Human PRO
325	20.6	50.2	3233	9	ADA96217	Ada96217 Human PRO
326	20.6	50.2	3233	9	ADA80789	Ada80789 Human PRO
327	20.6	50.2	3233	9	ADA95665	Ada95665 Human PRO
328	20.6	50.2	3233	9	ADB25974	Adb25974 cDNA enco
329	20.6	50.2	3233	9	ADB21459	Adb21459 Novel hum
330	20.6	50.2	3233	9	ADA77238	Ada77238 Human PRO
331	20.6	50.2	3233	9	ADB17978	Adb17978 cDNA enco
332	20.6	50.2	3233	9	ADA86661	Ada86661 Novel hum
333	20.6	50.2	3233	9	ADA87764	Ada87764 Novel hum
334	20.6	50.2	3233	9	ADA46152	Ada46152 Novel hum
335	20.6	50.2	3233	9	ADB28182	Adb28182 cDNA enco
336	20.6	50.2	3233	9	ADB28734	Adb28734 cDNA enco
337	20.6	50.2	3233	9	ADA76686	Ada76686 Human PRO
338	20.6	50.2	3233	9	ADA88316	Ada88316 Novel hum
339	20.6	50.2	3233	9	ADA97321	Ada97321 Human PRO
340	20.6	50.2	3233	9	ADB27078	Adb27078 cDNA enco
341	20.6	50.2	3233	9	ADB22011	Adb22011 Novel hum
342	20.6	50.2	3233	9	ADA66702	Ada66702 Human PRO
343	20.6	50.2	3233	9	ADB22563	Adb22563 Human PRO
344	20.6	50.2	3233	9	ADB23336	Adb23336 Human PRO
345	20.6	50.2	3233	9	ADA92058	Ada92058 Novel hum
346	20.6	50.2	3233	9	ADB15121	Adb15121 Human PRO
347	20.6	50.2	3233	9	ADB38373	Adb38373 Novel hum
348	20.6	50.2	3233	9	ADB37821	Adb37821 Novel hum
349	20.6	50.2	3233	10	ADB66293	Adb66293 Novel hum
350	20.6	50.2	3233	10	ADB89373	Adb89373 Human PRO
351	20.6	50.2	3233	10	ADB90105	Adb90105 Human PRO
352	20.6	50.2	3233	10	ADB39206	Adb39206 Novel hum
353	20.6	50.2	3233	10	ADB46829	Adb46829 Novel hum
354	20.6	50.2	3233	10	ADB86436	Adb86436 Human PRO
355	20.6	50.2	3233	10	ADB77041	Adb77041 Novel hum
356	20.6	50.2	3233	10	ADB34198	Adb34198 Human PRO
357	20.6	50.2	3233	10	ADB35302	Adb35302 Human PRO
358	20.6	50.2	3233	10	ADB33646	Adb33646 Human PRO
359	20.6	50.2	3233	10	ADB34750	Adb34750 Human PRO
360	20.6	50.2	3233	10	ADB35854	Adb35854 Human PRO
361	20.6	50.2	3233	10	ADB46249	Adb46249 Novel hum
362	20.6	50.2	3233	10	ADC50122	Adc50122 Novel hum
363	20.6	50.2	3233	10	ADC71669	Adc71669 Novel hum
364	20.6	50.2	3233	10	ADC59648	Adc59648 Novel hum
365	20.6	50.2	3233	10	ADC52655	Adc52655 Novel hum
366	20.6	50.2	3233	10	ADC57009	Adc57009 Novel hum
367	20.6	50.2	3233	10	ADC60200	Adc60200 Novel hum
368	20.6	50.2	3233	10	ADC50675	Adc50675 Novel hum
369	20.6	50.2	3233	10	ADC65202	Adc65202 Human PRO
370	20.6	50.2	3233	10	ADC54300	Adc54300 Novel hum
371	20.6	50.2	3233	10	ADC53261	Adc53261 Novel hum
372	20.6	50.2	3233	10	ADC58784	Adc58784 Novel hum
373	20.6	50.2	3233	10	ADC55662	Adc55662 Novel hum
374	20.6	50.2	3233	10	ADC58232	Adc58232 Novel hum
375	20.6	50.2	3233	10	ADD02906	Add02906 Novel hum
376	20.6	50.2	3233	10	ADC89898	Adc89898 Novel hum
377	20.6	50.2	3233	10	ADC69317	Adc69317 cDNA enco
378	20.6	50.2	3233	10	ADC48206	Adc48206 Human PRO
379	20.6	50.2	3233	10	ADD09735	Add09735 Human PRO
380	20.6	50.2	3233	10	ADD04310	Add04310 Novel hum
381	20.6	50.2	3233	10	ADC80266	Adc80266 Novel hum
382	20.6	50.2	3233	10	ADD10773	Add10773 Human PRO
383	20.6	50.2	3233	10	ADC47654	Adc47654 Human PRO
384	20.6	50.2	3233	10	ADC79714	Adc79714 Novel hum

385	20.6	50.2	3233	10	ADD09183	Add09183 Human PRO	458	20.6	50.2	3233	12	AD91418	Ade91418 Novel hum
386	20.6	50.2	3233	10	ADD40896	Add40896 Novel hum	459	20.6	50.2	3233	12	ADG01997	Adg01997 Human PRO
387	20.6	50.2	3233	10	ADD52035	Add52035 cDNA enco	460	20.6	50.2	3233	12	ADG21783	Adg21783 Novel hum
388	20.6	50.2	3233	10	ADD52775	Add52775 cDNA enco	461	20.6	50.2	3233	12	ADG19853	Adg19853 cDNA enco
389	20.6	50.2	3233	10	ADD53327	Add53327 Novel hum	462	20.6	50.2	3233	12	ADF97759	Adf97759 Human PRO
390	20.6	50.2	3233	10	ADD51483	Add51483 cDNA enco	463	20.6	50.2	3233	12	ADG23976	Adg23976 Novel hum
391	20.6	50.2	3233	10	ADD02282	Add02282 Human PRO	464	20.6	50.2	3233	12	ADF98330	Adf98330 Human PRO
392	20.6	50.2	3233	10	ADD01716	Add01716 Human PRO	465	20.6	50.2	3233	12	ADG03161	Adg03161 Human PRO
393	20.6	50.2	3233	10	ADD53898	Add53898 Novel hum	466	20.6	50.2	3233	12	ADF98882	Adf98882 Human PRO
394	20.6	50.2	3233	10	ADD92215	Add92215 Human PRO	467	20.6	50.2	3233	12	ADG16467	Adg16467 cDNA enco
395	20.6	50.2	3233	10	ADD91111	Add91111 Human PRO	468	20.6	50.2	3233	12	ADG04926	Adg04926 Human PRO
396	20.6	50.2	3233	10	ADE03725	Ade03725 Human PRO	469	20.6	50.2	3233	12	ADG19193	Adg19193 cDNA enco
397	20.6	50.2	3233	10	ADE32022	Ade32022 Novel hum	470	20.6	50.2	3233	12	ADG13030	Adg13030 cDNA enco
398	20.6	50.2	3233	10	ADE21954	Ade21954 cDNA enco	471	20.6	50.2	3233	12	ADG08087	Adg08087 Novel hum
399	20.6	50.2	3233	10	ADD79178	Add79178 cDNA enco	472	20.6	50.2	3233	12	ADG15257	Adg15257 cDNA enco
400	20.6	50.2	3233	10	ADE41714	Ade41714 Human PRO	473	20.6	50.2	3233	12	ADF96655	Adf96655 Human PRO
401	20.6	50.2	3233	10	ADE17531	Ade17531 Human PRO	474	20.6	50.2	3233	12	ADG05840	Adg05840 Human PRO
402	20.6	50.2	3233	10	ADD91663	Add91663 Human PRO	475	20.6	50.2	3233	12	ADG23424	Adg23424 Novel hum
403	20.6	50.2	3233	10	ADE33126	Ade33126 Novel hum	476	20.6	50.2	3233	12	ADG03713	Adg03713 Human PRO
404	20.6	50.2	3233	10	ADE33678	Ade33678 Novel hum	477	20.6	50.2	3233	12	ADG24614	Adg24614 Novel hum
405	20.6	50.2	3233	10	ADD79730	Add79730 cDNA enco	478	20.6	50.2	3233	12	ADG06911	Adg06911 Novel hum
406	20.6	50.2	3233	10	ADD92767	Add92767 Human PRO	479	20.6	50.2	3233	12	ADG07463	Adg07463 Novel hum
407	20.6	50.2	3233	10	ADE19187	Ade19187 Human PRO	480	20.6	50.2	3233	12	ADG54958	Adg54958 Novel hum
408	20.6	50.2	3233	10	ADE18635	Ade18635 Human PRO	481	20.6	50.2	3233	12	ADG60622	Adg60622 Novel hum
409	20.6	50.2	3233	10	ADE42831	Ade42831 Human PRO	482	20.6	50.2	3233	12	ADG61726	Adg61726 Novel hum
410	20.6	50.2	3233	10	ADD95620	Add95620 Human PRO	483	20.6	50.2	3233	12	ADG81927	Adg81927 Human PRO
411	20.6	50.2	3233	10	ADE22506	Ade22506 cDNA enco	484	20.6	50.2	3233	12	ADG57166	Adg57166 Novel hum
412	20.6	50.2	3233	10	ADD78624	Add78624 cDNA enco	485	20.6	50.2	3233	12	ADG56614	Adg56614 Novel hum
413	20.6	50.2	3233	10	ADE32574	Ade32574 Novel hum	486	20.6	50.2	3233	12	ADG55510	Adg55510 Novel hum
414	20.6	50.2	3233	10	ADE42266	Ade42266 Human PRO	487	20.6	50.2	3233	12	ADG58270	Adg58270 Novel hum
415	20.6	50.2	3233	10	ADD80282	Add80282 cDNA enco	488	20.6	50.2	3233	12	ADG70636	Adg70636 Novel hum
416	20.6	50.2	3233	10	ADD89310	Add89310 Human PRO	489	20.6	50.2	3233	12	ADG57718	Adg57718 Novel hum
417	20.6	50.2	3233	10	ADE40594	Ade40594 Human PRO	490	20.6	50.2	3233	12	ADG53302	Adg53302 Novel hum
418	20.6	50.2	3233	10	ADE04393	Ade04393 Human PRO	491	20.6	50.2	3233	12	ADG71188	Adg71188 Novel hum
419	20.6	50.2	3233	10	ADE92522	Ade92522 Human PRO	492	20.6	50.2	3233	12	ADG81375	Adg81375 Human PRO
420	20.6	50.2	3233	10	ADG21231	Adg21231 Novel hum	493	20.6	50.2	3233	12	ADH30337	Adh30337 Human PRO
421	20.6	50.2	3233	10	ADG22872	Adg22872 Novel hum	494	20.6	50.2	3233	12	ADH11704	Adh11704 Novel hum
422	20.6	50.2	3233	10	ADF97207	Adf97207 Human PRO	495	20.6	50.2	3233	12	ADG52126	Adg52126 Novel hum
423	20.6	50.2	3233	10	ADG80271	Adg80271 Human PRO	496	20.6	50.2	3233	12	ADG53854	Adg53854 Novel hum
424	20.6	50.2	3233	10	ADG79719	Adg79719 Human PRO	497	20.6	50.2	3233	12	ADG80823	Adg80823 Human PRO
425	20.6	50.2	3233	10	ADH55011	Adh55011 Novel hum	498	20.6	50.2	3233	12	ADG56062	Adg56062 Novel hum
426	20.6	50.2	3233	10	ADH55563	Adh55563 Novel hum	499	20.6	50.2	3233	12	ADH12328	Adh12328 Novel hum
427	20.6	50.2	3233	10	ADI63782	Adi63782 Novel hum	500	20.6	50.2	3233	14	ADZ03052	Adz03052 Human sec
428	20.6	50.2	3233	10	ADI64731	Adi64731 Novel hum							
429	20.6	50.2	3233	10	ADI63230	Adi63230 Novel hum							
430	20.6	50.2	3233	10	ADH81644	Adh81644 Novel hum							
431	20.6	50.2	3233	10	ADH81092	Adh81092 Novel hum							
432	20.6	50.2	3233	10	ACD23893	Acd23893 Novel hum							
433	20.6	50.2	3233	10	ACA67034	Aca67034 cDNA enco							
434	20.6	50.2	3233	11	ADM82261	Adm82261 Novel hum							
435	20.6	50.2	3233	11	ADN15660	Adn15660 Novel hum							
436	20.6	50.2	3233	11	ADN16289	Adn16289 Novel hum							
437	20.6	50.2	3233	11	ADN15108	Adn15108 Novel hum							
438	20.6	50.2	3233	11	ADN14556	Adn14556 Novel hum							
439	20.6	50.2	3233	12	ADC80818	Adc80818 Novel hum							
440	20.6	50.2	3233	12	ADD76266	Add76266 Human PRO							
441	20.6	50.2	3233	12	ADD87630	Add87630 Human PRO							
442	20.6	50.2	3233	12	ADD86034	Add86034 Human PRO							
443	20.6	50.2	3233	12	ADE75482	Ade75482 Human PRO							
444	20.6	50.2	3233	12	ADE23058	Ade23058 cDNA enco							
445	20.6	50.2	3233	12	ADE23610	Ade23610 cDNA enco							
446	20.6	50.2	3233	12	ADE24253	Ade24253 cDNA enco							
447	20.6	50.2	3233	12	ADD87078	Add87078 Human PRO							
448	20.6	50.2	3233	12	ADE88944	Ade88944 Human PRO							
449	20.6	50.2	3233	12	ADE18083	Ade18083 Human PRO							
450	20.6	50.2	3233	12	ADE88392	Ade88392 Human PRO							
451	20.6	50.2	3233	12	ADE94412	Ade94412 cDNA enco							
452	20.6	50.2	3233	12	ADE90823	Ade90823 Human PRO							
453	20.6	50.2	3233	12	ADE94964	Ade94964 cDNA enco							
454	20.6	50.2	3233	12	ADE93074	Ade93074 Human PRO							
455	20.6	50.2	3233	12	ADF34655	Adf34655 cDNA enco							
456	20.6	50.2	3233	12	ADE91970	Ade91970 Novel hum							
457	20.6	50.2	3233	12	ADE90271	Ade90271 Human PRO							

ALIGNMENTS

RESULT 1	
AAD30228	
ID	AAD30228 standard; DNA; 53522 BP.
XX	
AC	AAD30228;
XX	
DT	17-MAY-2002 (first entry)
XX	
DE	Human PKD1 gene.
XX	
KW	Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;
KW	acquired cystic disease; transgenic animal; chromosome 16; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200206529-A2.
XX	
PD	24-JAN-2002.
XX	
PF	13-JUL-2001; 2001WO-US022035.
XX	
PR	13-JUL-2000; 2000US-0218261P.
PR	13-APR-2001; 2001US-0283691P.
XX	
PA	(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Germino GG, Watnick TJ, Phakdeekitcharoen B;
PI WPI; 2002-179805/23.
XX Novel primer for diagnosing polycystic kidney disease-associated
PT disorder, comprises regions having sequence that selectively hybridizes
PT to polycystic kidney disease gene sequence.
XX Claim 20; Page 127-156; 192pp; English.
PS The present invention relates to compositions and methods useful for the
XX identification and detection of polycystic kidney disease (PKD1) gene
CC mutations. The invention also relates to primers comprising a 5' region
CC having a sequence that selectively hybridizes to a PKD1 gene sequence and
CC optionally, to a PKD1 homologue sequence and an adjacent 3' region having
CC a PKD1 homologue sequence. Primer pairs of the invention are useful for
CC detecting the presence or absence of a mutation in a PKD1 polynucleotide
CC in a sample, for identifying a subject at risk for a PKD1-associated
CC disorder such as autosomal dominant polycystic kidney disease (ADPKD) or
CC acquired cystic disease and for diagnosing a PKD1-associated disorder in
CC a subject. They are useful for selectively amplifying a region of a PKD1
CC gene. PKD1 DNA fragments are useful detecting the presence of a mutant
CC PKD1 polynucleotide in a sample, as a probe for an amplification
CC reaction, in hybridisation or amplification assays of biological samples
CC to detect abnormalities of PKD1 expression and for engineering transgenic
CC animals. The present sequence is human PKD1 gene located on chromosome 16
XX
SQ Sequence 53522 BP; 8486 A; 17664 C; 15766 G; 11606 T; 0 U; 0 Other;
Query Match 100.0%; Score 41; DB 6; Length 53522;
Best Local Similarity 97.6%; Pred. No. 0.0003;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCG 41
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCG 3340
RESULT 2
ADU03973
ID ADU03973 standard; DNA; 53522 BP.
XX
AC ADU03973;
XX
DT 30-DEC-2004 (first entry)
XX
DE Human polycystic kidney disease 1 (PKD-1) gene.
XX
KW mutation detection; polycystic kidney disease; PKD; PKD-1; biomarker;
KW autosomal dominant polycystic kidney disease; ADPKD; gene; ds.
XX
OS Homo sapiens.
XX
PN CA2461106-A1.
XX
PD 11-OCT-2004.
XX
PP 08-APR-2004; 2004CA-02461106.
XX
PR 11-APR-2003; 2003US-00411915.
XX
PA (ATHE-) ATHENA DIAGNOSTICS INC.
XX
PI Jones JG, Hennigan AN, Flynn KE, Garces JA, Seltzer WK;
PI Palatucci CM, Wang J, Curran JA, Allen SK, Robichaud NJ;
XX
DR WPI; 2004-776219/77.
XX
PT Novel nucleic acid comprising specific sequence capable of detecting
PT mutations in polycystic kidney disease-1 (PKD-1) or PKD-2 gene, useful
PT for detecting biomarkers of autosomal dominant polycystic kidney disease.

XX Disclosure; SEQ ID NO 1; 195pp; English.
PS The invention relates to a novel isolated nucleic acid capable of
XX detecting mutations in polycystic kidney disease (PKD-1) or PKD-2 gene,
CC comprising a specific sequence. The invention further comprises: a
CC nucleic acid biomarker for autosomal dominant polycystic kidney disease
CC (ADPKD), comprising a PKD-1 or PKD-2 nucleic acid sequence having one or
CC more novel nucleotide alterations chosen from identified ADPKD associated
CC alterations, as given in the specification; a polypeptide biomarker for
CC ADPKD, comprising a PKD-1 or PKD-2 polypeptide sequence having one or
CC more novel amino acid alterations chosen from identified ADPKD associated
CC alterations, as given in the specification; a method for diagnosing ADPKD
CC in an individual; and a method for determining in an individual the
CC presence or absence of a mutant PKD gene. The PKD mutation detecting
CC isolated nucleic acid or the ADPKD nucleic acid biomarker is useful in
CC diagnosing ADPKD in an individual, or determining the presence or absence
CC of a mutant PKD gene in an individual. This polynucleotide sequence
CC represents a human polycystic kidney disease 1 (PKD-1) gene of the
CC invention. Note: This sequence was not shown in the specification, but
CC was retrieved from Genbank by the indexer.
XX
SQ Sequence 53522 BP; 8486 A; 17664 C; 15766 G; 11606 T; 0 U; 0 Other;
Query Match 100.0%; Score 41; DB 13; Length 53522;
Best Local Similarity 97.6%; Pred. No. 0.0003;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCG 41
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCG 3340
RESULT 3
AEB35216
ID AEB35216 standard; DNA; 53522 BP.
XX
AC AEB35216;
XX
DT 06-OCT-2005 (first entry)
XX
DE Human Gefitinib sensitivity-related gene, PKD1 SEQ ID 80.
XX
KW Cancer; cytostatic; non-small-cell lung cancer; epidermal growth factor;
KW therapy; gefitinib; ds; gene.
XX
OS Homo sapiens.
XX
PN WO2005070020-A2.
XX
PD 04-AUG-2005.
XX
PP 24-JAN-2005; 2005WO-US002325.
XX
PR 23-JAN-2004; 2004US-0538682P.
XX
PA (COLS) UNIV COLORADO.
XX
PI Bunn PA, Coldren CD, Franklin WA, Geraci MW, Helfrich BA;
PI Hirsch FR, Lapadat R, Sugita M, Witta SE;
XX
DR WPI; 2005-533944/54.
XX
PT Selecting cancer patient who is predicted to benefit from administration
PT of epidermal growth factor receptor inhibitor or its agonist, by
PT providing sample of tumor cells from the patient and detecting expression
PT of genes from panel of genes.
XX
PS Claim 28; SEQ ID NO 80; 379pp; English.
XX
CC The invention relates to selecting a cancer patient who is predicted to
CC benefit from therapeutic administration of an EGFR inhibitor or agonist,
CC or a drug having similar biological activity as EGFR inhibitor,

CC comprising providing a sample of tumor cells from a patient to be tested,
CC and detecting in the sample the expression of genes chosen from a panel
CC of genes (that have been correlated with sensitivity or resistance to the
CC EGFR inhibitor) and selecting the patient as being predicted to benefit
CC from therapeutic administration of the EGFR inhibitor, if the expression
CC of the gene or genes in the patient's tumor cells is statistically more
CC similar to the expression levels of the gene or genes that has been
CC correlated with sensitivity to the EGFR inhibitor than to resistance to
CC the EGFR inhibitor. Also included are identifying molecules that interact
CC with the EGFR pathway to allow or enhance responsiveness to EGFR
CC inhibitors, polynucleotides (for detecting the expression of genes that
CC are indicative of sensitivity or resistance to gefitinib, or its agonist,
CC or a drug having substantially similar biological activity as gefitinib,
CC where the polynucleotides consist of at least two polynucleotides, where
CC each polynucleotide is at least 5 nucleotides in length, and where each
CC polynucleotide is complementary to an RNA transcript, or nucleotide
CC derived from it, of a gene that is regulated differently in gefitinib-
CC sensitive tumor cells as compared to gefitinib-resistant cells),
CC antibodies (or their antigen binding fragments or peptides) for detecting
CC the expression of genes that are indicative of sensitivity or resistance
CC to gefitinib (or its agonist, or a drug having substantially similar
CC biological activity as gefitinib, which antibody selectively binds to a
CC protein encoded by a gene comprising, or expressing a transcript
CC comprising, a nucleic acid sequence appearing as AEB35137-AEB35330,
CC identifying a compound with the potential to enhance the efficacy of EGFR
CC inhibitors and treating a patient suffering from cancer. The method is
CC useful in selecting a cancer patient (especially non-small-cell lung
CC cancer) who is predicted to benefit from therapeutic administration of an
CC EGFR inhibitor or its agonist, or a drug having similar biological
CC activity as EGFR inhibitor. The present sequence represents one of the
CC 194 genes that have been correlated with sensitivity or resistance to the
CC EGFR inhibitor.

XX
SQ Sequence 53522 BP; 8486 A; 17665 C; 15766 G; 11605 T; 0 U; 0 Other;

Query Match 100.0%; Score 41; DB 14; Length 53522;
Best Local Similarity 97.6%; Pred. No. 0.0003;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTGGCG 3340

RESULT 4
AAT94101
ID AAT94101 standard; DNA; 53526 BP.
XX
AC AAT94101;
XX
XX 25-MAR-2003 (revised)
DT 01-JUN-1998 (first entry)
XX
DE Human PKD1 gene.
XX
KW Human; polycystic kidney disease 1; PKD1; treatment;
KW autosomal dominant polycystic kidney disease; APKD; ss.
XX
OS Homo sapiens.
XX
PN WO9744457-A1.
XX
PD 27-NOV-1997.
XX
PF 22-MAY-1997; 97WO-US008799.
XX
XX 24-MAY-1996; 96US-00655360.
PR 04-JUN-1996; 96US-00658136.
XX
XX (GENZ) GENZYME CORP.
PA
XX Klinger K, Burn T, Connors T, Dackowski W, Germino G, Qian F;
PI
XX

DR WPI; 1998-018511/02.
XX
PT Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose
PT human autosomal or adult onset polycystic kidney disease.

PS Claim 2; Page 90-118; 257pp; English.

XX
CC The present sequence is the human polycystic kidney disease 1 (PKD1)
CC gene. The PKD1 gene or polypeptide may be used to treat autosomal
CC dominant polycystic kidney disease (APKD), and identify carriers of
CC mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies (Ab)
CC that distinguish between normal and mutant PKD1 sequences can also be
CC used in diagnostic tests. Anti-PKD1 Ab may also be used to perform
CC subcellular and histochemical localisation studies, and to block the
CC function of PKD1. Ab are also useful in rational drug design studies to
CC identify and test inhibitors of PKD1. Sense and antisense sequences
CC derived from the PKD1 gene may used for detection and therapy. (Updated
CC on 25-MAR-2003 to correct PR field.)

XX
SQ Sequence 53526 BP; 8486 A; 17665 C; 15768 G; 11607 T; 0 U; 0 Other;
Query Match 100.0%; Score 41; DB 2; Length 53526;
Best Local Similarity 97.6%; Pred. No. 0.0003;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTGGCG 3340

RESULT 5
AAT18551
ID AAT18551 standard; DNA; 53577 BP.

XX
AC AAT18551;

XX
DT 06-MAY-1997 (first entry)

XX
DE Human polycystic kidney disease normal PKD1 gene.

XX
KW Adult onset polycystic kidney disease; APKD; autosomal dominant; mutant;
KW transversion; transition; deletion; insertion; ds.

XX
OS Homo sapiens.

XX
PH Key Location/Qualifiers
FT misc_feature 4379. .5272
FT /*tag= a
FT /note= "specifically claimed region of intronless cDNA
FT identified by exon trapping"
FT old_sequence replace(50652. .50653, cg)
FT /*tag= b
FT old_sequence /note= "changes Val codon to Leu codon"
FT replace(50796. .50797, cg)
FT /*tag= c
FT old_sequence /note= "replaces Val codon by Leu codon"
FT replace(51827. .51828, cc)
FT /*tag= d
FT old_sequence /note= "insertion, results in frameshift"

XX
PN WO9612033-A1.

XX
PD 25-APR-1996.

XX
PF 11-OCT-1995; 95WO-US013357.

XX
XX 12-OCT-1994; 94US-00323443.

PR 31-JAN-1995; 95US-00381520.

XX
PA (IGIG-) IG LAB INC.

PA (UYJO) UNIV JOHNS HOPKINS.

XX
PI Klinger KW, Landes GM, Burn TC, Connors TD, Dackowski W;

PI Germino G, Qian F;
XX WPI; 1996-222017/22.
XX
PT Isolated human polycystic kidney diseases gene and its mutants - useful
PT for treatment of polycystic kidney disease and screening for carriers.
XX
PS Claim 1; Fig 1; 65pp; English.
XX
CC The present sequence is that of the normal human PKD1 gene from
CC chromosome 16. Mutations in this gene (e.g. transitions, transversions,
CC deletions and/or insertions) are associated with adult-onset polycystic
CC kidney disease (APKD). The PKD1 locus is GC-rich (62.4%). Comparison of
CC this sequence with a previously reported partial cDNA sequence revealed
CC differences at three locations (see features table). The most significant
CC difference is the presence of two additional cytosine residues on the
CC plus-strand at position 4566 of the previously reported sequence. The
CC insertion results in a frame-shift in the predicted protein coding
CC sequence, leading to replacement of 92 C-terminal amino acids with a
CC novel 12 amino acid C-terminus. The PKD1 gene contains 23 Alu repeats.
CC There is a region consisting of 17 tandem copies of a perfect 27 bp
CC repeat and two large CT-rich regions
XX
SQ Sequence 53577 BP; 8495 A; 17681 C; 15785 G; 11616 T; 0 U; 0 Other;

Query Match 100.0%; Score 41; DB 2; Length 53577;
Best Local Similarity 97.6%; Pred. No. 0.0003;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTGGCG 3340
|||||

RESULT 6
AAT94108
ID AAT94108 standard; DNA; 53577 BP.
XX
AC AAT94108;
XX
DT 25-MAR-2003 (revised)
DT 01-JUN-1998 (first entry)
XX
DE Human PKD1 locus between chromosomal markers ATPL (ATP6C) and D16S84.
XX
KW Human; polycystic kidney disease 1; PKD1; treatment;
KW autosomal dominant polycystic kidney disease; APKD; ss.
XX
OS Homo sapiens.
XX
PN WO9744457-A1.
XX
PD 27-NOV-1997.
XX
PF 22-MAY-1997; 97WO-US008799.
XX
PR 24-MAY-1996; 96US-00655360.
PR 04-JUN-1996; 96US-00658136.
XX
PA (GENZ) GENZYME CORP.
XX
PI Klinger K, Burn T, Connors T, Dackowski W, Germino G, Qian F;
XX WPI; 1998-018511/02.
XX
PT Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose
PT human autosomal or adult onset polycystic kidney disease.
XX
PS Example 5; Page 60-89; 257pp; English.
XX
CC The present sequence is the human polycystic kidney disease 1 (PKD1)
CC locus between chromosomal markers ATPL (ATP6C) and D16S84. The PKD1 gene
CC or polypeptide may be used to treat autosomal dominant polycystic kidney

CC disease (APKD), and identify carriers of mutant PKD1 genes, i.e. subjects
CC susceptible to APKD. Antibodies (Ab) that distinguish between normal and
CC mutant PKD1 sequences can also be used in diagnostic tests. Anti-PKD1 Ab
CC may also be used to perform subcellular and histochemical localisation
CC studies, and to block the function of PKD1. Ab are also useful in
CC rational drug design studies to identify and test inhibitors of PKD1.
CC Sense and antisense sequences derived from the PKD1 gene may be used for
CC detection and therapy. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 53577 BP; 8495 A; 17684 C; 15782 G; 11616 T; 0 U; 0 Other;

Query Match 100.0%; Score 41; DB 2; Length 53577;
Best Local Similarity 97.6%; Pred. No. 0.0003;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|||||
Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGTGGCG 3340
|||||

RESULT 7
ABQ16060/c
ID ABQ16060 standard; DNA; 623 BP.
XX
AC ABQ16060;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 2651.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for

CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 623 BP; 63 A; 93 C; 256 G; 211 T; 0 U; 0 Other;

Query Match 72.7%; Score 29.8; DB 6; Length 623;
Best Local Similarity 80.5%; Pred. No. 1.5;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|| ||||| || ||| ||||| ||||| ||||| : ||||
Db 462 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 422

RESULT 8
ABQ16061
ID ABQ16061 standard; DNA; 623 BP.
XX
AC ABQ16061;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 2652.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method

CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 623 BP; 211 A; 256 C; 93 G; 63 T; 0 U; 0 Other;

Query Match 72.7%; Score 29.8; DB 6; Length 623;
Best Local Similarity 80.5%; Pred. No. 1.5;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|| ||||| || ||| ||||| ||||| ||||| : ||||
Db 162 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 202

RESULT 9
ABL34569/c
ID ABL34569 standard; DNA; 6423 BP.
XX
AC ABL34569;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human metastasis associated gene SEQ ID NO: 122.
XX
KW Metastasis associated gene; cytostatic; gene therapy; cancer;
KW cytosine methylation; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200177376-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-EP003970.
XX
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-010922/01.
XX
PT New nucleic acid derived from chemically treated metastasis genes, useful
PT for diagnosis of cancers by analysis of cytosine methylation, also for
PT treatment.
XX
PS Claim 1; SEQ ID NO 122; 23pp + Sequence Listing; English.
XX
CC The present invention provides a number of human metastasis associated
CC genes which are modified by cytosine methylation. The sequences can be
CC used in the diagnosis and treatment of cancer. The present sequence is
CC one of the genes of the invention
XX
SQ Sequence 6423 BP; 1625 A; 292 C; 1756 G; 2750 T; 0 U; 0 Other;

Query Match 72.7%; Score 29.8; DB 6; Length 6423;
Best Local Similarity 80.5%; Pred. No. 1.6;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
|| ||||| || ||| ||||| ||||| ||||| : ||||
Db 1563 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 1523

RESULT 10
ABL70310/c
ID ABL70310 standard; DNA; 6423 BP.
XX
AC ABL70310;

XX 01-JUL-2002 (first entry)
DT Chemically treated cell signalling DNA sequence complementary to#100.
DE
XX Cell signalling; cytosine methylation; cell signalling disease; cancer;
KW tumour; cytostatic; ds.
XX Unidentified.
OS
XX WO200202807-A2.
PN
XX 10-JAN-2002.
PD
XX 29-JUN-2001; 2001WO-EP007471.
PF
XX 30-JUN-2000; 2000DE-01032529.
PR
XX 01-SEP-2000; 2000DE-01043826.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2002-154758/20.
DR
XX Nucleic acid, useful for diagnosis and therapy of diseases associated
PT with cell signaling e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with cell signaling.
PT
XX Claim 1; SEQ ID NO 200; 24pp + Sequence Listing; English.
PS
XX The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signalling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell
CC signalling, as well as oligonucleotides and/or PNA-oligomers for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 6423 BP; 1625 A; 292 C; 1756 G; 2750 T; 0 U; 0 Other;

Query Match 72.7%; Score 29.8; DB 6; Length 6423;
Best Local Similarity 80.5%; Pred. No. 1.6;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
Db ||||| ||||| ||||| ||||| ||||| ||||| :|||
1563 AAACCTCCGATACCAATCCCTCATCGCTAACCCGATCGCG 1523

RESULT 11
ADS99830/c
ID ADS99830 standard; DNA; 6423 BP.
XX
AC ADS99830;
XX
DT 02-DEC-2004 (first entry)
XX
DE Complement of bisulphite treated metastasis-associated human gene #61.
XX
KW Human; ds; gene; Bisulphite; metastasis; cancer; cytostatic;
KW DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;
KW electrospray; mass spectrometry; CpG dinucleotide; solid tumour.
XX

OS Homo sapiens.
XX
PN US2003148327-A1.
XX
PD 07-AUG-2003.
XX
PF 21-JAN-2003; 2003US-00240485.
XX
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
PR 06-APR-2001; 2001WO-EP003970.
XX
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-010922/01.
XX
PT New nucleic acid derived from chemically treated metastasis genes, useful
PT for diagnosis of cancers by analysis of cytosine methylation, also for
PT treatment.
XX
PS Claim 1; SEQ ID NO 122; 9pp; English.
XX
CC The invention relates to a nucleic acid comprising at least 18 bases from
CC a segment of the chemically pretreated DNA of genes associated with
CC metastasis, i.e. any of ADS99709-ADS99906 human genomic sequences or any
CC of the 19 sequences appearing as ADS99911-ADS99929. SEQ ID 2,4,6 etc are
CC the complements of SEQ ID 1,3,5, etc. Also included are an oligomer
CC (particularly an oligonucleotide or peptide nucleic acid) comprising at
CC least one base sequence of at least 9 bases which hybridises to (or is
CC identical with) the sequences referred to above, producing an array of
CC the oligomers on a carrier, obtaining genetic and/or epigenetic
CC parameters for diagnosis and/or therapy of diseases (or predisposition to
CC them) by analysis of cytosine methylation and a kit comprising a
CC bisulphite (disulphite or hydrogen sulphite) and the oligomers. In the
CC method of above 5-unmethylated cytosines in a genomic DNA sample are
CC converted chemically to uracil, or another base with hybridisation
CC properties different from those of cytosine, then fragments of the
CC treated DNA amplified (particularly by polymerase chain reaction) using
CC the oligomers and a polymerase (preferably heat stable) to produce
CC labelled amplicons. These are tested for hybridisation to an array of
CC oligomers and any hybridisation detected. The amplicons are labelled with
CC fluorescent or radioactive markers, or with a detachable mass marker to
CC allow their detection by mass spectrometry, specifically using the matrix
CC -assisted laser desorption/ionisation (MALDI) or electrospray techniques.
CC To improve detection in the mass spectrometer, fragments formed in the
CC instrument have only a single net charge (positive or negative). The
CC genomic DNA is from e.g. a cell line, biopsy sample, blood, or paraffin-
CC embedded tissue sample. Oligonucleotides or peptide-nucleic acids that
CC are complementary to (or identical with) parts of the nucleic acids listed
CC above may be used as primers for amplification of the nucleic acids or
CC their complements, and for determining cytosine methylation status and/or
CC single nucleotide polymorphisms in metastasis-related genes. They can be
CC used for analysis of diseases associated with methylation of CpG
CC dinucleotides and to determine (epi)genetic parameters for diagnosis
CC and/or therapy of disease (or predisposition). The genomic DNA sequences
CC are useful for diagnosis and therapy of solid tumours and cancer. The
CC present sequence is the complementary sequence to a bisulphite treated
CC human gene associated with metastasis. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030148327.
XX
SQ Sequence 6423 BP; 1625 A; 292 C; 1756 G; 2750 T; 0 U; 0 Other;

Query Match 72.7%; Score 29.8; DB 7; Length 6423;
Best Local Similarity 80.5%; Pred. No. 1.6;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAGCTCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|| ||||| || ||| ||||| ||||| ||||| : |||||
Db 1563 AAACCTCGAATACCAATCCCTCATCGCTAACCCGATCGCG 1523

RESULT 12
ACL66662/c
ID ACL66662 standard; DNA; 1424 BP.
XX
AC ACL66662;
XX
DT 02-JUN-2005 (first entry)
XX
DE M. xanthus gene sequence, seq id 3125.
XX
KW Transgenic plant; DNA replication; gene regulation; gene expression;
KW gene; ds.
XX
OS Myxococcus xanthus.
XX
PN US6833447-B1.
XX
PD 21-DEC-2004.
XX
PF 10-JUL-2001; 2001US-00902540.
XX
PR 10-JUL-2000; 2000US-0217883P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX
DR WPI; 2005-028716/03.
XX
PT New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
PS Example 2; SEQ ID NO 3125; 25pp; English.
XX

CC The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC set of about 7842 genes or partial genes from the genome of the bacterium
CC Myxococcus xanthus. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from USPTO

SQ Sequence 1424 BP; 195 A; 521 C; 501 G; 207 T; 0 U; 0 Other;
XX

Query Match 60.0%; Score 24.6; DB 14; Length 1424;
Best Local Similarity 74.4%; Pred. No. 85;
Matches 29; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|| ||||| ||||| ||||| ||||| ||||| : |||||
Db 606 GCGCGCGGGGCCAGGCCCTCGATGCTGGCCCGGTAGCG 568

RESULT 13
ACL64679/c
ID ACL64679 standard; DNA; 15268 BP.
XX
AC ACL64679;
XX
DT 02-JUN-2005 (first entry)
XX

DE M. xanthus DNA fragment, seq id 1142.
XX
KW Transgenic plant; DNA replication; gene regulation; gene expression; ds.
XX
OS Myxococcus xanthus.
XX
PN US6833447-B1.
XX
PD 21-DEC-2004.
XX
PF 10-JUL-2001; 2001US-00902540.
XX
PR 10-JUL-2000; 2000US-0217883P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX
DR WPI; 2005-028716/03.
XX
PT New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
PS Example 1; SEQ ID NO 1142; 25pp; English.
XX

CC The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1-1849 represent a
CC set of 1849 contig and singleton sequences comprising coding sequences,
CC DNA replication elements, promoters and other regulatory elements from
CC the genome of the bacterium Myxococcus xanthus. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO

XX
SQ Sequence 15268 BP; 2318 A; 5524 C; 5125 G; 2301 T; 0 U; 0 Other;
XX

Query Match 60.0%; Score 24.6; DB 14; Length 15268;
Best Local Similarity 74.4%; Pred. No. 95;
Matches 29; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
|| ||||| ||||| ||||| ||||| ||||| : |||||
Db 14450 GCGCGCGGGGCCAGGCCCTCGATGCTGGCCCGGTAGCG 14412

RESULT 14
ABL30357
ID ABL30357 standard; DNA; 2202 BP.
XX
AC ABL30357;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42544.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.

CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the 5912
CC bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present
CC sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137160

XX
SQ Sequence 413 BP; 88 A; 125 C; 124 G; 76 T; 0 U; 0 Other;

Query Match 56.1%; Score 23; DB 8; Length 413;
Best Local Similarity 71.8%; Pred. No. 2.8e+02;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
||| |||| ||||| ||||| ||||| ||||| ||||| : ||
Db 267 AACCAGCGGAGACCAGTCCACATGGCAGGCCCTGAAGC 229

RESULT 17
ADQ59193/c
ID ADQ59193 standard; DNA; 3750 BP.
XX
AC ADQ59193;
XX
DT 09-SEP-2004 (first entry)
XX
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:30.
KW coding mononucleotide repeat; cMNR; gene; antibody; MSI-H tumour;
KW MSI-H carcinoma; high microsatellite instability tumour;
KW high microsatellite instability carcinoma; cytostatic; ds.
XX
OS Homo sapiens.
XX
PN KR2004008012-A.
XX
PD 28-JAN-2004.
XX
PF 15-JUL-2002; 2002KR-00041304.
XX
PR 15-JUL-2002; 2002KR-00041304.
XX
PA (KIMH/) KIM H G.
PA (KIMN/) KIM N G.
PA (LEEJ/) LEE J S.
PA (RHEE/) RHEE H S.
XX
PI Kim HG, Kim NG, Lee JS, Rhee HS;
XX
DR WPI; 2004-386326/36.
XX
PT Genes containing coding mononucleotide repeats are useful in developing
PT an antibody against MSI-H (hugh (sic high) microsatellite instability)
PT tumor.
XX
PS Claim 3; SEQ ID NO 30; 578pp; Korean.
XX

CC The present invention describes genes containing coding mononucleotide
CC repeats (cMNRs). The genes are useful for the development of an antibody
CC against MSI-H (hugh microsatellite instability) tumour. Also described:
CC (1) cDNA genes containing cMNRs with 10 or more nucleotide sequences, and
CC selected from the cDNA genes having the nucleotide sequences of SEQ ID
CC NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35,
CC 37, 39, 41 and 43; (2) cDNA genes, which are frameshift mutated by
CC deletion or insertion of one or more base in the cMNRs; (3) genomic DNA

CC genes containing cMNRs with 10 or more nucleotide sequences, and selected
CC from the genomic DNA genes having the nucleotide sequences of SEQ ID
CC NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36,
CC 38, 40, 42 and 44; and (4) genomic DNA genes, which are frameshift
CC mutated by deletion or insertion of one or more base in the cMNRs. The
CC genes have cytostatic activity. The present sequence represents an MSI-H
CC carcinoma genomic DNA sequence from the present invention.

XX
SQ Sequence 3750 BP; 725 A; 1035 C; 1191 G; 799 T; 0 U; 0 Other;

Query Match 56.1%; Score 23; DB 12; Length 3750;
Best Local Similarity 71.8%; Pred. No. 3.1e+02;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||| |||| ||||| ||||| ||||| ||||| ||||| : |||
Db 1817 GGCTTCGGCGCCCTCCCGCGCGCGGGCCCGGGCGCG 1779

RESULT 18
ADT43870/c
ID ADT43870 standard; cDNA; 768 BP.
XX
AC ADT43870;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #18621.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX

PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 42308; 122pp; English.
XX

CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.

CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed human CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 22715 BP; 4607 A; 6738 C; 6685 G; 4685 T; 0 U; 0 Other;

Query Match 55.1%; Score 22.6; DB 9; Length 22715;
Best Local Similarity 73.0%; Pred. No. 4.5e+02;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGN 37
||||||| | ||||| ||||| ||||| | | :
Db 15385 AAGCCTCCGGTGGCAGCCCTCGTAGCTGTCTTGAG 15421

RESULT 21
ADB72590
ID ADB72590 standard; DNA; 22715 BP.
XX
AC ADB72590;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human CBX8 gene.
XX
KW human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX

OS Homo sapiens.
XX
PN WO2003008583-A2.
XX
PD 30-JAN-2003.
XX
PF 26-DEC-2001; 2001WO-US051291.
XX
PR 02-MAR-2001; 2001US-00798586.
PR 23-OCT-2001; 2001US-00004113.
PR 08-NOV-2001; 2001US-00052482.
PR 30-NOV-2001; 2001US-00997722.
PR 20-DEC-2001; 2001US-00034650.
XX

PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW, Engelhard EK;
XX
XX WPI; 2003-239337/23.
DR
XX
PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
PT cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
PS Claim 1; SEQ ID NO 418; 2304pp; English.
XX

CC The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytostatic
CC activity, and may have a use in gene therapy, or in a vaccine. The
CC recombinant nucleic acids and polypeptides are useful for treating
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC sarcomas. The present sequence represents a human gene of the invention.
XX

SQ Sequence 22715 BP; 4607 A; 6738 C; 6685 G; 4685 T; 0 U; 0 Other;

Query Match 55.1%; Score 22.6; DB 10; Length 22715;
Best Local Similarity 73.0%; Pred. No. 4.5e+02;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGN 37

Db 15385 AAGCCTCCGGTGGCAGCCCTCGTAGCTGTCTTGAG 15421
||||||| | ||||| ||||| ||||| | | :
RESULT 22
ADC85331
ID ADC85331 standard; DNA; 22715 BP.
XX
AC ADC85331;
XX
DT 01-JAN-2004 (first entry)
XX
DE Mouse Cbx8 coding sequence.
XX
KW Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;
KW secreted; transmembrane; intracellular; ds.
XX
OS Mus sp.
XX
PN WO2003045230-A2.
XX
PD 05-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038582.
XX
PR 30-NOV-2001; 2001US-00997722.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW, Engelhard EK;
XX
DR WPI; 2003-513603/48.
XX

PT New recombinant nucleic acid comprising a nucleotide sequence of any of
PT the carcinoma-associated (CA) genes, useful for screening for drug
PT candidates for diagnosing or treating carcinomas.
XX
PS Claim 1; SEQ ID NO 117; 983pp; English.
XX
CC The invention relates to a recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the fully defined carcinoma-
CC associated (CA) genes from the 50 tables given in the specification. The
CC CA proteins are secreted, transmembrane or intracellular proteins. The
CC recombinant nucleic acids are useful for screening for drug candidates
CC for diagnosing or treating carcinomas. Sequences given in ADC85215-
CC ADC85514 represent CA genes of the invention.
XX
SQ Sequence 22715 BP; 4607 A; 6738 C; 6685 G; 4685 T; 0 U; 0 Other;

Query Match 55.1%; Score 22.6; DB 10; Length 22715;
Best Local Similarity 73.0%; Pred. No. 4.5e+02;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGN 37
||||||| | ||||| ||||| ||||| | | :
Db 15385 AAGCCTCCGGTGGCAGCCCTCGTAGCTGTCTTGAG 15421

RESULT 23
ADM74447
ID ADM74447 standard; DNA; 22715 BP.
XX
AC ADM74447;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human carcinoma associated (CA) nucleic acid #58.
XX
KW Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
KW carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
KW cytostatic.
XX
OS Homo sapiens.

XX US2004072154-A1.
PN 15-APR-2004.
XX
PD 30-NOV-2001; 2001US-00997722.
XX
PF 22-DEC-2000; 2000US-00747377.
XX
PR 02-MAR-2001; 2001US-00798586.
XX
XX (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
XX
PI Morris DW, Engelhard EK;
XX
DR WPI; 2004-328562/30.
XX
XX New carcinoma associated gene or protein, useful for preparing a
PT composition for diagnosing or treating carcinoma e.g., leukemia or
PT lymphoma.
XX
PS Claim 1; SEQ ID NO 118; 29pp; English.
XX
CC The invention relates to new recombinant nucleic acids. The invention
CC also relates to a host cell comprising a recombinant nucleic acid or
CC expression vector, an expression vector comprising a recombinant nucleic
CC acid, a recombinant protein, a method of screening for drug candidates, a
CC method of screening for a bioactive agent capable of binding to a
CC carcinoma associated protein (CAP) encoded by a nucleotide sequence, a
CC method of screening for a bioactive agent capable of modulating the
CC activity of a CAP, a method of evaluating the effect of a candidate
CC carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting
CC the activity of a CAP, a method of treating carcinomas, a method of
CC neutralising the effect of a CAP and a method of diagnosing carcinoma or
CC propensity to carcinoma. A method of evaluating the effect of a candidate
CC carcinoma drug comprises administering the drug to a patient, removing a
CC cell sample from the patient and determining alterations in the
CC expression or activation of a gene comprising the nucleotide sequence. A
CC method of diagnosing carcinoma comprises determining the expression of
CC one or more genes comprising the nucleic acid sequence in a first tissue
CC type of a first individual and comparing the expression of the gene from
CC a second normal tissue type from the first individual or a second
CC unaffected individual, where a difference in the expression indicates
CC that the first individual has carcinoma. A method of inhibiting the
CC activity of a CAP comprises binding an inhibitor to the CAP. Treating
CC carcinomas comprises administering to a patient an inhibitor of CAP.
CC Neutralising the effect of a CAP comprises contacting an agent specific
CC for the CAP. The polypeptide specifically binds to the protein encoded by
CC the nucleic acid. It comprises an antibody that specifically binds to the
CC protein encoded by the nucleic acid. The nucleic acids are useful for
CC preparing a composition for diagnosing or treating carcinoma e.g.,
CC leukaemia or lymphoma. This sequence represents a human carcinoma
CC associated (CA) nucleic acid of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 22715 BP; 4607 A; 6738 C; 6685 G; 4685 T; 0 U; 0 Other;

Query Match 55.1%; Score 22.6; DB 12; Length 22715;
Best Local Similarity 73.0%; Pred. No. 4.5e+02;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGN 37
||||||| ||||| ||||| ||||| ||||| :
Db 15385 AAGCCTCCCGGTGCCAGCCCTCGTAGCTGTCTTGAG 15421

RESULT 24
ADK57630/c
ID ADK57630 standard; DNA; 622 BP.
XX
AC ADK57630;

XX 06-MAY-2004 (first entry)
DT
XX
DE Plant DNA sequence which confers altered metabolic characteristic #5013.
XX
KW altered metabolic characteristic; plant; acid metabolism;
KW alcohol metabolism; fatty acid metabolism; alkaloid metabolism;
KW branched fatty acid metabolism; ester metabolism; glyceride metabolism;
KW amino acid metabolism; carbohydrate metabolism; sterol metabolism;
KW phenolic metabolism; isoprenoid metabolism; alkene metabolism;
KW terpene metabolism; hydrocarbon metabolism; ketone metabolism;
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
OS Unidentified.
XX
XX WO2003020936-A1.
PN 13-MAR-2003.
XX
PD 30-AUG-2002; 2002WO-US027884.
PF 31-AUG-2001; 2001US-0316471P.
PR (DOWC) DOW CHEM CO.
XX (DOWC) DOW AGROSCIENCES LLC.
PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX WPI; 2003-313091/30.
XX
PT Novel genes that confer altered metabolic characteristics in Nicotiana
PT benthamiana plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX
PS Claim 1; SEQ ID NO 5013; 2576pp; English.
XX
CC The invention comprises DNA sequences which confer an altered metabolic
CC characteristic when they are expressed in a plant. The DNA sequences of
CC the invention are useful for producing plants with an altered metabolic
CC characteristic, such as: altered acid metabolism, alcohol metabolism,
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC base metabolism, altered amino acid metabolism, altered ester metabolism,
CC altered glyceride metabolism, altered sterol, oxygenated terpene, or
CC carbohydrate metabolism, alkene or alkyne metabolism, hydrocarbon
CC isoprenoid metabolism, ketone or quinone metabolism. The DNA sequences of the
CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a
CC DNA sequence of the invention.
XX
SQ Sequence 622 BP; 151 A; 156 C; 172 G; 143 T; 0 U; 0 Other;

Query Match 54.6%; Score 22.4; DB 10; Length 622;
Best Local Similarity 70.0%; Pred. No. 4.5e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
||||||| ||||| ||||| ||||| ||||| :
Db 126 AGCCTCCCGATGCCAAGCCACAGATTGGTGGCGCCGCG 87

RESULT 25
ABD04866/c
ID ABD04866 standard; DNA; 1269 BP.
XX
AC ABD04866;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #3470.
XX

KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO71295.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 3470; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1269 BP; 222 A; 421 C; 428 G; 198 T; 0 U; 0 Other;

Query Match 54.6%; Score 22.4; DB 11; Length 1269;
Best Local Similarity 70.0%; Pred. No. 4.7e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
Db 998 AGGCTCATGATGCCAGCCCCCGATGCCAGACCCGCTCGCG 959

RESULT 26
ADF28721
ID ADF28721 standard; cDNA; 2940 BP.
XX
AC ADF28721;
XX
DT 12-FEB-2004 (first entry)
XX
DE Guanylate kinase-associated cDNA - SED ID 631.
XX
KW neuroprotective; nootropic; cerebroprotective; antiparkinsonian;
KW neurological; spinal cord injury; cranial; cerebral trauma; stroke;
KW Alzheimer's disease; anxiety; autism; Parkinson's; tardive dyskinesia;
KW paralysis; seizure; memory disorder; adiponectin; C1q domain;
KW complement C1Q; speract receptor; Wilm's tumour; synapsin; annexin;
KW leupin; serpin; NGRHy; PRO; leucine-rich repeat; scavenger; neural IgCAM;
KW Ig; FN3; somatotropin; prolactin; somatostatin;
KW chorionic somatomammotropin hormone; NGAL; mucolipin; peroxidasin; otx1;

KW SAPAP; ss; gene.
XX
OS Unidentified.
XX
PN WO2003048326-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038526.
XX
PR 03-DEC-2001; 2001US-00005499.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ghosh M, Tang YT, Wang JR, Wang Z, Zhao QA, Xu C, Mulero JJ;
PI Boyle BJ;
XX
DR WPI; 2003-513756/48.
DR P-PSDB; ADF28722.
XX
PT New polynucleotides and polypeptides, useful for useful for treating
PT neurological conditions, e.g. spinal cord injury, cranial or cerebral
PT trauma, stroke, Alzheimer's disease, anxiety, autism, Parkinson's
PT disease, or paralysis.
XX
PS Claim 1; SEQ ID NO 631; 396pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising any
CC of the 87 sequences fully defined in the specification or its mature
CC protein-coding portion. The polynucleotide of the invention demonstrates
CC neuroprotective, nootropic, cerebroprotective and antiparkinsonian
CC activities whilst the polynucleotides, polypeptides and compounds may be
CC useful for treating neurological conditions including spinal cord injury,
CC cranial or cerebral trauma, stroke, Alzheimer's disease, anxiety, autism,
CC Parkinson's disease, tardive dyskinesia, paralysis, seizures or memory
CC disorders. The current sequence is that of the cDNA of the invention.
XX
SQ Sequence 2940 BP; 546 A; 1007 C; 956 G; 431 T; 0 U; 0 Other;

Query Match 54.6%; Score 22.4; DB 10; Length 2940;
Best Local Similarity 70.0%; Pred. No. 4.9e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGC 40
Db 1538 AAGACGACGACTGCCTGCCCTCTCGCTACCCCTGCCGC 1577

RESULT 27
ADF28719
ID ADF28719 standard; cDNA; 3568 BP.
XX
AC ADF28719;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human SAPAP-like cDNA - SED ID 629.
XX
KW neuroprotective; nootropic; cerebroprotective; antiparkinsonian;
KW neurological; spinal cord injury; cranial; cerebral trauma; stroke;
KW Alzheimer's disease; anxiety; autism; Parkinson's; tardive dyskinesia;
KW paralysis; seizure; memory disorder; adiponectin; C1q domain;
KW complement C1Q; speract receptor; Wilm's tumour; synapsin; annexin;
KW leupin; serpin; NGRHy; PRO; leucine-rich repeat; scavenger; neural IgCAM;
KW Ig; FN3; somatotropin; prolactin; somatostatin;
KW chorionic somatomammotropin hormone; NGAL; mucolipin; peroxidasin; otx1;
KW SAPAP; ss; gene; human.
XX
OS Homo sapiens.
XX
PN WO2003048326-A2.
XX
PD 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038526.
XX
PR 03-DEC-2001; 2001US-00005499.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Ghosh M, Tang YT, Wang JR, Wang Z, Zhao QA, Xu C, Mulero JJ;
PI Boyle BJ;
XX
DR WPI; 2003-513756/48.
XX P-PSDB; ADF28720.
XX
PT New polynucleotides and polypeptides, useful for useful for treating
PT neurological conditions, e.g. spinal cord injury, cranial or cerebral
PT trauma, stroke, Alzheimer's disease, anxiety, autism, Parkinson's
PT disease, or paralysis.
XX
XX Claim 1; SEQ ID NO 629; 396pp; English.
PS
XX The invention relates to a novel isolated polynucleotide comprising any
XX of the 87 sequences fully defined in the specification or its mature
CC protein-coding portion. The polynucleotide of the invention demonstrates
CC neuroprotective, neurotropic, cerebroprotective and antiparkinsonian
CC activities whilst the polynucleotides, polypeptides and compounds may be
CC useful for treating neurological conditions including spinal cord injury,
CC cranial or cerebral trauma, stroke, Alzheimer's disease, anxiety, autism,
CC Parkinson's disease, tardive dyskinesia, paralysis, seizures or memory
CC disorders. The current sequence is that of the cDNA of the invention.
XX
SQ Sequence 3568 BP; 624 A; 1278 C; 1128 G; 538 T; 0 U; 0 Other;
Query Match 54.6%; Score 22.4; DB 10; Length 3568;
Best Local Similarity 70.0%; Pred. No. 4.9e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
Db 1538 AAGACGACGACTGCCTGCCCTCCTCGCTACCCCTGCCGC 1577
RESULT 28
ADS09784
ID ADS09784 standard; DNA; 3568 BP.
XX
AC ADS09784;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human therapeutic DNA - SEQ ID 21.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX
OS Homo sapiens.
XX
PN WO2004080148-A2.
XX
PD 23-SEP-2004.
XX
PF 30-SEP-2003; 2003WO-US030720.
XX
PR 02-OCT-2002; 2002US-0416186P.
XX
PA (NUVE-) NUVELO INC.
XX
PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI; 2004-668857/65.
DR P-PSDB; ADS10468.
XX

PT New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
PS Claim 1; SEQ ID NO 21; 718pp; English.
XX
CC The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic DNA of
CC the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 3568 BP; 624 A; 1278 C; 1128 G; 538 T; 0 U; 0 Other;
Query Match 54.6%; Score 22.4; DB 13; Length 3568;
Best Local Similarity 70.0%; Pred. No. 4.9e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
Db 1538 AAGACGACGACTGCCTGCCCTCCTCGCTACCCCTGCCGC 1577
RESULT 29
ADC51948
ID ADC51948 standard; DNA; 3705 BP.
XX
AC ADC51948;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human postsynaptic density protein encoding DNA SEQ ID NO:6.
XX
KW ds; gene; human; N-methyl-D-aspartic acid; NMDA;
KW receptor signal transfer; neuroprotective; neurotropic; antiParkinsonian;
KW gene therapy; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; postsynaptic density.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..3059
FT /*tag= a
FT /product= "postsynaptic density protein"
XX
PN WO2003044196-A1.
XX
PD 30-MAY-2003.
XX
PF 20-NOV-2002; 2002WO-JP012102.
XX
PR 20-NOV-2001; 2001JP-00354678.
PR 22-FEB-2002; 2002JP-00046786.
PR 07-AUG-2002; 2002JP-00229863.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
PA (KAZU-) KAZUSA DNA RES INST FOUND.
XX
PI Ohara O, Nagase T, Ohishi M, Yokota H, Arai Y;
XX WPI; 2003-468772/44.
DR P-PSDB; ADC51945.
XX
PT Agent for controlling N-methyl-D-aspartic acid receptor signal transfer
PT for treatment of Alzheimer's and Parkinson's disease.
XX
PS Claim 28; Page 126-129; 140pp; Japanese.
XX

CC The invention relates to a novel agent for controlling, inhibiting or
 CC promoting N-methyl-D-aspartic acid (NMDA) receptor signal transfer. The
 CC agent inhibits or promotes binding of NMDA with a 576 residue polypeptide
 CC sequence (S1) and/or inhibits or promotes interaction between (S1) and a
 CC 979 residue amino acid sequence (S3), both given in the specification. A
 CC protein of the invention has neuroprotective, neurotropic, and
 CC antiParkinsonian activity. A polynucleotide encoding a protein of the
 CC invention may have a use in gene therapy. The agent is useful for
 CC treatment and prevention of neurodegenerative diseases such as
 CC Alzheimer's disease and also for Parkinson's disease. The present
 CC sequence encodes a postsynaptic density protein of the invention.
 XX
 SQ Sequence 3705 BP; 657 A; 1314 C; 1171 G; 563 T; 0 U; 0 Other;

Query Match	54.6%	Score 22.4;	DB 10;	Length 3705;
Best Local Similarity	70.0%;	Pred. No. 4.9e+02;		
Matches 28; Conservative	1;	Mismatches 11;	Indels 0;	Gaps 0;

Claim 5; Page 191-192; 195pp; English.

The present invention relates to a new intracellular signalling molecule (INTSIG) polypeptide. The polypeptides and polynucleotides of the invention are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of INTSIG, such as cell proliferative diseases (e.g. cancer, atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS (acquired immunodeficiency syndrome), allergies), neurological disorders (e.g. stroke, Parkinson's disease, epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. endometriosis), developmental, vesicle trafficking disorders, and infections (e.g. bacterial, viral, parasitic, protozoal). These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of INTSIG. The INTSIG or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles. The present nucleic acid sequence encodes a human INSTIG protein of the invention

XX 01-AUG-2002 (first entry)
XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 425.
DE Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
XX disease; crop; thale cress; tolerance factor; insect; pathogen;
KW nutrition; ds.
KW Arabidopsis thaliana.
XX
OS
XX
XX US2002023281-A1.
XX 21-FEB-2002.
XX
XX 26-JAN-2001; 2001US-00770445.
XX
XX 27-JAN-2000; 2000US-0178472P.
PR
XX (GORL/) GORLACH J.
PA (ANYV/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYI/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX
PI Goriach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
XX WPI; 2002-403163/43.
XX
XX New Arabidopsis thaliana nucleic acid for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of protein.
XX
PS Claim 1; SEQ ID NO 425; 49pp + Sequence Listing; English.
XX
XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridising under stringent conditions
CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
CC given in the specification or its fragment. A polypeptide (II) encoded by
CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
CC useful for screening a candidate agent for its biological effect. (I) is
CC useful in identifying homologous or related genes, in producing
CC compositions that modulate the expression or function of its encoded
CC protein, mapping functional regions of the protein and in studying
CC associated physiological pathways. (I) is also useful for the genetic
CC manipulation of cells, particularly plant cells. (I) is also useful in
CC screening assays of various plant strains to determine the strains that
CC are best capable of withstanding a particular disease or environmental
CC stress. (II) and (III) are useful for screening of biologically active
CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
CC pathways. The screened agents are useful in improved methods of treating
CC crops to prevent or treat disease. (II) are also useful in screening
CC programs to identify agents that mimic or enhance the action of tolerance
CC factors. Such agents are useful in improved methods of treating crops to
CC enhance their tolerance to environmental stress. (I) is also useful for

CC enhancing or inhibiting production of a biosynthetic product in a plant.
CC (III) is useful for identifying other mediators that may induce
CC expression of proteins of interest, for establishing the extent to which
CC any specific insect and/or pathogen is responsible for damage to a
CC particular plant, for identifying other mediators that enhance or induce
CC tolerance to environmental stress, for identifying factors involved in
CC biosynthetic pathways of nutritional, commercial, or medicinal value and
CC for identifying productions of nutritional, commercial or medicinal
CC value. (IV) is useful in the study of genetic function and regulation,
CC for alteration of the cellular metabolism and for screening compounds
CC that may affect the biological function of the gene or gene products.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=999909770445
XX
SQ Sequence 918 BP; 264 A; 226 C; 151 G; 270 T; 0 U; 7 Other;

Query Match 53.7%; Score 22; DB 6; Length 918;
Best Local Similarity 71.1%; Pred. No. 6.3e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGNCG 39
||| ||| ||| ||| ||| ||| ||| ||| :||
Db 508 AGCTTCGGAGTGCATGTCCTCGATCGCTGGCTCGTACG 471

RESULT 37
ACL70733
ID ACL70733 standard; DNA; 1281 BP.
XX
AC ACL70733;
XX
DT 02-JUN-2005 (first entry)
XX
DE M. xanthus gene sequence, seq id 7196.
XX
KW Transgenic plant; DNA replication; gene regulation; gene expression;
KW gene; ds.
XX
OS Myxococcus xanthus.
XX
XX US6833447-B1.
PN
XX 21-DEC-2004.
PD
XX 10-JUL-2001; 2001US-00902540.
PF
XX 10-JUL-2000; 2000US-0217883P.
PR
XX (MONS) MONSANTO TECHNOLOGY LLC.
PA
XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
PI
XX WPI; 2005-028716/03.
DR
XX New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
PS Example 2; SEQ ID NO 7196; 25pp; English.
XX
XX The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1850-9691 represent a
CC set of about 7842 genes or partial genes from the genome of the bacterium
CC Myxococcus xanthus. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from USPTO

```
XX
SQ      Sequence 1281 BP; 200 A; 447 C; 443 G; 191 T; 0 U; 0 Other;

      Query Match          53.7%;   Score 22;   DB 14;   Length 1281;
      Best Local Similarity 80.0%;   Pred. No. 6.4e+02;
      Matches 24;   Conservative 1;   Mismatches 5;   Indels 0;   Gaps 0;

QY      12 TGCCAGTCCTCATCGCTGGCCCGGCGCG 41
      | | | | | | | | | | | | | | | | | |
Db      742 TACAAGTACCTCAACGCCGCGCGCGCGCG 771

RESULT 38
ABA20206
ID      ABA20206 standard; DNA; 1441 BP.
XX
AC      ABA20206;
XX
DT      23-JAN-2002 (first entry)
XX
DE      Human nervous system related polynucleotide SEQ ID NO 12537.
XX
KW      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW      immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW      antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW      antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW      antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW      antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW      neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS      Homo sapiens.
XX
PN      WO200159063-A2.
XX
PD      16-AUG-2001.
XX
PF      17-JAN-2001; 2001WO-US001334.
XX
PR      31-JAN-2000; 2000US-0179065P.
PR      04-FEB-2000; 2000US-0180628P.
PR      24-FEB-2000; 2000US-0184664P.
PR      02-MAR-2000; 2000US-0186350P.
PR      16-MAR-2000; 2000US-0189874P.
PR      17-MAR-2000; 2000US-0190076P.
PR      18-APR-2000; 2000US-0198123P.
PR      19-MAY-2000; 2000US-0205515P.
PR      07-JUN-2000; 2000US-0209467P.
PR      28-JUN-2000; 2000US-0214886P.
PR      30-JUN-2000; 2000US-0215135P.
PR      07-JUL-2000; 2000US-0216647P.
PR      07-JUL-2000; 2000US-0216880P.
PR      11-JUL-2000; 2000US-0217487P.
PR      11-JUL-2000; 2000US-0217496P.
PR      14-JUL-2000; 2000US-0218290P.
PR      26-JUL-2000; 2000US-0220963P.
PR      26-JUL-2000; 2000US-0220964P.
PR      14-AUG-2000; 2000US-0224518P.
PR      14-AUG-2000; 2000US-0224519P.
PR      14-AUG-2000; 2000US-0225213P.
PR      14-AUG-2000; 2000US-0225214P.
PR      14-AUG-2000; 2000US-0225266P.
PR      14-AUG-2000; 2000US-0225267P.
PR      14-AUG-2000; 2000US-0225268P.
PR      14-AUG-2000; 2000US-0225270P.
PR      14-AUG-2000; 2000US-0225447P.
PR      14-AUG-2000; 2000US-0225757P.
PR      14-AUG-2000; 2000US-0225758P.
PR      14-AUG-2000; 2000US-0225759P.
PR      18-AUG-2000; 2000US-0226279P.
PR      22-AUG-2000; 2000US-0226681P.
PR      22-AUG-2000; 2000US-0226868P.
PR      22-AUG-2000; 2000US-0227182P.
PR      23-AUG-2000; 2000US-0227009P.
PR      31-JAN-2000; 2000US-0179065P.
PR      04-FEB-2000; 2000US-0180628P.
PR      24-FEB-2000; 2000US-0184664P.
PR      02-MAR-2000; 2000US-0186350P.
PR      16-MAR-2000; 2000US-0189874P.
PR      17-MAR-2000; 2000US-0190076P.
PR      18-APR-2000; 2000US-0198123P.
PR      19-MAY-2000; 2000US-0205515P.
PR      07-JUN-2000; 2000US-0209467P.
PR      28-JUN-2000; 2000US-0214886P.
PR      30-JUN-2000; 2000US-0215135P.
PR      07-JUL-2000; 2000US-0216647P.
PR      07-JUL-2000; 2000US-0216880P.
PR      11-JUL-2000; 2000US-0217487P.
PR      11-JUL-2000; 2000US-0217496P.
PR      14-JUL-2000; 2000US-0218290P.
PR      26-JUL-2000; 2000US-0220963P.
PR      26-JUL-2000; 2000US-0220964P.
PR      14-AUG-2000; 2000US-0224518P.
PR      14-AUG-2000; 2000US-0224519P.
PR      14-AUG-2000; 2000US-0225213P.
PR      14-AUG-2000; 2000US-0225214P.
PR      14-AUG-2000; 2000US-0225266P.
PR      14-AUG-2000; 2000US-0225267P.
PR      14-AUG-2000; 2000US-0225268P.
PR      14-AUG-2000; 2000US-0225270P.
PR      14-AUG-2000; 2000US-0225447P.
PR      14-AUG-2000; 2000US-0225757P.
PR      14-AUG-2000; 2000US-0225758P.
PR      14-AUG-2000; 2000US-0225759P.
PR      18-AUG-2000; 2000US-0226279P.
PR      22-AUG-2000; 2000US-0226681P.
PR      22-AUG-2000; 2000US-0226868P.
PR      22-AUG-2000; 2000US-0227182P.
PR      23-AUG-2000; 2000US-0227009P.
PR      30-AUG-2000; 2000US-0228924P.
PR      01-SEP-2000; 2000US-0229287P.
PR      01-SEP-2000; 2000US-0229343P.
PR      01-SEP-2000; 2000US-0229344P.
PR      01-SEP-2000; 2000US-0229345P.
PR      05-SEP-2000; 2000US-0229509P.
PR      05-SEP-2000; 2000US-0229513P.
PR      06-SEP-2000; 2000US-0230437P.
PR      06-SEP-2000; 2000US-0230438P.
PR      08-SEP-2000; 2000US-0231242P.
PR      08-SEP-2000; 2000US-0231243P.
PR      08-SEP-2000; 2000US-0231244P.
PR      08-SEP-2000; 2000US-0231413P.
PR      08-SEP-2000; 2000US-0231414P.
PR      08-SEP-2000; 2000US-0232080P.
PR      08-SEP-2000; 2000US-0232081P.
PR      12-SEP-2000; 2000US-0231968P.
PR      14-SEP-2000; 2000US-0232397P.
PR      14-SEP-2000; 2000US-0232398P.
PR      14-SEP-2000; 2000US-0232399P.
PR      14-SEP-2000; 2000US-0232400P.
PR      14-SEP-2000; 2000US-0232401P.
PR      14-SEP-2000; 2000US-0233063P.
PR      14-SEP-2000; 2000US-0233064P.
PR      14-SEP-2000; 2000US-0233065P.
PR      21-SEP-2000; 2000US-0234223P.
PR      21-SEP-2000; 2000US-0234274P.
PR      25-SEP-2000; 2000US-0234997P.
PR      25-SEP-2000; 2000US-0234998P.
PR      26-SEP-2000; 2000US-0235484P.
PR      27-SEP-2000; 2000US-0235834P.
PR      27-SEP-2000; 2000US-0235836P.
PR      29-SEP-2000; 2000US-0236327P.
PR      29-SEP-2000; 2000US-0236367P.
PR      29-SEP-2000; 2000US-0236368P.
PR      29-SEP-2000; 2000US-0236369P.
PR      29-SEP-2000; 2000US-0236370P.
PR      02-OCT-2000; 2000US-0236802P.
PR      02-OCT-2000; 2000US-0237037P.
PR      02-OCT-2000; 2000US-0237038P.
PR      02-OCT-2000; 2000US-0237039P.
PR      02-OCT-2000; 2000US-0237040P.
PR      13-OCT-2000; 2000US-0239935P.
PR      13-OCT-2000; 2000US-0239937P.
PR      20-OCT-2000; 2000US-0240960P.
PR      20-OCT-2000; 2000US-0241785P.
PR      20-OCT-2000; 2000US-0241786P.
PR      20-OCT-2000; 2000US-0241787P.
PR      20-OCT-2000; 2000US-0241809P.
PR      20-OCT-2000; 2000US-0241826P.
PR      20-OCT-2000; 2000US-0242221P.
PR      01-NOV-2000; 2000US-0244617P.
PR      08-NOV-2000; 2000US-0246474P.
PR      08-NOV-2000; 2000US-0246475P.
PR      08-NOV-2000; 2000US-0246476P.
PR      08-NOV-2000; 2000US-0246477P.
PR      08-NOV-2000; 2000US-0246478P.
PR      08-NOV-2000; 2000US-0246523P.
PR      08-NOV-2000; 2000US-0246524P.
PR      08-NOV-2000; 2000US-0246525P.
PR      08-NOV-2000; 2000US-0246526P.
PR      08-NOV-2000; 2000US-0246527P.
PR      08-NOV-2000; 2000US-0246528P.
PR      08-NOV-2000; 2000US-0246532P.
PR      08-NOV-2000; 2000US-0246609P.
PR      08-NOV-2000; 2000US-0246610P.
PR      08-NOV-2000; 2000US-0246611P.
PR      08-NOV-2000; 2000US-0246613P.
PR      17-NOV-2000; 2000US-0249207P.
PR      17-NOV-2000; 2000US-0249208P.
PR      17-NOV-2000; 2000US-0249209P.
PR      17-NOV-2000; 2000US-0249210P.
```



```
Best Local Similarity 71.1%; Pred.No. 6.5e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
Db 985 AGGCATCGAGGGCAGGCCGCTCACGGCGCGCGGCCG 948

RESULT 40
ADR42106/c
ID ADR42106 standard; cDNA; 2423 BP.
XX
AC ADR42106;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer inhibiting protein PP8857-encoding cDNA, SEQ ID NO:21.
XX
KW Human; PP8857; cancer inhibiting protein; recombinant preparation;
KW gene therapy; cancer; tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1863..2378
FT /*tag= a
FT /product= "Human cancer inhibiting protein PP8857"
XX
PN CN1368511-A.
XX
PD 11-SEP-2002.
XX
PF 08-FEB-2001; 2001CN-00105312.
XX
PR 08-FEB-2001; 2001CN-00105312.
XX
PA (SHAN-) SHANGHAI INST ONCOLOGY.
XX
PI Gu J;
XX
DR WPI; 2003-248949/25.
XX
DR P-PSDB; ADR42065.
XX
PT New human protein with cancer inhibiting function for treating diseases,
PT such as, cancer.
XX
PS Claim 5; SEQ ID NO 21; 40pp; Chinese.
XX
CC The invention relates to 12 novel human proteins with cancer inhibiting
CC functions, and to the polynucleotides encoding them. The invention also
CC relates to the recombinant preparation of the proteins, antagonists of
CC the proteins, and the use of the proteins, polynucleotides and
CC antagonists in therapeutic applications for treating diseases such as
CC cancers. The present sequence represents a specifically claimed cDNA
CC encoding a human cancer inhibiting protein of the invention. Note: The
CC present sequence is identical to SEQ ID NO:19 (ADR42064) referred to in
CC example 3.
XX
SQ Sequence 2423 BP; 473 A; 859 C; 729 G; 362 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 11; Length 2423;
Best Local Similarity 71.1%; Pred.No. 6.6e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
Db 209 AGCCCCGGATGCCGGCCCGGAGCGCTGGGGGGCCG 172

RESULT 41
ADR42064/c
ID ADR42064 standard; cDNA; 2423 BP.
XX
```

```
AC ADR42064;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human cancer inhibiting protein PP8857-encoding cDNA, SEQ ID NO:19.
XX
KW Human; PP8857; cancer inhibiting protein; recombinant preparation;
KW gene therapy; cancer; tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1863..2378
FT /*tag= a
FT /product= "Human cancer inhibiting protein PP8857"
XX
PN CN1368511-A.
XX
PD 11-SEP-2002.
XX
PF 08-FEB-2001; 2001CN-00105312.
XX
PR 08-FEB-2001; 2001CN-00105312.
XX
PA (SHAN-) SHANGHAI INST ONCOLOGY.
XX
PI Gu J;
XX
DR WPI; 2003-248949/25.
DR P-PSDB; ADR42065.
XX
PT New human protein with cancer inhibiting function for treating diseases,
PT such as, cancer.
XX
PS Example 3; SEQ ID NO 19; 40pp; Chinese.
XX
CC The invention relates to 12 novel human proteins with cancer inhibiting
CC functions, and to the polynucleotides encoding them. The invention also
CC relates to the recombinant preparation of the proteins, antagonists of
CC the proteins, and the use of the proteins, polynucleotides and
CC antagonists in therapeutic applications for treating diseases such as
CC cancers. The present sequence represents a cDNA encoding a human cancer
CC inhibiting protein of the invention. Note: The present sequence is
CC identical to SEQ ID NO:21 (ADR42106), which is claimed in Claim 5.
XX
SQ Sequence 2423 BP; 473 A; 859 C; 729 G; 362 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 11; Length 2423;
Best Local Similarity 71.1%; Pred.No. 6.6e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
Db 209 AGCCCCGGATGCCGGCCCGGAGCGCTGGGGGGCCG 172

RESULT 42
ABZ12243
ID ABZ12243 standard; DNA; 2979 BP.
XX
AC ABZ12243;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 48.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.
```

XX 24-AUG-2001; 2001WO-US026685.
PF
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
DR WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
PS Claim 144; SEQ ID NO 48; 577pp + Sequence Listing; English.
XX
CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 2979 BP; 817 A; 658 C; 633 G; 871 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 6; Length 2979;
Best Local Similarity 71.1%; Pred. No. 6.6e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCG 39
||| ||| ||| ||| ||| ||| ||| ||| ||| :||
Db 2598 AGCTTCGAGTGCATGTCTCTCGATCGCTGGCTCGTACG 2635

RESULT 43
ADS45922
ID ADS45922 standard; cDNA; 4257 BP.
XX
AC ADS45922;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #665.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 24352; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 4257 BP; 773 A; 1425 C; 1449 G; 610 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 13; Length 4257;
Best Local Similarity 71.1%; Pred. No. 6.7e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
||| ||| ||| ||| ||| ||| ||| ||| ||| :|||
Db 126 GCGCTGGCGGCCAGTCCCTCTTCCCGTCCCGCCGC 163

RESULT 44
AAK84334/C
ID AAK84334 standard; DNA; 6052 BP.
XX
AC AAK84334;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39146.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
DR
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 39146; 3071pp + Sequence Listing; English.
XX

CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 75252 BP; 16571 A; 19384 C; 19541 G; 19756 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 11; Length 75252;
Best Local Similarity 71.1%; Pred. No. 7.6e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGNCGC 40
Db 50417 GGCCCTGGATGCCACACCCCTCATCTCCTGCCCCGTTTAC 50380

RESULT 48
ADJ72363
ID ADJ72363 standard; DNA; 90597 BP.

XX
AC ADJ72363;

XX
DT 06-MAY-2004 (first entry)

XX
DE Streptomyces roseosporus daptomycin biosynthetic gene cluster DNA.

XX ds; gene; antibacterial; gene therapy;
KW daptomycin biosynthesis gene cluster;
KW daptomycin non-ribosomal peptide synthetase; DptBC;
KW gram-positive bacterial infection.

XX Streptomyces roseosporus.

XX WO2003014297-A2.

XX
PD 20-FEB-2003.

XX
PF 31-JUL-2002; 2002WO-US024310.

XX
PR 06-AUG-2001; 2001US-0310385P.

PR 17-OCT-2001; 2001WO-US032354.

PR 10-MAY-2002; 2002US-0379866P.

XX
PA (CUBI-) CUBIST PHARM INC.

XX
PI Miao VPW, Brian P, Baltz RH, Coeffet-Legal MF;

XX
DR WPI; 2003-268192/26.

XX New isolated nucleic acid molecule encoding a daptomycin non-ribosomal
PT peptide synthetase, useful for treatment of a gram-positive bacterial
PT infection of skeletal muscle, skin, bloodstream, kidneys, heart, lung and
PT bone.

XX
PS Disclosure; SEQ ID NO 1; 292pp; English.

XX The invention relates to new isolated nucleic acid (NA) molecules from
CC the Streptomyces roseosporus daptomycin biosynthesis gene cluster,
CC especially a daptomycin non-ribosomal peptide synthetase (NRPS) or its
CC subunit, where the (NA) molecule encodes DptBC, and is not PRHB159. The
CC methods and compositions of the present invention are useful for
CC treatment of a gram-positive bacterial infection of any organ or tissue
CC in the body, including skeletal muscle, skin, bloodstream, kidneys,
CC heart, lung and bone. This sequence represents the daptomycin
CC biosynthesis gene cluster sequence.

XX
SQ Sequence 90597 BP; 12671 A; 32312 C; 31569 G; 14045 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 10; Length 90597;
Best Local Similarity 71.1%; Pred. No. 7.7e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGNCGCG 41
Db 14303 CCTCCGATGGTGCCACACGCGGGTCCCGGCCCG 14340

RESULT 49
ABQ78872
ID ABQ78872 standard; DNA; 90600 BP.

XX
AC ABQ78872;

XX
DT 23-OCT-2002 (first entry)

XX S. roseosporus daptomycin biosynthetic gene cluster 90kb region.

KW Daptomycin biosynthetic gene cluster; thioesterase; antibacterial;
KW fungicide; virucide; antiparasitic; immunomodulator; antilipemic;
KW cytostatic; gene therapy; antimitotic; immunomodulatory; siderophore;
KW anti-cholesterolemic; agrochemical; gene; ds.

XX Streptomyces roseosporus.

XX WO200259322-A2.

XX
PN 01-AUG-2002.

XX
PF 17-OCT-2001; 2001WO-US032354.

XX
PR 17-OCT-2000; 2000US-0240879P.

PR 28-FEB-2001; 2001US-0272207P.

PR 06-AUG-2001; 2001US-0310385P.

XX (MIAO/) MIAO V P W.

PA (BRIA/) BRIAN P.

PA (BALT/) BALTZ R H.

PA (SILV/) SILVA C J.

XX Miao VPW, Brian P, Baltz RH, Silva CJ;

XX WPI; 2002-599794/64.

XX
PS Claim 7; Page 142-165; 227pp; English.

XX The invention relates to a novel isolated nucleic acid molecule
CC comprising a sequence that encodes a thioesterase or thioesterase domain,
CC derived from a bacterial daptomycin biosynthetic gene cluster. The
CC proteins of the invention have antibacterial, fungicide, virucide,
CC antiparasitic, immunomodulator, antilipemic, and cytostatic activity. The
CC polynucleotides may have a use in gene therapy. The compositions and
CC methods of the present invention are useful for generating novel linear
CC and cyclic peptides and improving yield of a product in a cell expressing
CC an daptomycin non-ribosomal peptide synthetase (NRPS) to be used as new
CC compounds or in producing new compounds, such as antibiotics,

CC antifungals, antivirals, antiparasitics, antimitotics, antitumour agents,
CC immunomodulatory agents, anti-cholesterolemic agents, siderophores,
CC agrochemicals and cytostatics. The sequence represents the 90kb region of
CC the S. roseosporus daptomycin biosynthetic gene cluster

XX
SQ Sequence 90600 BP; 12671 A; 32312 C; 31571 G; 14046 T; 0 U; 0 Other;

Query Match 53.7%; Score 22; DB 6; Length 90600;
Best Local Similarity 71.1%; Pred. No. 7.7e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGNCGCG 41

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
Db 162 AAGTTTCCGATGTTAGTTTTTTATCGTTGGTTCGGTCGCG 202

RESULT 52
ABQ16059/c
ID ABQ16059 standard; DNA; 623 BP.
XX AC ABQ16059;
XX 12-JUL-2002 (first entry)
DT XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 2650.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX

CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 623 BP; 226 A; 246 C; 93 G; 58 T; 0 U; 0 Other;

Query Match 53.2%; Score 21.8; DB 6; Length 623;
Best Local Similarity 68.3%; Pred. No. 7.2e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
Db 462 AAGTTTCCGATGTTAGTTTTTTATCGTTGGTTCGGTCGCG 422

RESULT 53
ACL72417
ID ACL72417 standard; DNA; 687 BP.
XX AC ACL72417;
XX 02-JUN-2005 (first entry)
DT XX
DE M. xanthus gene sequence, seq id 8880.
XX
KW Transgenic plant; DNA replication; gene regulation; gene expression;
KW gene; ds.
XX
OS Myxococcus xanthus.
XX
PN US6833447-B1.
XX
PD 21-DEC-2004.
XX
PF 10-JUL-2001; 2001US-00902540.
XX
PR 10-JUL-2000; 2000US-0217883P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX
DR WPI; 2005-028716/03.
XX
PT New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
PS Example 2; SEQ ID NO 8880; 25pp; English.
XX

CC The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1850-9691 represent a
CC set of about 7842 genes or partial genes from the genome of the bacterium
CC Myxococcus xanthus. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from USPTO
XX
SQ Sequence 687 BP; 97 A; 255 C; 232 G; 103 T; 0 U; 0 Other;

Query Match 53.2%; Score 21.8; DB 14; Length 687;
Best Local Similarity 68.3%; Pred. No. 7.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
Db 110 ACGCCTCCGGCGCCCGCCCTTCATCGAGCGCCCGCGGTG 150

RESULT 54
ADX65687/c
ID ADX65687 standard; cDNA; 963 BP.
XX AC ADX65687;
XX 21-APR-2005 (first entry)
DT XX
DE Plant full length insert polynucleotide seqid 36530.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;

KW Metastasis associated gene; cytostatic; gene therapy; cancer;
KW cytosine methylation; gene; ds.
XX Homo sapiens.
OS
XX WO200177376-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-EP003970.
PF
XX 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-010922/01.
DR
XX New nucleic acid derived from chemically treated metastasis genes, useful
PT for diagnosis of cancers by analysis of cytosine methylation, also for
PT treatment.
PT
XX
PS Claim 1; SEQ ID NO 121; 23pp + Sequence Listing; English.
XX
XX The present invention provides a number of human metastasis associated
CC genes which are modified by cytosine methylation. The sequences can be
CC used in the diagnosis and treatment of cancer. The present sequence is
CC one of the genes of the invention
XX
SQ Sequence 6423 BP; 1244 A; 292 C; 1798 G; 3089 T; 0 U; 0 Other;

Query Match 53.2%; Score 21.8; DB 6; Length 6423;
Best Local Similarity 68.3%; Pred. No. 8e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||| | ||||| ||| | ||||| ||||| ||||| ||||| |||||
Db 4861 AAGTTTCGGATGTTAGTTTTTTATCGTTGTTTCGGTCGCG 4901

RESULT 57
ABL70309
ID ABL70309 standard; DNA; 6423 BP.
XX
AC ABL70309;
XX
XX 01-JUL-2002 (first entry)
DT
XX Chemically treated cell signalling DNA sequence#100.
DE
XX Cell signalling; cytosine methylation; cell signalling disease; cancer;
KW tumour; cytostatic; ds.
KW
XX Unidentified.
OS
XX WO200202807-A2.
XX
PN 10-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-EP007471.
PF
XX 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2002-154756/20.
DR

XX Nucleic acid, useful for diagnosis and therapy of diseases associated
PT with cell signaling e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with cell signaling.
XX
PS Claim 1; SEQ ID NO 199; 24pp + Sequence Listing; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signalling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell
CC signalling, as well as oligonucleotides and/or PNA-oligomers for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL70111-ABL70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office
XX
SQ Sequence 6423 BP; 1244 A; 292 C; 1798 G; 3089 T; 0 U; 0 Other;

Query Match 53.2%; Score 21.8; DB 6; Length 6423;
Best Local Similarity 68.3%; Pred. No. 8e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||| | ||||| ||| | ||||| ||||| ||||| ||||| |||||
Db 4861 AAGTTTCGGATGTTAGTTTTTTATCGTTGTTTCGGTCGCG 4901

RESULT 58
ADS99829
ID ADS99829 standard; DNA; 6423 BP.
XX
AC ADS99829;
XX
XX 02-DEC-2004 (first entry)
DT
XX Bisulphite treated human gene associated with metastasis #61.
DE
XX Human; ds; gene; Bisulphite; metastasis; cancer; cytostatic;
KW DNA methylation; matrix-assisted laser desorption/ionisation; MALDI;
KW electrospray; mass spectrometry; CpG dinucleotide; solid tumour.
XX
OS Homo sapiens.
XX
XX US2003148327-A1.
PN
XX 07-AUG-2003.
PD
XX 21-JAN-2003; 2003US-00240485.
PF
XX 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
PR 06-APR-2001; 2001WO-EP003970.
PR
XX (OLEK/) OLEK A.
PA (PIEP/) PIEPENROCK C.
PA (BERL/) BERLIN K.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-010922/01.
DR
XX New nucleic acid derived from chemically treated metastasis genes, useful
PT for diagnosis of cancers by analysis of cytosine methylation, also for

PT treatment.

PS Claim 1; SEQ ID NO 121; 9pp; English.

XX

CC The invention relates to a nucleic acid comprising at least 18 bases from

CC a segment of the chemically pretreated DNA of genes associated with

CC metastasis, i.e. any of ADS99709-ADS99906 human genomic sequences or any

CC of the 19 sequences appearing as ADS99911-ADS99929. SEQ ID 2,4,6 etc are

CC the complements of SEQ ID 1,3,5, etc. Also included are an oligomer

CC (particularly an oligonucleotide or peptide nucleic acid) comprising at

CC least one base sequence of at least 9 bases which hybridises to (or is

CC identical with) the sequences referred to above, producing an array of

CC the oligomers on a carrier, obtaining genetic and/or epigenetic

CC parameters for diagnosis and/or therapy of diseases (or predisposition to

CC them) by analysis of cytosine methylation and a kit comprising a

CC bisulphite (disulphite or hydrogen sulphite) and the oligomers. In the

CC method of above 5-unmethylated cytosines in a genomic DNA sample are

CC converted chemically to uracil, or another base with hybridisation

CC properties different from those of cytosine, then fragments of the

CC treated DNA amplified (particularly by polymerase chain reaction) using

CC the oligomers and a polymerase (preferably heat stable) to produce

CC labelled amplicons. These are tested for hybridisation to an array of

CC oligomers and any hybridisation detected. The amplicons are labelled with

CC fluorescent or radioactive markers, or with a detachable mass marker to

CC allow their detection by mass spectrometry, specifically using the matrix

CC -assisted laser desorption/ionisation (MALDI) or electrospray techniques.

CC To improve detection in the mass spectrometer, fragments formed in the

CC instrument have only a single net charge (positive or negative). The

CC genomic DNA is from e.g. a cell line, biopsy sample, blood, or paraffin-

CC embedded tissue sample. Oligonucleotides or peptide-nucleic acids that

CC are complementary to (or identical with) parts of the nucleic acids listed

CC above may be used as primers for amplification of the nucleic acids or

CC their complements, and for determining cytosine methylation status and/or

CC single nucleotide polymorphisms in metastasis-related genes. They can be

CC used for analysis of diseases associated with methylation of CpG

CC dinucleotides and to determine (epi)genetic parameters for diagnosis

CC and/or therapy of disease (or predisposition). The genomic DNA sequences

CC are useful for diagnosis and therapy of solid tumours and cancer. The

CC present sequence is a bisulphite treated human gene associated with

CC metastasis. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly

CC from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030148327.

XX

SQ Sequence 6423 BP; 1244 A; 292 C; 1798 G; 3089 T; 0 U; 0 Other;

Query Match 53.2%; Score 21.8; DB 7; Length 6423;

Best Local Similarity 68.3%; Pred. No. 8e+02;

Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41

Db 4861 AAGTTTTCGGATGTTAGTTTTATCGTTGTTGTCGTCGCG 4901

RESULT 59

ABL02587

ID ABL02587 standard; cDNA; 6492 BP.

XX

AC ABL02587;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2243.

XX

XX Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ss.

KW

XX Drosophila melanogaster.

OS

XX WO200171042-A2.

PN

XX 27-SEP-2001.

PD

XX

PF 23-MAR-2001; 2001WO-US009231.

XX

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

XX

PI WPI; 2001-656860/75.

DR P-PSDB; ABB58484.

DR

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell

PT interactions.

PT

XX Claim 1; SEQ ID NO 2243; 2lpp + Sequence Listing; English.

PS

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-

CC ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 6492 BP; 1838 A; 1579 C; 1755 G; 1320 T; 0 U; 0 Other;

Query Match 53.2%; Score 21.8; DB 4; Length 6492;

Best Local Similarity 68.3%; Pred. No. 8e+02;

Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41

Db 238 AAGTCGCCGGATGCCCTCACCTCCCTGTTGGCCCGAAGAG 278

RESULT 60

AAA81461

ID AAA81461 standard; DNA; 9941 BP.

XX

AC AAA81461;

XX

DT 04-DEC-2000 (first entry)

XX

DE N. meningitidis partial DNA sequence gnm_9 SEQ ID NO:9.

XX

KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;

KW antigen; vaccine; diagnosis; infection; antibacterial; identification;

KW Meningococcus B; MenB; ds.

XX

OS Neisseria meningitidis.

XX

XX WO200022430-A2.

PN

XX

PD 20-APR-2000.

XX

XX

PF 08-OCT-1999; 99WO-US023573.

XX

XX

PR 09-OCT-1998; 98US-0103794P.

PR 30-APR-1999; 99US-0132068P.

XX

XX (CHIR) CHIRON CORP.

PA

XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;

PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;

PI Rappuoli R, Pizza M;

XX

XX WPI; 2000-318079/27.

DR

XX

PT Isolated nucleotide sequences of Neisseria meningitidis which can be used
PT in the diagnosis and treatment of N. meningitidis infection and other
PT Neisserial infections, for example, N.gonorrhoea.

PS Claim 7; Page 326-329; 1760pp; English.

XX The present invention describes methods of obtaining immunogenic proteins
CC from Neisseria genomic sequences. AAA81453 to AAA82414 represent
CC specifically claimed Neisseria meningitidis genomic DNA sequences;
CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA
CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
CC Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to Neisserial bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against Meningococcus B; against all serotypes; and/or against all
CC pathogenic Neissariae. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious Meningococcus B
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions

XX Sequence 9941 BP; 2330 A; 2662 C; 2649 G; 2300 T; 0 U; 0 Other;

SQ Query Match 53.2%; Score 21.8; DB 3; Length 9941;
Best Local Similarity 68.3%; Pred. No. 8.2e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41

Db 1752 AAGCCGCCGCTGCGAGTACGGTATGCGGGCGCGGATGCG 1792

RESULT 61

ACL64482/c

ID ACL64482 standard; DNA; 10528 BP.

XX ACL64482;

AC ACL64482;

XX 02-JUN-2005 (first entry)

DT M. xanthus DNA fragment, seq id 945.

DE Transgenic plant; DNA replication; gene regulation; gene expression; ds.

XX Myxococcus xanthus.

OS US6833447-B1.

XX 21-DEC-2004.

PF 10-JUL-2001; 2001US-00902540.

XX 10-JUL-2000; 2000US-0217883P.

PR (MONS) MONSANTO TECHNOLOGY LLC.

XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

PI WPI; 2005-028716/03.

XX New substantially purified Myxococcus xanthus nucleic acid molecule

PT encoding a nitrite reductase, useful for determining gene expression,

PT identifying mutations in a gene of interest, and for constructing

PT mutations in a gene of interest.

XX Example 1; SEQ ID NO 945; 25pp; English.

PS The invention relates to a substantially purified nucleic acid molecule
XX encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1-1849 represent a
CC set of 1849 contig and singleton sequences comprising coding sequences,
CC DNA replication elements, promoters and other regulatory elements from
CC the genome of the bacterium Myxococcus xanthus. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO

XX Sequence 10528 BP; 1463 A; 3512 C; 3806 G; 1747 T; 0 U; 0 Other;

SQ Query Match 53.2%; Score 21.8; DB 14; Length 10528;

Best Local Similarity 68.3%; Pred. No. 8.2e+02;

Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41

Db 8588 ACGCCTCCGGGCCAGGCCCTTCATCGAGCGCCCGCGGTG 8548

RESULT 62

ABL02586

ID ABL02586 standard; cDNA; 16105 BP.

XX ABL02586;

AC ABL02586;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2240.

XX Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ss.

XX Drosophila melanogaster.

OS WO200171042-A2.

XX 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

PA Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR P-PSDB; ABB58483.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell

PT interactions.

XX Claim 1; SEQ ID NO 2240; 21pp + Sequence Listing; English.

PS The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-

DR WPI; 2000-013262/01.

XX Isolation of polynucleotides from mycobacterial genomes, useful for

PT detection of Mycobacteria and for combating tuberculosis.

XX

PS Claim 23; Page 90; 161pp; English.

XX

CC The present invention describes a method for isolating a polynucleotide

CC of interest that is present or is expressed in a genome of a first

CC mycobacterium strain and that is absent or altered in a genome of a

CC second mycobacterium strain, which is different from the first strain

CC using a bacterial artificial chromosome (BAC) vector. Recombinant BAC

CC vectors, which are preferably immobilised, can be used to detect

CC mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological

CC samples. The polynucleotides identified are useful as probes or primers

CC for detecting a given mycobacterium of interest. By aligning the

CC polynucleotides contained in the recombinant BAC vectors it is possible

CC to physically map a polynucleotide of mycobacterial origin in a

CC biological sample. The methods and vectors from the present invention are

CC useful in providing information for combating tuberculosis. It is

CC possible to compare genomes between different strains or species and

CC their non-pathogenic strains or species counterparts. ABQ62492 to

CC ABQ63228 and ABB81227 to ABB81230 represent sequences used in the

CC exemplification of the present invention

XX

SQ Sequence 230 BP; 39 A; 87 C; 59 G; 43 T; 0 U; 2 Other;

Query Match 52.7%; Score 21.6; DB 3; Length 230;

Best Local Similarity 72.2%; Pred. No. 8.1e+02;

Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 TCCGGATGCCAGTCCTCATCGCTGCCCGGCGCG 41

DB 33 TCCGGATTCTGGGCTTCATCGCTCGCGCGTGGCG 68

RESULT 66

ADQ54664

ID ADQ54664 standard; DNA; 562 BP.

XX

AC ADQ54664;

XX

DT 21-OCT-2004 (first entry)

XX

DE Novel canine microarray-related DNA sequence SeqID5966.

XX

KW canine microarray; drug screening; toxicity assay;

KW environmental pollutant; cellular response; gene expression profile;

KW toxic response; liver necrosis; fatty liver disease;

KW protein adduct formation; hepatitis; dog; ds.

XX

OS Canis familiaris.

XX

PN WO2004063324-A2.

XX

PD 29-JUL-2004.

XX

PF 05-MAY-2003; 2003WO-US013853.

XX

PR 03-MAY-2002; 2002US-0377240P.

XX

PA (GENE-) GENE LOGIC INC.

PA (PFIZ) PFIZER PROD INC.

XX

PI Diggins JC, Porter M, Wei T;

XX

DR WPI; 2004-561890/54.

XX

PT New isolated nucleic acid molecule, useful for drug screening and

PT toxicity assays or for assessing the impact, including toxicity, of a

PT compound, pharmaceutical agent or environmental pollutant on a cell or

PT living organism.

XX

PS Claim 1; SEQ ID NO 5966; 41pp; English.

XX

CC This invention is related to a novel isolated canine nucleic acid

CC sequences and the construction of canine microarrays containing a

CC significant portion of the canine genome. The isolated canine nucleic

CC acid sequences of the invention may be useful for drug screening and

CC toxicity assays. The invention is therefore useful for assessing the

CC impact, including toxicity, of a compound, pharmaceutical agent or

CC environmental pollutant on a cell or living organism. The methods are

CC useful for detecting genes that are up- or down-regulated in canines in a

CC disease state. The sequences are useful as diagnostic agents or markers

CC to detect a cellular response in a sample individually or as part of a

CC gene expression profile. It is also useful as a target for agents that

CC modulate gene expression or activity. The database is useful for

CC producing electronic Northernns that allow the user to determine the cell

CC type or tissue in which a given gene is expressed and to allow

CC determination of the abundance or expression level of a given gene in a

CC particular tissue or cell. The methods are useful for determining the

CC similarity of a toxic response to one or more individual compounds. The

CC methods are useful for predicting at least one toxic response or the

CC likelihood that a compound or test agent will induce various specific

CC pathologies such as those of the liver (liver necrosis, fatty liver

CC disease, protein adduct formation or hepatitis), those of the kidney,

CC heart, brain or testes, or other pathologies associated with at least one

CC of the toxins. The methods are also useful for predicting or elucidating

CC the potential cellular pathways influenced, induced or modulated by the

CC compound or test agent due to the similarity of the expression profile

CC compared to the profile induced by a known toxin. The present sequence is

CC that of a canine DNA sequence which was claimed for use during the

CC production of a canine microarray of the invention.

XX

SQ Sequence 562 BP; 136 A; 177 C; 152 G; 96 T; 0 U; 1 Other;

Query Match 52.7%; Score 21.6; DB 13; Length 562;

Best Local Similarity 72.2%; Pred. No. 8.4e+02;

Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCTCATCGCTGGCCCGGN 37

DB 298 AGCTCCGCCGCCCAAGTTCCTCCAGCTCTGGCCCGGT 333

RESULT 67

ACL66884

ID ACL66884 standard; DNA; 1689 BP.

XX

AC ACL66884;

XX

DT 02-JUN-2005 (first entry)

XX

DE M. xanthus gene sequence, seq id 3347.

XX

KW Transgenic plant; DNA replication; gene regulation; gene expression;

KW gene; ds.

XX

OS Myxococcus xanthus.

XX

PN US6833447-B1.

XX

PD 21-DEC-2004.

XX

PF 10-JUL-2001; 2001US-00902540.

XX

PR 10-JUL-2000; 2000US-0217883P.

XX

PA (MONS) MONSANTO TECHNOLOGY LLC.

XX

PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX

DR WPI; 2005-028716/03.

XX

PT New substantially purified Myxococcus xanthus nucleic acid molecule

PT encoding a nitrite reductase, useful for determining gene expression,

PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
PS Example 2; SEQ ID NO 3347; 25pp; English.
XX
CC The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1850-9691 represent a
CC set of about 7842 genes or partial genes from the genome of the bacterium
CC Myxococcus xanthus. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from USPTO
XX
SQ Sequence 1689 BP; 302 A; 592 C; 611 G; 184 T; 0 U; 0 Other;

Query Match 52.7%; Score 21.6; DB 14; Length 1689;
Best Local Similarity 72.2%; Pred. No. 8.8e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNC 38
||| ||| || ||||| || ||||| ||| ||||| :|
Db 765 GCCCCGGTGCCCGTCCCTCCGCGCGCGCCGCC 800

RESULT 68
ACL64694
ID ACL64694 standard; DNA; 18537 BP.
XX
AC ACL64694;
XX
DT 02-JUN-2005 (first entry)
XX
DE M. xanthus DNA fragment, seq id 1157.
XX
KW Transgenic plant; DNA replication; gene regulation; gene expression; db.
XX
OS Myxococcus xanthus.
XX
PN US6833447-B1.
XX
PD 21-DEC-2004.
XX
PF 10-JUL-2001; 2001US-00902540.
XX
PR 10-JUL-2000; 2000US-0217883P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
XX
DR WPI; 2005-028716/03.
XX
PT New substantially purified Myxococcus xanthus nucleic acid molecule
PT encoding a nitrite reductase, useful for determining gene expression,
PT identifying mutations in a gene of interest, and for constructing
PT mutations in a gene of interest.
XX
PS Example 1; SEQ ID NO 1157; 25pp; English.
XX
CC The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 1-1849 represent a
CC set of 1849 contig and singleton sequences comprising coding sequences,
CC DNA replication elements, promoters and other regulatory elements from
CC the genome of the bacterium Myxococcus xanthus. Note: The sequence data

CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO
XX
SQ Sequence 18537 BP; 2809 A; 6703 C; 6248 G; 2777 T; 0 U; 0 Other;

Query Match 52.7%; Score 21.6; DB 14; Length 18537;
Best Local Similarity 72.2%; Pred. No. 9.8e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNC 38
||| ||| || ||||| || ||||| ||| ||||| :|
Db 1169 GCCCCGGTGCCCGTCCCTCCGCGCGCGCCGCC 1204

RESULT 69
ABD33069
ID ABD33069 standard; DNA; 24883 BP.
XX
AC ABD33069;
XX
DT 18-NOV-2004 (first entry)
XX
DE Murine cancer-associated (CA) gene MD07-001.
XX
KW Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW ds; cancer; cytostatic.
XX
OS Mus musculus.
XX
PN WO2004058146-A2.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040081.
XX
PR 17-DEC-2002; 2002US-00322281.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-499109/47.
XX
PT Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS Disclosure; SEQ ID NO 1; 182pp; English.
XX
CC The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a murine CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 24883 BP; 5917 A; 5582 C; 5819 G; 6459 T; 0 U; 1106 Other;

Query Match 52.7%; Score 21.6; DB 13; Length 24883;
Best Local Similarity 72.2%; Pred. No. 9.9e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCGCCGCGNC 39
||||| ||||| || ||| || ||| ||||| :||

Db 6088 CCTCAGGATGACTGTCACTTAAGGCTGCCCGGTACG 6123

RESULT 70
ABQ81846/c
ID ABQ81846 standard; DNA; 349980 BP.
XX
AC ABQ81846;
XX
DT 19-NOV-2002 (first entry)
XX
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.
XX
KW Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;
KW anti-diarrheic; antibacterial; inhibitor of Salmonella; detection;
KW identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;
KW rotavirus; food composition; pharmaceutical composition; gene; ds.
XX
OS Bifidobacterium longum.
OS Synthetic.
XX
PN EP1227152-A1.
XX
PD 31-JUL-2002.
XX
PF 30-JAN-2001; 2001EP-00102050.
XX
PR 30-JAN-2001; 2001EP-00102050.
XX
PA (NEST) SOC PROD NESTLE SA.
XX
DR WPI; 2002-668397/72.
XX
PT Novel polynucleotide comprising Bifidobacterium genome sequence useful as
PT a probe or primer for detecting and/or identifying Bifidobacterium longum
PT in a biological sample.
XX
PS Disclosure; SEQ ID NO 1102; 80pp; English.
XX
CC The present invention describes a polynucleotide (I) comprising a
CC sequence of a Bifidobacterium genome selected from the nucleotide
CC sequences given in ABQ81842 and ABQ81843, or a sequence exhibiting at
CC least 90% identity or which hybridises with the sequences given in
CC ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding a
CC fusion protein, comprising a sequence selected from 1097 sequences given
CC in ABP65258 to ABP66354 ligated in frame to a polynucleotide encoding a
CC heterologous polypeptide. (I) has anti-diarrheic and antibacterial
CC activities, and can be used as an inhibitor of Salmonella. (I) (which is
CC a probe) is useful for the detection and/or identification of
CC Bifidobacterium longum in a biological sample. A carrier containing the
CC lactic acid bacterium Bifidobacterium longum NCC2705 (NCIM I-2618) can be
CC used for preventing and/or treating diarrhoea brought about by pathogenic
CC bacteria and/or rotavirus. The carrier is a food composition selected
CC from milk, yogurt, curd, cheese, fermented milks, milk based fermented
CC products, ice-creams, fermented cereal based products, milk based
CC powders, infant formula, pet food or a pharmaceutical composition
CC selected from tablets, liquid bacterial suspensions, dried oral
CC supplement, wet oral supplement, dry tube feeding or wet tube feeding.
CC (I) is useful in DNA arrays or chips to carry out analysis of the
CC expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent
CC Bifidobacterium related nucleotide sequences given in the Sequence
CC Listing from the present invention but not mentioned further within the
CC specification. N.B. The sequence data for this patent is not represented
CC in the printed specification but is based on sequence information
CC supplied by the European Patent Office
XX
SQ Sequence 349980 BP; 69200 A; 103414 C; 105147 G; 72219 T; 0 U; 0 Other;

Query Match 52.7%; Score 21.6; DB 6; Length 349980;
Best Local Similarity 72.2%; Pred. No. 1.1e+03;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39

Db 195457 CCTCCGAAAGCCACAGCCTGATCGCGCGCTGTCCG 195422

RESULT 71
ABD06358
ID ABD06358 standard; DNA; 234 BP.
XX
AC ABD06358;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #4962.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO72787.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 4962; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 234 BP; 33 A; 76 C; 77 G; 48 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 11; Length 234;
Best Local Similarity 69.2%; Pred. No. 9.4e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
Db 93 GCCCGCGAATTCCACTCGCTCTTCACTCCGCTTGGCCGCG 131

RESULT 72
ABQ99123/c
ID ABQ99123 standard; DNA; 292 BP.
XX

XX AC ABX51132;
XX DT 25-FEB-2003 (first entry)
XX DE Bovine EST associated with lactation/muscle/fat deposition #1061.
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX OS Bos Taurus.
XX PN US2002137160-A1.
XX PD 26-SEP-2002.
XX PF 26-OCT-2001; 2001US-00983965.
PR 17-DEC-1998; 98US-0113678P.
PR 15-DEC-1999; 99US-00465231.
XX (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
PI WPI; 2003-102386/09.
XX Purified nucleic acid molecules, useful for genome mapping, gene
PT identification and analysis, cattle breeding or preparation of constructs
PT for cattle gene expression and genetically improved cattle.
XX Claim 2; SEQ ID NO 1061; 38pp; English.
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 5912 nucleotide sequences,
CC appearing as ABX50072-ABX55983, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 5912 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the 5912
CC bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present
CC sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137160
XX SQ Sequence 381 BP; 80 A; 118 C; 111 G; 72 T; 0 U; 0 Other;
Query Match 52.2%; Score 21.4; DB 8; Length 381;
Best Local Similarity 69.2%; Pred. No. 9.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 2 AGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
Db 261 AACCAGCGAGACCAGTCCCACTTGGCAGCCCTGAAGC 223

RESULT 75
ABX50790
ID ABX50790 standard; cDNA; 381 BP.
XX AC ABX50790;
XX DT 25-FEB-2003 (first entry)
XX DE Bovine EST associated with lactation/muscle/fat deposition #719.
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX OS Bos Taurus.
XX PN US2002137160-A1.
XX PD 26-SEP-2002.
XX PF 26-OCT-2001; 2001US-00983965.
PR 17-DEC-1998; 98US-0113678P.
PR 15-DEC-1999; 99US-00465231.
XX (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
PI WPI; 2003-102386/09.
XX Purified nucleic acid molecules, useful for genome mapping, gene
PT identification and analysis, cattle breeding or preparation of constructs
PT for cattle gene expression and genetically improved cattle.
XX Claim 2; SEQ ID NO 719; 38pp; English.
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 5912 nucleotide sequences,
CC appearing as ABX50072-ABX55983, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 5912 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the 5912
CC bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present
CC sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137160
XX SQ Sequence 381 BP; 70 A; 113 C; 119 G; 79 T; 0 U; 0 Other;
Query Match 52.2%; Score 21.4; DB 8; Length 381;
Best Local Similarity 69.2%; Pred. No. 9.6e+02;

ABA311177
ID ABA311177 standard; DNA; 572 BP.
XX
AC ABA311177;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #9643 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 1; SEQ ID NO 9643; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 572 BP; 116 A; 135 C; 187 G; 134 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 4; Length 572;
Best Local Similarity 69.2%; Pred. No. 9.8e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
Db 134 GCATTGGATGCTGGTCCCGCAAGGCTGGCGAGGCCACG 172

RESULT 83
AAK12507
ID AAK12507 standard; DNA; 572 BP.
XX
AC AAK12507;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 12498.
XX

KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 12498; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 572 BP; 116 A; 135 C; 187 G; 134 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 4; Length 572;
Best Local Similarity 69.2%; Pred. No. 9.8e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
Db 134 GCATTGGATGCTGGTCCCGCAAGGCTGGCGAGGCCACG 172

RESULT 84
ADD68671/C
ID ADD68671 standard; DNA; 597 BP.
XX
AC ADD68671;
XX
DT 15-JAN-2004 (first entry)
XX
DE Murine DNA amplification-related DNA - SEQ ID 28.
XX
KW PCR; DNA amplification; ds; mouse; murine.
XX
OS Mus sp.
XX
PN JP2002315583-A.
XX
PD 29-OCT-2002.
XX
PF 29-JUN-2001; 2001JP-00197813.
XX
PR 29-JUN-2000; 2000JP-00196242.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.

XX WPI; 2003-375838/36.
XX
PT Amplification of a DNA, a gene encoding the repeated sequence of an amino
PT acid sequence.
XX
PS Example 3; SEQ ID NO 28; 33pp; Japanese.
XX
CC The invention relates to a novel method for amplifying a DNA using
CC polymerase chain reaction (PCR) comprising synthesising the first region
CC of a base sequence to be amplified by designing a pair of primers so as
CC to place the first region between them and to anneal each other at the 3'
CC -end and carrying out a polymerase chain reaction (PCR) using the
CC primers. Subsequently, the second region is synthesised by designing a
CC pair of primers so as to place the second region partly overlapping with
CC the first region of the base sequence between them and to anneal each
CC other at the 3'-end and carrying out a PCR using the primers. Finally,
CC the first region is annealed to the second region generating the template
CC to carry out a PCR and thus to synthesize a base sequence containing the
CC first and the second regions. The method of the invention may be useful
CC for amplifying a DNA sequence. The current sequence is that of the murine
CC DNA amplification-related DNA of the invention.
XX
SQ Sequence 597 BP; 135 A; 169 C; 174 G; 119 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 10; Length 597;
Best Local Similarity 69.2%; Pred. No. 9.8e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
||||| ||| ||||| | ||||| ||||| :|||
Db 130 AGCCTCTGGAGTCCAGTAGCGTGCCGTGGCGGGCGC 92

RESULT 85
AAX81396/c
ID AAX81396 standard; cDNA to mRNA; 630 BP.
XX
AC AAX81396;
XX
DT 24-AUG-1999 (first entry)
XX
DE Polynucleotide used in the preparation of heparin-combining protein.
KW Heparin-combining protein; sugar chain; heat resistance; acid resistance;
KW sugar chain-added type heparin-combining protein; alkali resistance;
KW protease resistance; ds.
XX
OS Unidentified.
XX
PN JP11137255-A.
XX
PD 25-MAY-1999.
XX
PF 10-NOV-1997; 97JP-00307721.
XX
PR 10-NOV-1997; 97JP-00307721.
XX
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
XX
DR WPI; 1999-374376/32.
DR P-PSDB; AAY22980.
XX
XX Sugar chain-added type heparin-combining protein - useful in drug
PT composition for production of high function protein.
PT
PS Disclosure; Page 19; 28pp; Japanese.
XX
CC The specification describes a heparin-combining protein produced by
CC covalently combining a sugar chain. The protein is prepared by linking a
CC cDNA coding a peptide which can be added by a sugar chain with a cDNA
CC coding a heparin-combining protein, recombinating the linked cDNA to an
CC expression vector, introducing the expression vector to a host cell

CC having a sugar chain adding path, and expressing the heparin-combining
CC protein in which a sugar chain is covalently combined through a peptide
CC which can be added by a sugar chain. The new sugar chain-added type
CC heparin-combining protein has excellent heat resistance, acid resistance,
CC alkali resistance and protease resistance. The present sequence is used
CC in the course of the invention
XX
SQ Sequence 630 BP; 148 A; 159 C; 191 G; 132 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 2; Length 630;
Best Local Similarity 69.2%; Pred. No. 9.9e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
||||| ||| ||||| | ||||| ||||| :|||
Db 130 AGCCTCTGGAGTCCAGTAGCGTGCCGTGGCGGGCGC 92

RESULT 86
ABD14505/c
ID ABD14505 standard; DNA; 654 BP.
XX
AC ABD14505;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #13109.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO80934.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 13109; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 654 BP; 110 A; 231 C; 208 G; 105 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 11; Length 654;
Best Local Similarity 69.2%; Pred. No. 9.9e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
||| ||| ||| ||| ||| ||| ||| ||| : |||
Db 390 GCAACCGAGGCCAGTTCTCTCGTCGCGCCAGCCAGCG 352

RESULT 87
ABD14229
ID ABD14229 standard; DNA; 738 BP.
XX
AC ABD14229;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #12833.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO80658.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 12833; 455pp; English.
XX

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 738 BP; 126 A; 230 C; 254 G; 128 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 11; Length 738;
Best Local Similarity 69.2%; Pred. No. 9.9e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
||| ||| ||| ||| ||| ||| ||| ||| : |||
Db 310 GCAACCGAGGCCAGTTCTCTCGTCGCGCCAGCCAGCG 348

RESULT 88
ABD11508/c
ID ABD11508 standard; DNA; 816 BP.
XX
AC ABD11508;
XX
DT 29-JUL-2004 (first entry)
XX

DE Pseudomonas aeruginosa polynucleotide #10112.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO77937.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 10112; 455pp; English.
XX

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX

SQ Sequence 816 BP; 161 A; 299 C; 233 G; 123 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 11; Length 816;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCGCG 41
||| ||| ||| ||| ||| ||| ||| ||| : |||
Db 82 GCCACCTGATGCCAGGACAGCTTGACCGCCTGGCGCG 44

RESULT 89
ABD11440/c
ID ABD11440 standard; DNA; 834 BP.
XX
AC ABD11440;
XX

PR 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO80773.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 12948; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 966 BP; 168 A; 333 C; 298 G; 167 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 11; Length 966;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCCGNCGCG 41
|| ||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 604 GCAACCGCAGCCAGTTCCTCGTCGTCGCCAGCCAGCG 566

RESULT 92
ADT47081/c
ID ADT47081 standard; cDNA; 1236 BP.
XX
AC ADT47081;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #21832.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 45519; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1236 BP; 167 A; 426 C; 446 G; 197 T; 0 U; 0 Other;

Query Match 52.2%; Score 21.4; DB 13; Length 1236;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCCGNCGCG 41
|| ||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 476 GCCTCCGGTCCGACAGAGGCTCATCGCCGTCAGGTGTCG 438

RESULT 93
ADA48031/c
ID ADA48031 standard; DNA; 1305 BP.
XX
AC ADA48031;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene conferring disease resistance in plants.
XX
KW disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant.
XX
OS Oryza sativa.
XX
PN WO2003000906-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-IB002453.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 26-SEP-2001; 2001US-0352277P.
PR 22-MAR-2002; 2002US-0366535P.

XX PF 15-AUG-2003; 2003WO-US026073.
XX PR 15-AUG-2002; 2002US-0404311P.
XX PA (FUNC-) FUNCTIONAL GENETICS INC.
XX PI Li L, Aghdasi B;
XX DR WPI; 2004-269214/25.
XX PT New purified mammalian rapamycin resistance and tumorigenesis (RapR7)
PT protein, useful for diagnosing and/or treating diseases or conditions
PT associated with rapamycin resistance, cancer and tumorigenesis.
XX PS Disclosure; SEQ ID NO 19; 128pp; English.
XX CC The present invention describes a purified mammalian rapamycin resistance
CC and tumorigenesis (RapR7) protein. RapR7 has cytostatic activity.
CC Methods and compositions of the present invention are useful for the
CC diagnosis and/or treatment of diseases or conditions associated with
CC rapamycin resistance, cancer and tumorigenesis, and for identifying
CC agents for treating these conditions. The present sequence represents a
CC human RapR7 regulatory region nucleotide sequence, which is used in the
CC exemplification of the present invention.
XX SQ Sequence 1440 BP; 216 A; 460 C; 519 G; 245 T; 0 U; 0 Other;
Query Match 52.2%; Score 21.4; DB 12; Length 1440;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGNCGCG 41
Db 1029 GCGCCCGCCCGCGCCCTCGCGCGCCCGGGGCG 991
RESULT 98
ABQ91417
ID ABQ91417 standard; DNA; 1470 BP.
XX AC ABQ91417;
XX DT 01-OCT-2002 (first entry)
XX DE M. capsulatus gene #1402 for DNA array.
XX KW Micro array; gene; ds; differential expression; gene expression.
XX OS Methylococcus capsulatus.
XX PN WO200255655-A2.
XX PD 18-JUL-2002.
XX PF 14-JAN-2002; 2002WO-NO000019.
XX PR 12-JAN-2001; 2001NO-00000235.
XX PR 12-JAN-2001; 2001NO-00000239.
XX PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
XX PA (TIGR-) TIGR.
XX PI Birkeland NK, Eidhammer I, Jonassen I, Jensen HB, Lien T;
PI Lillehaug JR, Lossius I, Eisen JA, Fraser CM, Durkin AS;
PI Salzberg SL;
XX WPI; 2002-557818/59.
XX Novel DNA array useful for determining differential expression of
PT Methylococcus capsulatus genes, comprises polynucleotides or
PT oligonucleotides representative for a selective number of Methylococcus
PT capsulatus genes.

XX PS Claim 14; Page 556-557; 678pp; English.
XX CC The invention relates to a novel DNA array giving a representation of a
CC number of Methylococcus capsulatus genes. The method of the invention is
CC useful for determination of the differential expression of the genes of
CC M. capsulatus, and for studying gene expression on a genomic scale and in
CC gene expression assays of M. capsulatus genes. The sequences shown in
CC ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
CC invention
XX SQ Sequence 1470 BP; 252 A; 460 C; 477 G; 281 T; 0 U; 0 Other;
Query Match 52.2%; Score 21.4; DB 6; Length 1470;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGGNCGC 40
Db 86 AGCCGCGCGGACCTCGACCCCTCAACGCTGCGCGCGCGC 124
RESULT 99
ABL19573
ID ABL19573 standard; DNA; 1861 BP.
XX AC ABL19573;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 10192.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX PS Claim 1; SEQ ID NO 10192; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1861 BP; 525 A; 495 C; 510 G; 331 T; 0 U; 0 Other;
Query Match 52.2%; Score 21.4; DB 4; Length 1861;
Best Local Similarity 69.2%; Pred. No. 1e+03;

Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0; Job time : 301 secs

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGCTGCCCGGNCG 39
||| | ||||| ||||| ||||| : |
Db 1589 AACCAACGATGCCAGTTCCTCAAGGTGGCCCAATTG 1627

RESULT 100
ACL36154
ID ACL36154 standard; cDNA; 2000 BP.
XX
AC ACL36154;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice stress-regulated promoter SEQ ID NO:14717.
XX
KW ss; abiotic stress tolerance; transgenic plant; cereal;
KW agriculture.
XX

OS Oryza sativa.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
DR WPI; 2003-248011/24.
XX

PT New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
PS Claim 48; SEQ ID NO 14717; 89pp; English.
XX

CC The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX

SQ Sequence 2000 BP; 412 A; 709 C; 524 G; 354 T; 0 U; 1 Other;

Query Match 52.2%; Score 21.4; DB 11; Length 2000;
Best Local Similarity 69.2%; Pred. No. 1e+03;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGCCCGGNCGG 41
||| | ||||| ||||| ||||| : ||
Db 1098 GCCACACAGTCCACGCGGTACCGGTGCCGTCCCG 1136

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model
Run on: May 9, 2006, 22:17:45 ; Search time 1878 Seconds
(without alignments)
1021.443 Million cell updates/sec
Title: US-09-904-968A-1_N3336_COPY_3300_3340
Perfect score: 41
Sequence: 1 aagcctccgatgccagtc.....tcatcgctggccgncgcg 41

Scoring table: IDENTITY_NUCDX
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries
Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_htc: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gse1: *
10: gb_gse2: *
11: gb_gse3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	39.4	96.1	340	9	AQ939774 NR5-118R
C 2	28.4	69.3	702	9	BZ892025 Hml2_0104
C 3	24.8	60.5	611	8	DN393531 LIB3934-0
C 4	24.4	59.5	690	10	CG190773 PUILD25TD
C 5	24.2	59.0	890	2	BG772871 602721069
C 6	24	58.5	445	7	CO336372 EN12413.5
C 7	24	58.5	555	5	BQ384615 NISC_mn07
C 8	24	58.5	745	10	AL206826 Tetraodon
C 9	24	58.5	806	5	BU279692 603865894
C 10	23.8	58.0	1101	10	CNS000K2
C 11	23.6	57.6	356	9	BH841209 Drosophil
C 12	23.6	57.6	584	10	CE771255 tigr-gss-
C 13	23.6	57.6	646	8	CX775930 UI-EH-HG2
C 14	23.6	57.6	727	3	BI888178 ZF637-1-0
C 15	23.6	57.6	730	8	CX774191 UI-EH-HG1
C 16	23.6	57.6	884	10	AG848813 Oryza sat
C 17	23.6	57.6	917	3	BI662946 603286312
C 18	23.4	57.1	483	7	CO983269 GM89018A2
C 19	23.4	57.1	576	6	CF246184 TgESTzyl5
C 20	23.4	57.1	1209	8	DN684120 CGX34-A07
C 21	23.4	57.1	1404	8	DN655453 CEC17-B09
C 22	23.2	56.6	374	5	BY278985 BY278985

96	22.4	54.6	415	3	BM721516	BM721516 UI-E-E01-	C 169	22	53.7	624	10	CW026783
97	22.4	54.6	482	2	BG717495	BG717495 602689259	C 170	22	53.7	633	2	BE410885
98	22.4	54.6	554	5	BQ785316	BQ785316 saq76a07.	171	22	53.7	633	11	CNS0710Q
99	22.4	54.6	638	10	CW579372	CW579372 OA_ABa010	172	22	53.7	635	2	BI064629
C 100	22.4	54.6	680	10	AG104213	AG104213 Pan trogl	173	22	53.7	641	10	CG037953
	22.4	54.6	692	10	CW592639	CW592639 OA_ABA012	174	22	53.7	642	9	BZ779785
C 102	22.4	54.6	727	9	AZ074798	AZ074798 RPCI-23-4	175	22	53.7	647	2	BE386619
	22.4	54.6	737	10	CZ722561	CZ722561 OC_Ba004	176	22	53.7	675	5	BU393876
103	22.4	54.6	753	10	CZ726194	CZ726194 OC_Ba005	177	22	53.7	684	8	DN256838
C 105	22.4	54.6	759	3	BI967604	BI967604 GMB30002B	178	22	53.7	688	8	DR006928
	22.4	54.6	771	10	CL542062	CL542062 OB_Ba006	179	22	53.7	693	6	CA415230
107	22.4	54.6	791	1	AI765898	AI765898 wh66h06.x	180	22	53.7	704	3	BP450095
C 108	22.4	54.6	798	3	BI825415	BI825415 603072344	181	22	53.7	709	10	CL819350
	22.4	54.6	821	7	CO796485	CO796485 AGENCOURT	182	22	53.7	718	2	BE390186
110	22.4	54.6	901	8	DN784286	DN784286 92288392	183	22	53.7	720	8	CV804593
C 111	22.4	54.6	902	9	BZ553902	BZ553902 pacsl-60	184	22	53.7	728	7	CK359451
	22.4	54.6	989	9	CC222573	CC222573 CH261-48E	185	22	53.7	733	8	DR081743
C 112	22.4	54.6	1034	2	BE866354	BE866354 601678814	186	22	53.7	737	2	BG760245
C 113	22.4	54.6	1166	6	CD500566	CD500566 CDA45-G03	187	22	53.7	743	2	BG427686
C 114	22.4	54.6	1166	6	CD500566	CD500566 CDA45-G03	187	22	53.7	743	2	BG427686
C 115	22.2	54.1	387	10	CZ394778	CZ394778 ZMMBF0174	188	22	53.7	758	3	BP441623
C 116	22.2	54.1	654	6	CA680933	CA680933 wlm24.pk0	189	22	53.7	765	8	DN124579
C 117	22.2	54.1	661	6	CD924532	CD924532 G750.113G	190	22	53.7	773	7	CK771392
118	22.2	54.1	675	7	CO121308	CO121308 GR_EB02H	191	22	53.7	778	8	DR081806
119	22.2	54.1	677	10	CZ234435	CG234435 OGVC086TH	192	22	53.7	783	7	CK597420
C 120	22.2	54.1	689	6	CD893289	CD893289 G118.123F	193	22	53.7	783	10	CZ528157
C 121	22.2	54.1	695	6	CD927723	CD927723 GR45.102P	194	22	53.7	798	7	CK603037
122	22.2	54.1	712	6	CD454178	CD454178 WHE0987-0	195	22	53.7	800	9	AQ864214
C 123	22.2	54.1	724	6	CD869974	CD869974 AZO2.113C	196	22	53.7	816	2	BE733889
124	22.2	54.1	769	7	CO442891	CO442891 MZCCL1005	197	22	53.7	818	2	BE727035
125	22.2	54.1	805	5	BX453231	BX453231 BX453231	198	22	53.7	831	2	BE379548
C 126	22.2	54.1	869	5	BX444778	BX444778 BX444778	199	22	53.7	873	10	AG878594
127	22.2	54.1	869	10	CL901826	CL901826 CSHC1201	200	22	53.7	874	2	BG474208
C 128	22.2	54.1	966	2	BF203427	BF203427 601865857	201	22	53.7	911	5	BX354894
129	22.2	54.1	1378	3	BM909928	BM909928 AGENCOURT	202	22	53.7	922	2	BG764905
130	22	53.7	121	9	BZ591412	BZ591412 3590_1.84	203	22	53.7	924	5	BO948154
131	22	53.7	200	8	D84460	D84460 D84460_Forc	204	22	53.7	936	10	CL502260
C 132	22	53.7	235	2	BF818549	BF818549 MR3-CJ018	205	22	53.7	939	2	BG768730
133	22	53.7	259	2	BF713700	BF713700 ESTPBL276	206	22	53.7	940	2	BG766674
C 134	22	53.7	293	7	CO991983	CO991983 UMC-pd6en	207	22	53.7	948	2	BG331308
135	22	53.7	296	1	AI569263	AI569263 tn42f05.x	208	22	53.7	970	5	BU557844
136	22	53.7	298	3	BP949304	BP949304 BP949304	209	22	53.7	978	5	BX449417
C 137	22	53.7	314	7	CN257914	CN257914 170004243	210	22	53.7	1030	5	BU857719
138	22	53.7	319	11	DE116312	DE116312 Oryzias_1	211	22	53.7	1089	5	BX841390
C 139	22	53.7	344	1	AI833890	AI833890 605096G08	212	22	53.7	1153	2	BG330655
C 140	22	53.7	351	2	BI223040	BI223040 602943373	213	22	53.7	1194	2	BG330027
141	22	53.7	351	2	BE501829	BE501829 hw35g06.x	214	22	53.7	1204	5	BU145784
142	22	53.7	351	2	BE501849	BE501849 hw36a06.x	215	22	53.7	1497	10	CL973192
C 143	22	53.7	363	6	CB212298	CB212298 OML02578	216	22	53.7	2423	4	AF318366
C 144	22	53.7	369	3	BM659181	BM659181 IIU602653	217	21.8	53.2	152	6	CF615655
145	22	53.7	400	9	BM758990	BM758990 013_5_T7	218	21.8	53.2	185	9	CC970216
C 146	22	53.7	401	3	BM847402	BM847402 K-EST0126	219	21.8	53.2	212	8	FI3632
147	22	53.7	404	10	CG464579	CG464579 KRIBB_2D_	220	21.8	53.2	275	10	CZ333013
148	22	53.7	406	9	AQ017724	AQ017724 CIT-HSP-2_	221	21.8	53.2	280	9	CC181170
149	22	53.7	428	6	CF2226963	CF2226963 IH089_sub	222	21.8	53.2	301	10	CL316143
C 151	22	53.7	431	9	BZ913711	BZ913711 CH240_54N	223	21.8	53.2	344	7	CF965417
C 152	22	53.7	468	6	CF648588	CF648588 3530_1_56	224	21.8	53.2	359	9	CC979211
C 153	22	53.7	491	6	CB209983	CB209983 OML00263	225	21.8	53.2	380	9	AQ852358
C 154	22	53.7	520	5	BU074427	BU074427 im75f03.x	226	21.8	53.2	404	9	CC930910
155	22	53.7	522	1	AI995067	AI995067 701501658	227	21.8	53.2	426	5	BY504611
C 155	22	53.7	548	2	BI211309	BI211309 IPI_59_B0	228	21.8	53.2	465	6	CF308748
156	22	53.7	551	3	BQ246302	BQ246302 TaeI5013F	229	21.8	53.2	476	9	BH900639
C 157	22	53.7	551	11	CR839827	CR839827 GROAA8BG	230	21.8	53.2	483	5	BW964069
158	22	53.7	559	2	BG362665	BG362665 sac07b03_	231	21.8	53.2	491	2	BI076018
159	22	53.7	568	6	CD877766	CD877766 AZO4.101A	232	21.8	53.2	503	7	CK008657
160	22	53.7	575	1	AJ449183	AJ449183 AJ449183	233	21.8	53.2	505	2	BI211383
161	22	53.7	575	3	BM440722	BM440722 pgrln.pk0	234	21.8	53.2	520	7	CN432728
162	22	53.7	582	1	AJ274024	AJ274024 AJ274024	235	21.8	53.2	526	6	CB441818
C 163	22	53.7	585	1	AV523351	AV523351 AV523351	236	21.8	53.2	551	2	BE683491
	22	53.7	613	10	CW307597	CW307597 104_795_1	237	21.8	53.2	553	1	AA696508
165	22	53.7	616	1	AJ450894	AJ450894 AJ450894_1	238	21.8	53.2	579	6	CB617041
166	22	53.7	621	5	BX671154	BX671154 BX671154	239	21.8	53.2	579	8	DN215609
167	22	53.7	624	5	BX671378	BX671378 BX671378	240	21.8	53.2	593	7	CO889267
168	22	53.7	624	6	CD214780	CD214780 pgm2n.pk0	241	21.8	53.2	600	5	BX901538

CW026783 104_253_1
BE410885 601303506
AL424320 T7 end of
BI064629 pgfln.pk0
CG037953 PUKBH96TD
BZ779785 i134e11.g
BE386619 601274315
BU393876 603512776
DN256838 Meso02807
DR006928 TC106643
CA415230 UI-H-EUI-
BP450095 BP450095
CL819350 OR_CBa003
BE390186 601286191
CV804593 AGENCOURT
CK359451 AGENCOURT
DR081743 RTFEP1_3
BG760245 602716644
BG427686 602500144
BP441623 BP441623
DN124579 1125493 M
CK771392 959664 MA
DR081806 RTFEP1_3
CK597420 AGENCOURT
CZ528157 SRAA-aac5
CK603037 AGENCOURT
AQ864214 nbeb0022N
BE733889 601568350
BE727035 601563705
BE379548 601238164
AG878594 Oryza sat
BG474208 602516820
BX354894 BX354894
BG764905 602737342
BQ948154 AGENCOURT
CL502260 SAIL_70_F
BG768730 602743175
BG766674 602739958
BG331308 602432036
BU557844 AGENCOURT
BX449417 BX449417
BU857719 AGENCOURT
BX841390 BX841390
BG330655 602430060
BG330027 602429790
BU145784 AGENCOURT
CL973192 OsIFCC042
AF318366 Homo sapi
CF615655 CES014044
CC970216 ZUAD525TH
FI3632 HSF1G075 St
CZ333013 ZMMBF0041
CC181170 JSalBAC_0
CL316143 ZMMBBC050
CF965417 10998rslc
CC979211 ZUAF377TH
AQ852358 LMAJFV1_1
CC930910 ZMMBBC054
BY504611 BY504611
CF308748 ABF--02-K
BH900639 Otb00181
BW964069 BW964069
BI076018 IPI_24_C1
CK008657 26269rslc
BI211383 IPI_60_A1
CN432728 BE030003A
CB441818 692331 MA
BE683491 183294 MA
AA696508 GM07807_5
CB617041 3529_1_67
DN215609 MEST971_C
CO889267 BovGen_17
BX901538 BX901538

C 242	21.8	53.2	603	5	BW967108	BW967108	BW967108	C 315	21.8	53.2	967	10	CG270097	CG270097	CG270097	OG3CF04TV
C 243	21.8	53.2	604	2	BI076019	BI076019	IP1_24_C1	C 316	21.8	53.2	975	10	CZ360147	CZ360147	CZ360147	ZMMBF0101
244	21.8	53.2	604	7	CK979453	CK979453	4110876_B	C 317	21.8	53.2	986	10	CZ390986	CZ390986	CZ390986	ZMMBF0168
245	21.8	53.2	625	7	CK347658	CK347658	zmrsubl_0	318	21.8	53.2	988	9	CC328125	CC328125	CC328125	OGPAX34TV
246	21.8	53.2	627	2	BG844411	BG844411	1024006C1	C 319	21.8	53.2	995	7	CF880021	CF880021	CF880021	trIC021xj
247	21.8	53.2	628	7	CO891823	CO891823	BovGen_20	C 320	21.8	53.2	1012	10	CL009044	CL009044	CL009044	ZMMBBb054
C 248	21.8	53.2	628	10	CZ273742	CZ273742	ZMMBF0054	C 321	21.8	53.2	1018	10	CZ390651	CZ390651	CZ390651	ZMMBF0168
249	21.8	53.2	629	9	CC930765	CC930765	ZMMBBc054	C 322	21.8	53.2	1022	10	CL008298	CL008298	CL008298	ZMMBBb054
250	21.8	53.2	639	9	CC995805	CC995805	ZUACD86TV	C 323	21.8	53.2	1033	10	CG900908	CG900908	CG900908	ZMMBBb051
C 251	21.8	53.2	639	9	CC998626	CC998626	ZUAD535TH	C 324	21.8	53.2	1052	8	CX106299	CX106299	CX106299	BI125O19
252	21.8	53.2	643	3	BI723642	BI723642	1031067D0	325	21.8	53.2	1053	10	CZ362781	CZ362781	CZ362781	ZMMBF0141
C 253	21.8	53.2	645	6	CD228430	CD228430	CCC1_7_D0	326	21.8	53.2	1069	6	CD507199	CD507199	CD507199	CDA83-E10
254	21.8	53.2	646	10	CG270073	CG270073	OG2AF34TV	327	21.8	53.2	1184	2	BG828347	BG828347	BG828347	602753790
C 255	21.8	53.2	647	10	CG270061	CG270061	OG2AF34TH	328	21.8	53.2	1485	10	CL971743	CL971743	CL971743	OsIFCC022
256	21.8	53.2	652	6	CB860712	CB860712	HH05L24w	C 329	21.8	53.2	2230	4	AY107496	AY107496	AY107496	Zea_mays
C 257	21.8	53.2	660	6	CB021779	CB021779	px32d08.Y	C 330	21.8	53.2	2346	10	CL973685	CL973685	CL973685	OsIFCC024
258	21.8	53.2	663	9	CC974899	CC974899	ZUAF817TV	C 331	21.6	52.7	327	3	BM346050	BM346050	BM346050	rr1lf05.Y
C 259	21.8	53.2	669	10	CZ272611	CZ272611	ZMMBF0052	C 332	21.6	52.7	357	10	CL916119	CL916119	CL916119	OA_ABa001
C 260	21.8	53.2	689	10	CW375084	CW375084	fsbb001f0	333	21.6	52.7	374	8	DN324202	DN324202	DN324202	LIB3173-0
C 261	21.8	53.2	698	6	CD462178	CD462178	SAl_39_D0	C 334	21.6	52.7	375	1	AI682183	AI682183	AI682183	tp48f11.x
C 262	21.8	53.2	704	7	CK783762	CK783762	UI-D-GC1-	C 335	21.6	52.7	377	10	CW405808	CW405808	CW405808	fsbb001f0
263	21.8	53.2	712	10	CG438217	CG438217	OGVGI58TH	336	21.6	52.7	385	1	AI611360	AI611360	AI611360	tt67a01.x
C 264	21.8	53.2	718	2	BG409469	BG409469	S10-1-A8	337	21.6	52.7	402	1	AI612076	AI612076	AI612076	tt64b03.x
265	21.8	53.2	719	7	CV682501	CV682501	sjs3-003	338	21.6	52.7	402	7	CR363905	CR363905	CR363905	CR363905
C 266	21.8	53.2	726	10	CZ348290	CZ348290	ZMMBF0123	339	21.6	52.7	421	7	CN747277	CN747277	CN747277	SAL_US025
267	21.8	53.2	729	5	BW967388	BW967388	BW967388	340	21.6	52.7	458	5	BQ803765	BQ803765	BQ803765	WHE2841_F
268	21.8	53.2	731	8	DN213255	DN213255	MEST962_H	341	21.6	52.7	477	9	BH275187	BH275187	BH275187	CH230-13M
269	21.8	53.2	731	8	DN214783	DN214783	MEST890_D	C 342	21.6	52.7	480	7	CV159681	CV159681	CV159681	SCARABAEU
C 270	21.8	53.2	736	10	CZ819141	CZ819141	OC_Ba019	343	21.6	52.7	480	7	CV160137	CV160137	CV160137	SCARABAEU
271	21.8	53.2	752	9	CC181171	CC181171	Jsa1BAC_0	344	21.6	52.7	488	2	BE591027	BE591027	BE591027	WHE1655-1
272	21.8	53.2	757	8	DN217654	DN217654	MEST1054	345	21.6	52.7	524	1	AW395907	AW395907	AW395907	sh07c04.Y
273	21.8	53.2	771	4	AY808838	AY808838	Schistoso	346	21.6	52.7	530	5	BQ741326	BQ741326	BQ741326	saq17b04.
C 274	21.8	53.2	776	10	CG438222	CG438222	OGVGI58TV	347	21.6	52.7	533	6	CA684366	CA684366	CA684366	wlm96.pk0
C 275	21.8	53.2	777	9	BZ752345	BZ752345	PUDBI50TB	C 348	21.6	52.7	543	6	CA684883	CA684883	CA684883	wlm96.pk0
C 276	21.8	53.2	780	7	CO028521	CO028521	EST806905	349	21.6	52.7	546	6	CA684883	CA684883	CA684883	wlm96.pk0
C 277	21.8	53.2	785	10	CZ780037	CZ780037	OC_Ba014	350	21.6	52.7	548	3	BI972371	BI972371	BI972371	sag90e10.
278	21.8	53.2	787	9	CC778455	CC778455	ZMMBBc042	C 351	21.6	52.7	550	7	CK046319	CK046319	CK046319	46009rsic
C 279	21.8	53.2	793	9	CC710769	CC710769	OGULS59TH	C 352	21.6	52.7	552	7	CO694324	CO694324	CO694324	DG11-73f1
280	21.8	53.2	795	10	CZ354264	CZ354264	ZMMBF0091	C 353	21.6	52.7	552	9	AQ143805	AQ143805	AQ143805	HS_3075_B
281	21.8	53.2	796	9	BZ503797	BZ503797	BONMR74TF	C 354	21.6	52.7	555	7	CO609850	CO609850	CO609850	DG8-89h24
C 282	21.8	53.2	805	10	CZ340698	CZ340698	ZMMBF0110	C 355	21.6	52.7	555	7	CO712413	CO712413	CO712413	DG14-188n
C 283	21.8	53.2	811	2	BF210356	BF210356	601874433	C 356	21.6	52.7	560	7	CO652941	CO652941	CO652941	Syl384O15
C 284	21.8	53.2	818	9	CC606893	CC606893	OGWEF90TV	C 357	21.6	52.7	563	2	BG263479	BG263479	BG263479	WHE2342_E
285	21.8	53.2	826	6	CD436565	CD436565	EL01N0359	C 358	21.6	52.7	564	7	CO687338	CO687338	CO687338	DG11-230C
C 286	21.8	53.2	826	7	CK846866	CK846866	969420_MA	C 359	21.6	52.7	566	7	CO672414	CO672414	CO672414	DG33-95b1
C 287	21.8	53.2	833	9	CC627937	CC627937	OGWCE01TH	C 360	21.6	52.7	570	8	DN151187	DN151187	DN151187	5210_G03
288	21.8	53.2	834	6	CB653377	CB653377	OSJNEC04F	C 361	21.6	52.7	576	7	CO707225	CO707225	CO707225	DG32-75j1
289	21.8	53.2	846	9	CC642237	CC642237	OGMAN18TH	C 362	21.6	52.7	581	10	CW571588	CW571588	CW571588	OA_ABa009
290	21.8	53.2	855	9	CC627946	CC627946	OGWCE01TV	C 363	21.6	52.7	581	10	CL540317	CL540317	CL540317	OB_Ba006
291	21.8	53.2	855	10	CG024289	CG024289	ZMMBBc056	C 364	21.6	52.7	585	2	BG906820	BG906820	BG906820	TaLr1154A
C 292	21.8	53.2	862	10	CG378140	CG378140	OG1DR51TH	365	21.6	52.7	591	7	CO525694	CO525694	CO525694	3530_1_17
293	21.8	53.2	865	9	CC371573	CC371573	PUEHG67TD	C 366	21.6	52.7	596	6	CB826014	CB826014	CB826014	rq97h08.Y
294	21.8	53.2	866	9	BZ742036	BZ742036	OGFAS80TC	C 367	21.6	52.7	596	1	AL823350	AL823350	AL823350	AL823350
295	21.8	53.2	869	10	AG863307	AG863307	Oryza_sat	C 368	21.6	52.7	607	8	CX358301	CX358301	CX358301	ssalrgb52
296	21.8	53.2	873	10	CZ333376	CZ333376	ZMMBF0042	C 369	21.6	52.7	608	3	BJ227137	BJ227137	BJ227137	BJ227137
C 297	21.8	53.2	873	10	CZ334247	CZ334247	ZMMBF0043	370	21.6	52.7	622	9	BZ107573	BZ107573	BZ107573	CH230-134
C 298	21.8	53.2	875	10	CG017435	CG017435	ZUABG54TV	371	21.6	52.7	634	8	DN441159	DN441159	DN441159	LIB5338-1
C 299	21.8	53.2	879	11	CNS035KX	CNS035KX	Tetraodon	372	21.6	52.7	637	5	BX866130	BX866130	BX866130	BX866130
300	21.8	53.2	883	10	CL317692	CL317692	ZMMBBc010	373	21.6	52.7	642	6	CA609890	CA609890	CA609890	wrl.pk010
C 301	21.8	53.2	889	9	CC442083	CC442083	PUHPO58TB	C 375	21.6	52.7	653	11	CR960793	CR960793	CR960793	Homo_sapi
302	21.8	53.2	893	9	CC442087	CC442087	PUHPO58TD	C 376	21.6	52.7	658	2	BB646450	BB646450	BB646450	BB646450
C 303	21.8	53.2	897	7	CO455639	CO455639	MZCCL2000	C 377	21.6	52.7	661	9	AZ494752	AZ494752	AZ494752	1M0330P07
C 304	21.8	53.2	898	9	CC642244	CC642244	OGMAN18TV	378	21.6	52.7	662	5	BY727465	BY727465	BY727465	BY727465
305	21.8	53.2	908	10	CG001577	CG001577	ZUAD47TV	C 379	21.6	52.7	675	10	AG314010	AG314010	AG314010	Mus_muscu
306	21.8	53.2	909	6	CD437082	CD437082	EL01N0368	380	21.6	52.7	682	8	DR476763	DR476763	DR476763	WS00968.C
C 307	21.8	53.2	910	10	CL205625	CL205625	ZMMBBb056	381	21.6	52.7	685	7	CV064565	CV064565	CV064565	WNE112e2
308	21.8	53.2	916	5	BU168477	BU168477	AGENCOURT	C 382	21.6	52.7	687	9	AQ201663	AQ201663	AQ201663	RPC111-58
C 309	21.8	53.2	917	9	CC983015	CC983015	ZUABH69TV	C 383	21.6	52.7	696	1	AV602088	AV602088	AV602088	AV602088
310	21.8	53.2	923	9	CC987764	CC987764	ZUAFT62TH	C 384	21.6	52.7	699	6	CF134013	CF134013	CF134013	WHE4366_D
C 311	21.8	53.2	925	9	CC689609	CC689609	OGKAQ04TH	385	21.6	52.7	701	5	BX869408	BX869408	BX869408	BX869408
312	21.8	53.2	951	6	CD796551	CD796551	EST667912	386	21.6	52.7	706	8	CX353542	CX353542	CX353542	ssalrgb52
C 313	21.8	53.2	957	10	CL994032	CL994032	ZMMBHf000	387	21.6	52.7	707	6	CB169571	CB169571	CB169571	RUC603000
314	21.8	53.2	958	10	CG451948	CG451948	OG									

388	21.6	52.7	707	8	DN745300	GL-CF-209
389	21.6	52.7	715	5	BX861274	BX861274
390	21.6	52.7	718	8	DN877273	nael2e04.
391	21.6	52.7	721	5	BQ750888	EST631451
392	21.6	52.7	721	11	CR153925	Reverse s
393	21.6	52.7	726	5	BX305013	BX305013
394	21.6	52.7	732	7	CO249789	AGENCOURT
395	21.6	52.7	734	6	CA500056	WHE4014 G
396	21.6	52.7	735	6	CA800066	sat77b08.
397	21.6	52.7	742	5	BX859070	BX859070
398	21.6	52.7	743	7	CR367877	CR367877
c 399	21.6	52.7	749	2	BE659880	GM700011A
400	21.6	52.7	750	7	CR367234	CR367234
401	21.6	52.7	753	7	CR368280	CR368280
402	21.6	52.7	754	5	BX880804	BX880804
403	21.6	52.7	754	7	CR366178	CR366178
c 404	21.6	52.7	755	8	CX702411	gmrtDrNS0
405	21.6	52.7	766	8	CX720042	1326836 N
406	21.6	52.7	771	5	BX879765	BX879765
407	21.6	52.7	773	5	BX913656	BX913656
408	21.6	52.7	787	6	CB169689	RUC603000
409	21.6	52.7	811	7	CR363328	CR363328
410	21.6	52.7	831	11	CNS04937	AL280060 Tetraodon
c 411	21.6	52.7	837	8	CX702136	gmrtDrNS0
412	21.6	52.7	876	3	BI951111	HVSMEL002
413	21.6	52.7	909	5	BQ647220	AGENCOURT
c 414	21.6	52.7	965	5	BQ960212	AGENCOURT
c 415	21.6	52.7	973	2	BG704332	602687562
c 416	21.6	52.7	992	5	BX428794	BX428794
417	21.6	52.7	1054	3	BM562329	AGENCOURT
418	21.6	52.7	1083	8	DR150985	49245386
419	21.6	52.7	1096	11	CNS0683Q	AL411468 T3 end of
c 420	21.6	52.7	1174	5	BQ898019	AGENCOURT
421	21.6	52.7	1683	3	BM550161	AGENCOURT
c 422	21.6	52.7	1718	3	BM477352	AGENCOURT
c 423	21.6	52.7	3095	4	BC051240	Mus muscu
c 424	21.4	52.2	132	8	DN155128	GCA006N19
c 425	21.4	52.2	161	6	CB394113	OSTRI31H5
426	21.4	52.2	168	1	AA895494	vy34c07.r
c 427	21.4	52.2	192	7	CR537202	DKFp459K
c 428	21.4	52.2	307	1	AW015190	UI-H-B1Op
429	21.4	52.2	316	7	CO778035	BL002D A0
430	21.4	52.2	328	1	AA450647	vf80c06.r
c 431	21.4	52.2	330	1	AU093949	AU093949
c 432	21.4	52.2	331	1	AI867834	wb39c06.x
c 433	21.4	52.2	340	5	BY128882	BY128882
434	21.4	52.2	359	5	BY045091	BY045091
435	21.4	52.2	367	8	W34032	mb78d09.r1
436	21.4	52.2	368	2	BF775989	286309 MA
437	21.4	52.2	378	2	BE428065	MTD002.H0
438	21.4	52.2	378	2	BE428414	MTD006.G0
c 439	21.4	52.2	385	6	CD631207	56049790H
c 440	21.4	52.2	388	5	BU785612	in48a06.x
c 441	21.4	52.2	391	7	CK074479	71301rsic
442	21.4	52.2	395	6	CA648703	wreIn.pk0
443	21.4	52.2	399	8	CX620883	GABR1.54
444	21.4	52.2	400	1	AL364430	AL364430
c 445	21.4	52.2	405	9	CE205796	tigr-gss-
446	21.4	52.2	408	1	AI121642	ud12e06.r
447	21.4	52.2	434	1	AJ612119	AJ612119
448	21.4	52.2	435	5	BX511680	BX511680
449	21.4	52.2	436	6	CA640445	wreIn.pk0
450	21.4	52.2	436	9	CE164404	tigr-gss-
451	21.4	52.2	437	1	AA797791	vw33d02.r
452	21.4	52.2	439	1	AA620244	vo64e09.r
453	21.4	52.2	446	1	AA529473	vi36f02.r
c 454	21.4	52.2	448	10	CW617838	OA_ABa016
c 455	21.4	52.2	450	5	BQ459319	HA01109r
456	21.4	52.2	455	5	BY490206	BY490206
457	21.4	52.2	455	7	CK834994	4059136 B
c 458	21.4	52.2	457	3	BJ757841	BJ757841
c 459	21.4	52.2	461	10	CZ696047	OC_Ba000
460	21.4	52.2	462	1	AI316608	uk62c02.y

461	21.4	52.2	473	1	AA059965	AA059965
c 462	21.4	52.2	475	9	BZ351204	hv20a05.g
c 463	21.4	52.2	477	3	BI674742	949066G05
c 464	21.4	52.2	480	7	CN449423	GUO_cDNA
c 465	21.4	52.2	488	6	CD906816	G468.105I
c 466	21.4	52.2	489	3	BP149818	BP149818
c 467	21.4	52.2	493	10	CW034680	104_264_1
468	21.4	52.2	496	7	CN671566	A0907H11-
c 469	21.4	52.2	498	3	BI830382	603073431
c 470	21.4	52.2	501	2	BE219383	hv57b05.x
c 471	21.4	52.2	501	7	CF984174	18444rsrc
472	21.4	52.2	503	2	BF443144	260525 MA
c 473	21.4	52.2	505	10	CL195402	104_420_1
c 474	21.4	52.2	506	6	CB783367	AMGNNUC:N
c 475	21.4	52.2	510	7	CV043059	dbai4b10.
476	21.4	52.2	511	10	CW575705	OA_ABa010
c 477	21.4	52.2	516	2	BE926700	QV2-BT063
478	21.4	52.2	516	3	BM125744	id74g04.y
c 479	21.4	52.2	525	6	CA065029	SCACAD103
480	21.4	52.2	525	6	CA065105	SCACAD103
481	21.4	52.2	529	5	BQ462644	HI01J05T
482	21.4	52.2	530	7	CV043920	dbai4b10.
c 483	21.4	52.2	532	7	CO598811	DG8-171j2
c 484	21.4	52.2	535	3	BM630654	170006875
485	21.4	52.2	542	5	BQ553736	H4024A01-
486	21.4	52.2	543	7	CK309078	SB02048A2
487	21.4	52.2	544	1	AI292468	GH15379.5
488	21.4	52.2	553	2	BF618790	HVSMEC000
489	21.4	52.2	554	1	AW653994	102953 MA
490	21.4	52.2	556	3	BM255475	517220 MA
491	21.4	52.2	561	7	CK332540	H8202C09-
492	21.4	52.2	563	2	BE594382	PI1_32_G0
c 493	21.4	52.2	564	2	BG047966	OVI_26_A0
c 494	21.4	52.2	564	6	CA359548	632516_NC
c 495	21.4	52.2	564	7	CK310598	SB02006A2
c 496	21.4	52.2	571	6	CA086375	SCMCAM208
c 497	21.4	52.2	574	2	BE592199	WS1_89_F1
c 498	21.4	52.2	580	10	CZ313421	ZMMBF0011
c 499	21.4	52.2	581	10	CZ301795	ZMMBF0077
c 500	21.4	52.2	587	11	CR892938	Sus scrof

ALIGNMENTS

RESULT 1	340 bp	DNA	linear	GSS 23-AUG-2000
AAQ939774/c	NR5-118R	Human	NotI clones	Homo sapiens genomic, genomic survey
LOCUS	AAQ939774	sequence.		
DEFINITION	AAQ939774	AAQ939774.1	GI:7216152	
ACCESSION	AAQ939774	GSS.		
VERSION	AAQ939774.1	Homo sapiens (human)		
KEYWORDS	GSS.	Homo sapiens		
SOURCE	Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
ORGANISM	Homo sapiens	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
REFERENCE	1 (bases 1 to 340)	Hominidae; Homo.		
AUTHORS	Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie,L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N., Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.			
TITLE	NotI clones in the analysis of the human genome			
JOURNAL	Nucleic Acids Res. 28 (7), 1635-1639 (2000)			
PUBMED	10710430			
COMMENT	Contact: Podowski RM			
	Center for Genomics Research			
	Karolinska Institute			
	17177 Stockholm, Sweden			
	Tel: +46-8-728-6372			
	Fax: +46-8-337983			
	Email: Raf.Podowski@cgr.ki.se			

Class: NotI site.

FEATURES
source
Location/Qualifiers
1..340
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"

ORIGIN

Query Match 96.1%; Score 39.4; DB 9; Length 340;
Best Local Similarity 95.1%; Pred. No. 0.016;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
|||||
Db 236 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCTGGTCGCG 196
|||||

RESULT 2
BZ892025 702 bp DNA linear GSS 30-JUL-2003
LOCUS Hm12_0104.x1.011.ab1 Hm pUC18 Library Haloarcula marismortui ATCC
DEFINITION 43049 genomic 5', genomic survey sequence.
ACCESSION BZ892025
VERSION BZ892025.1 GI:33342658
KEYWORDS GSS.
SOURCE Haloarcula marismortui ATCC 43049
ORGANISM Haloarcula marismortui ATCC 43049
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloarcula.

REFERENCE
AUTHORS Goo,Y., Roach,J., Glusman,G., Baliga,N.S., Deutsch,K., Pan,M.,
DasSarma,S., Ng,W.V. and Hood,L.
TITLE Low-pass Sequencing for Microbial Comparative Genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Goo Y
Institute for Systems Biology
1441 North 34th Street, Seattle, WA 98103, USA
Tel: 206 732 1412
Fax: 206 732 1299
Email: ygoosystemsbiology.org
Seq primer: M13 Forward
Class: shotgun.

FEATURES
source
Location/Qualifiers
1..702
/organism="Haloarcula marismortui ATCC 43049"
/mol_type="genomic DNA"
/strain="ATCC 43049"
/db_xref="taxon:272569"
/clone_lib="Hm pUC18 Library"
/note="Vector: pUC18; Site_1: SmaI; A shotgun library was
constructed from Haloarcula marismortui genomic DNA using
pUC18/SmaI/BAP plasmid"

ORIGIN

Query Match 69.3%; Score 28.4; DB 9; Length 702;
Best Local Similarity 81.6%; Pred. No. 61;
Matches 31; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
|||||
Db 311 GCCTCCGAAGCGGTCTCTCATCGCTGACCGGCCG 348
|||||

RESULT 3
DN393531/c 611 bp mRNA linear EST 07-MAR-2005
LOCUS DN393531
DEFINITION LIB3934-056-A1-K1-F1 LIB3934 Canis familiaris cDNA clone
CLN12937122, mRNA sequence.
ACCESSION DN393531
VERSION DN393531.1 GI:60574752
KEYWORDS EST.
SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 611)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.

FEATURES
source
Location/Qualifiers
1..611
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/clone="CLN12937122"
/tissue_type="brain"
/lab_host="DH10B"
/clone_lib="LIB3934"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; brain
from normal dog"

ORIGIN

Query Match 60.5%; Score 24.8; DB 8; Length 611;
Best Local Similarity 77.8%; Pred. No. 9e+02;
Matches 28; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
|||||
Db 160 GCCTCCTGCTGCCGCCGCCCAACGCTGCCCGGCC 125
|||||

RESULT 4
CG190773/c 690 bp DNA linear GSS 21-AUG-2003
LOCUS PUID25TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0608E02,
DEFINITION genomic survey sequence.
ACCESSION CG190773
VERSION CG190773.1 GI:34081834
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 690)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUID25TB
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..690
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0608E02"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"

ORIGIN

Query Match 59.5%; Score 24.4; DB 10; Length 690;
Best Local Similarity 79.4%; Pred. No. 1.2e+03;
Matches 27; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 CTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
| | | | | | | | | | | | | | | | | | | | : |
Db 297 CGCCGGATGCCAGGCCTTCATCGCCGCCCGCGC 264

RESULT 5
BG772871 890 bp mRNA linear EST 15-MAY-2001
LOCUS 602721069F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4838104 5',
DEFINITION mRNA sequence.

ACCESSION BG772871
VERSION BG772871 GI:14083524
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 890)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10771 row: i. column: 17
High quality sequence stop: 72.

FEATURES
source Location/Qualifiers
1..890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4838104"
/lab_host="DH10B"
/clone_lib="NIH_MGC 97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN
Query Match 59.0%; Score 24.2; DB 2; Length 890;
Best Local Similarity 75.7%; Pred. No. 1.4e+03;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
| | | | | | | | | | | | | | | | | | | | : |
Db 60 GCCTCTGTATGCCAGCTCCTCTTCCCGGCGCGCGC 96

RESULT 6
CO336372 445 bp mRNA linear EST 05-OCT-2004
LOCUS EN12413.5prime Exelixis FlyTag MN08 Bluescript Drosophila
DEFINITION melanogaster cDNA clone EN12413 5, mRNA sequence.

ACCESSION CO336372
VERSION CO336372.1 GI:49396647
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 445)
AUTHORS Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Platt, D.
and Swimmer, C.
TITLE Exelixis FlyTag EST Project MN08 Library
JOURNAL Unpublished (2004)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: EN.124 row: B column: 1
High quality sequence stop: 351.

FEATURES
source Location/Qualifiers
1..445
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EN12413"
/cell_line="mbn2"
/clone_lib="Exelixis FlyTag MN08 Bluescript"
/note="Vector: pBluescript; Site_1: NotI; Site_2: XhoI;
oligodT primed from LPS induced mbn2 cell line."

ORIGIN
Query Match 58.5%; Score 24; DB 7; Length 445;
Best Local Similarity 72.5%; Pred. No. 1.6e+03;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 40
| | | | | | | | | | | | | | | | | | | | : |
Db 374 ACGGCTCCGGCGGCCACTCCCTCCTCGCGGCCCTTGAGC 335

RESULT 7
BQ384615/c 555 bp mRNA linear EST 22-MAY-2002
LOCUS NISC mn07g01.y1 NICHD_XGC_Ov1 Xenopus laevis cDNA clone
DEFINITION IMAGE:5049408 5', mRNA sequence.
ACCESSION BQ384615
VERSION BQ384615.1 GI:21072302
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 555)
AUTHORS NIH-XGC http://image.llnl.gov/image/html/xenopuslib_info.shtml.
TITLE National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
JOURNAL Unpublished (2002)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAM11134 row: N column: 1
Seq primer: M13RP1 reverse primer (ABI).

FEATURES
source Location/Qualifiers
1..555

RESULT 10
CNS000K2
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR02P13 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL058270
VERSION
AL058270.1 GI:4930724
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR02P13"
/clone_lib="RPCI-98"
/note="end : T7"
ORIGIN
Query Match 58.0%; Score 23.8; DB 10; Length 1101;
Best Local Similarity 77.1%; Pred. No. 2e+03;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCGGNC 38
Db 629 CCTCCGGATTTCAGATCCTCATAGCTGGCCCTATC 663
REFERENCE
BH841209
LOCUS
BH841209 356 bp DNA linear GSS 13-JUN-2002
DEFINITION
TC3-55C20.TP TC3 Trypanosoma cruzi genomic clone TC3-55C20, genomic
survey sequence.
ACCESSION
BH841209
VERSION
BH841209.1 GI:21408424
KEYWORDS
GSS.
SOURCE
Trypanosoma cruzi
ORGANISM
Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
REFERENCE
1 (bases 1 to 356)
AUTHORS
Myler,P.J., Aggarwal,G., Fazelinia,G., Mack,J., Marty,A.,
Munden,H., Nelson,S., Pentony,M., Rinta,J., Robertson,L.,
Seyler,A., Sisk,E., Stuart,K., Vogt,C., Worthey,E., El-Sayed,N.M.,
Ghedin,E. and Andersson,B.
Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing
TITLE
Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing

JOURNAL
COMMENT
Unpublished (2001)
Other GSSs: TC3-55C20.TV
Contact: Peter Myler
Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109, USA
Tel: 206 284 8846
Fax: 206 284 0313
Email: mylerpj@sbri.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seq primer: SP6
Class: BAC ends.
FEATURES
Location/Qualifiers
1..356
/organism="Trypanosoma cruzi"
/mol_type="genomic DNA"
/strain="CL Brener"
/db_xref="taxon:5693"
/clone="TC3-55C20"
/clone_lib="TC3"
/note="Vector: pBelobAC11; Site 1: Hin dIII; Constructed
for Uppsala University by Marie-Christine Le Paslier in
the laboratory of Denis Le Paslier at the Centre d'Etude
du Polymorphisme Humain (CEPH), Paris, France. Briefly,
Trypanosoma cruzi CL-Brener agarose embedded DNA (obtained
from Dr. Franco da Silveira) was partially digested with
Hin dIII. High molecular weight fragments were ligated in
pBelobAC11 digested with Hin dIII. The average insert
size is 100 kb. Total clone coverage: approx. 33 X the
haploid genome."
ORIGIN
Query Match 57.6%; Score 23.6; DB 9; Length 356;
Best Local Similarity 73.7%; Pred. No. 2.1e+03;
Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCGGNC 40
Db 88 GCCCTGGAAACGACAGTCCCAAAACGCTGGCCAGCCG 51
RESULT 12
CE771255/c
LOCUS
CE771255 584 bp DNA linear GSS 30-SEP-2003
DEFINITION
tigr-gss-dog-17000330592266 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION
CE771255
VERSION
CE771255.1 GI:37112019
KEYWORDS
GSS.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
1 (bases 1 to 584)
AUTHORS
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE
The dog genome: survey sequencing and comparative analysis
JOURNAL
Science 301 (5641), 1898-1903 (2003)
PUBMED
14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
Location/Qualifiers
1..584
/organism="Canis familiaris"

/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5320370"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 57.6%; Score 23.6; DB 3; Length 917;
Best Local Similarity 73.7%; Pred. No. 2.2e+03;
Matches 28; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
||||| ||| | ||||| ||||| ||||| :|||
Db 510 GCCTCCCTTTGCACGCACCTCAGCGCTGGCCCGACCGC 547

RESULT 18

CO983269/c
LOCUS
DEFINITION
CO983269 483 bp mRNA linear EST 13-SEP-2004
GM89018A2B01.r1 Gm-r1089 Glycine max CDNA clone Gm-r1089-6578 3,
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 483)
Vodkin, L., Shoemaker, R., Keim, P., Polacco, J.C., Retzel, E.,
Khanna, A., Shealy, R., Clough, S., Thibaud-Nissen, F., Coryell, V.,
Erpelding, J., Gonzalez, D.O., Stromvik, M., Rodriguez-Huete, A.M.,
Schweitzer, P., Gong, G. and Liu, L.
A Functional Genomics Program for Soybean (NSF 9872565) (2004)
Unpublished (2004)

TITLE

JOURNAL

COMMENT

Other_ESTs: BM893189 corresponding to Gm-cl069-3072 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for
Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional
Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
Email: l-vodkin@uiuc.edu
Plate: GM89018A2 row: B column: 01
Seq primer: 5'-TTTTTTTTTTTTTTTTTT(A/C/G)-3'
High quality sequence stop: 483.

FEATURES

source

1. .483
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="Gm-r1089-6578"
/clone_lib="Gm-r1089"
/note="The library Gm-r1089 is a sequence-driven, reracked
set of 9,216 low redundancy clones selected from 38
different cDNA libraries constructed from various tissues
and stages of development of soybean including 973 cDNAs
from germinating cotyledons(source library Gm-cl069,
Gm-cl076, and Gm-cl077); 1,465 cDNAs from various tissue
and organ systems of the adult plant; 476 cDNAs from adult
stem tissue (source library Gm-cl062); 1340 cDNAs from
tissue culture derived somatic embryos (source libraries

Gm-cl036 and Gm-cl075); 2918 cDNAs from hypocotyls or
young seedlings; 742 cDNAs from germinating seedlings,
shoot tips, or leaves exposed to various stresses(source
libraries Gm-cl065, Gm-cl066, and Gm-cl068); 839 cDNAs
from young leaves or hypocotyls exposed to bacterial and
fungal pathogens (source libraries Gm-cl072, Gm-cl073,
Gm-cl074; and Gm-cl084); and 463 from roots of young
plants grown in hydroponic media without phosphate (source
library Gm-cl087). The 5' ESTs of the source clones from
the different libraries were used to select singletons, or
a representative of each contig, which were reracked to
form library Gm-r1089 and the cDNA clones of the reracked
Gm-r1089 library were then sequencing at the 3' end. The
unigene selection and 3' sequencing was funded by NSF
Plant Genome project #9872565
(http://soybean.genomics.crops.csi.uiuc.edu/) as part of
creation of a low redundancy soybean cDNA set. The source
cDNA libraries were constructed by the laboratories of
Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa
State University, and Paul Keim, Northern Arizona
University as part of the Public EST project,
http://129.186.26.94/soybeanest.html. The contig analysis
to select unique genes was performed by the laboratory of
Ernest Retzel, Center for Computational Genomics and
Bioinformatics, University of Minnesota.
http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and 3'
sequencing were conducted by services of the University of
Illinois Keck Center for Comparative and Functional
Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The
corresponding 5' EST from each clone in the Gm-r1089
library is listed in the 'OTHER EST' field. The detailed
information on the source library for each clone can also
be obtained by referring to the clone ID of the original
cDNA library that is also listed under 'OTHER EST'."

ORIGIN

Query Match 57.1%; Score 23.4; DB 7; Length 483;
Best Local Similarity 70.7%; Pred. No. 2.5e+03;
Matches 29; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
||||| ||||| ||| ||||| ||||| :|||
Db 266 AGGCCACCGGATTCTCTCTCTCTCGCGGCGCTGCCGCG 226

RESULT 19

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF246184 576 bp mRNA linear EST 07-AUG-2003
TgESTzyi59e09.y1 TgMAS Tachyzoite cDNA Library Toxoplasma gondii
cDNA clone TgESTzyi59e09.y1 5', mRNA sequence.
CF246184
CF246184.1 GI:33477821
EST.
Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
1 (bases 1 to 576)
Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioke, J.A., White, M.,
Clifton, S., Pape, D., Martin, J., Wyllie, T., Dante, M., Marra, M.,
Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M.,
Ritter, E., Bennett, J., Franklin, C., Tsagaris, R., Ronko, I.,
Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
Toxoplasma EST Project
Unpublished (2001)
Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxoe@borcim.wustl.edu) for further

/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CEC"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTTCTAGATCGGAGCGCGCCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:
http://www.openbiosystems.com/stickleback"

ORIGIN

Query Match 57.1%; Score 23.4; DB 8; Length 1404;
Best Local Similarity 70.7%; Pred. No. 2.7e+03;
Matches 29; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCGGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 742 AAGTCCCCGGCTGCAAGTCTCCGTTCCGTGCGCCCGCCACG 702

RESULT 22

BY278985/c
LOCUS BY278985 374 bp mRNA linear EST 11-DEC-2002
DEFINITION BY278985 RIKEN full-length enriched, visual cortex Mus musculus
ACCESSION BY278985
VERSION BY278985.1 GI:26469322
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 374)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Oeato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Perteza,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,K., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

TITLE

JOURNAL
PUBMED
COMMENT

Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosawa,Wako-shi,Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

Source

Location/Qualifiers
1..374
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K430335O06"
/tissue type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"

ORIGIN

Query Match 56.6%; Score 23.2; DB 5; Length 374;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
| ||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 55 GTC TCACATGCCGGTGGCTCACGGCTGCCCCGGCC 20

RESULT 23

CN039111/c
LOCUS CN039111 608 bp mRNA linear EST 29-MAR-2004
DEFINITION nm_30_m13_t3_Math Ambystoma mexicanum cDNA, mRNA sequence.
ACCESSION CN039111
VERSION CN039111.1 GI:45809482
KEYWORDS EST.
SOURCE Ambystoma mexicanum (axolotl)
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae; Ambystoma.
REFERENCE 1 (bases 1 to 608)

AUTHORS Putta,S., Smith,J.J., Walker,J.A., Rondet,M., Weisrock,D., Monaghan,J., Samuels,A.K., Kump,K., King,D.C., Maness,N.J., Habermann,B., Tanaka,E., Bryant,S.V., Gardiner,D.M., Parichy,D.M. and Voss,S.R.

TITLE From biomedicine to natural history research: EST resources for ambystomatid salamanders

JOURNAL BMC Genomics 5 (1), 54 (2004)

PUBMED 15310388

COMMENT Contact: SR Voss
Department of Biology
University of Kentucky
TH Morgan Building, Lexington, KY 40506, USA
Tel: 859 257 9888
Fax: 859 257 1717
Email: srvooss@uky.edu
The EST is quality trimmed at the ends with a 20 base window and quality threshold of 15 (phred quality score).Please visit http://salamander.uky.edu For any information(trace,quality files etc) regarding this EST.

FEATURES
source location/Qualifiers
1. .608
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Limb Blastema and Proximal Limb Tissue collected from larvae on days 1-6 of regeneration"
/clone_lib="Math"

ORIGIN

Query Match 56.6%; Score 23.2; DB 7; Length 608;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
||||| | ||||| | ||| | ||||| :||
Db 215 CCTCCGGCTCCAGTACTTCACCACCTTGCCCGTCCG 180

RESULT 24
CO701815/c

LOCUS CO701815 709 bp mRNA linear EST 26-JUL-2004

DEFINITION DG32-214a13 DG32-liver Canis familiaris cDNA 3', mRNA sequence.

ACCESSION CO701815

VERSION CO701815.1 GI:50650483

KEYWORDS EST.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 709)
Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H., Henrich,J. and Loebbert,R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LION bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.

FEATURES
source location/Qualifiers
1. .709
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG32-liver"
/note="Organ: liver; Vector: Dog pBluescript LION"

ORIGIN

Query Match 56.6%; Score 23.2; DB 7; Length 799;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||||| | ||||| | ||| | ||||| :|
Db 171 GCCTCCGTCTGCCTGTCCCTCCCGCGCGCCGCTC 206

Query Match 56.6%; Score 23.2; DB 7; Length 709;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGN 37
||||| | ||||| | ||| | ||| | ||||| :|
Db 684 AGCTCCGGCCCCCAAGTTCCCGAGCTCTGGCCCGGT 649

RESULT 25
CO931079

LOCUS CO931079 799 bp mRNA linear EST 16-AUG-2004

DEFINITION AGENCOURT_30433863 NIH_ZGC_14 Danio rerio cDNA clone IMAGE:7405062 5', mRNA sequence.

ACCESSION CO931079

VERSION CO931079.1 GI:51285756

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 799)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John Ngai, Nancy Freeman, NIDCD
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM15602 row: j column: 04
High quality sequence start: 9
High quality sequence stop: 148.
Location/Qualifiers
1. .799
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7405062"
/tissue_type="olfactory epithelium"
/lab_host="DH10B Tona"
/clone_lib="NIH_ZGC_14"
/note="Organ: olfactory epithelium; Vector: pME18S-FL3; Site 1: DraIII; Site 2: DraIII; 1st strand cDNA was primed with an oligo(dT) primer
[GCGGCTGAAGACGGCTATGTGGCCTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor [GGCCUACUGG], digested and directionally cloned into distinct DraIII sites of the pME18S-FL3. Library was size selected for 1.0 kb, with a average insert size of ~1.2kb. Library constructed by Yutaka Suzuki (University of Tokyo Institute of Medical Science). Custom primers recommended for sequencing: 5' end primer 5'-GGATGTTGCCTTTACTTCA-3' and 3' end primer 5'-CGACCTGCAGTCGACACA-3'. Note: This is a Zebrafish Gene Collection (ZGC) library"

ORIGIN

Query Match 56.6%; Score 23.2; DB 7; Length 799;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||||| | ||||| | ||| | ||||| :|
Db 171 GCCTCCGTCTGCCTGTCCCTCCCGCGCGCCGCTC 206

RESULT 26
BX408897
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BX408897 903 bp mRNA linear EST 03-MAY-2004
BX408897 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA
clone CS0DH007YC09 5-PRIME, mRNA sequence.
BX408897
BX408897.2 GI:46951017
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 903)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30656780.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 994.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnafs=CS0BAA0132C12_CS01244_l&c=994.f.

FEATURES
source
1. .903
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DH007YC09"
/tissue type="T CELLS (JURKAT CELL LINE)"
/cell_line="JURKAT CELL LINE"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 56.6%; Score 23.2; DB 5; Length 903;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 35 CTCCCGAGGCCAGGCCACAAACGCCGCCCTACCGC 70

RESULT 27
CC377365
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CC377365 177 bp DNA linear GSS 19-MAY-2003
PUHMX92TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa487P16,
genomic survey sequence.
CC377365
CC377365.1 GI:30850982
GSS.
Zea mays
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 177)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and

TITLE
JOURNAL
COMMENT
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUHMX92TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .177
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa487P16"
/clone_lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"

ORIGIN
Query Match 56.1%; Score 23; DB 9; Length 177;
Best Local Similarity 71.8%; Pred. No. 3.3e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 41
||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 124 GCCTTCGCCACCAGTTCTCTGTCGCCGCCGACGCGC 162

RESULT 28
CC604446
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CC604446 234 bp DNA linear GSS 18-JUN-2003
OGCDB86TM ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0146P04,
genomic survey sequence.
CC604446
CC604446.1 GI:31965867
GSS.
Zea mays
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 234)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGCD86TC
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. .234
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0146P04"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2002)
Other_GSSs: OGCD86TC
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. .234
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0146P04"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES
source
1. .234
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0146P04"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 56.6%; Score 23.2; DB 5; Length 903;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 27; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Query Match 56.1%; Score 23; DB 9; Length 234;
Best Local Similarity 71.8%; Pred. No. 3.3e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 91 GCCTTCGGCCACCAGTTCCTCGTCGCCGGCAGCAGCG 129

RESULT 29
CC604439/c
LOCUS
DEFINITION CC604439 257 bp DNA linear GSS 18-JUN-2003
OGCDB86TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0146P04,
genomic survey sequence.
ACCESSION CC604439
VERSION CC604439.1 GI:31965860
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 257)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGCD86TMT
Contact: Cathy Whitelaw
TIGR
7112 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
FEATURES
source Location/Qualifiers
1..257
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0146P04"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 56.1%; Score 23; DB 9; Length 257;
Best Local Similarity 71.8%; Pred. No. 3.3e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 130 GCCTTCGGCCACCAGTTCCTCGTCGCCGGCAGCAGCG 92

RESULT 30
CW120817
LOCUS
DEFINITION CW120817 526 bp DNA linear GSS 29-OCT-2004
104_498_11109551_148_34655_090 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 11109551, genomic survey
sequence.
ACCESSION CW120817
VERSION CW120817.1 GI:54813364
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 526)

AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 498 row: h column: 23
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 526.
FEATURES
source Location/Qualifiers
1..526
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11109551"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
Query Match 56.1%; Score 23; DB 10; Length 526;
Best Local Similarity 71.8%; Pred. No. 3.4e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||
Db 92 GCCTCCGGCAGGGAGACCCGCATCTGTGTCTCGGCCGCG 130

RESULT 31
CG264881
LOCUS
DEFINITION CG264881 577 bp DNA linear GSS 25-AUG-2003
OG5CJ96TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0830O24,
genomic survey sequence.
ACCESSION CG264881
VERSION CG264881.1 GI:34177022
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 577)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
FEATURES
source Location/Qualifiers
1..577

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0830024"
/clone_lib="ZM 0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
ORIGIN
Query Match 56.1%; Score 23; DB 10; Length 577;
Best Local Similarity 71.8%; Pred. No. 3.4e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||| ||||| ||||| ||||| ||||| :|||
Db 28 GCCTTCGGCCACCAGTTCCTCGTCGCCGCGCAGCAGCG 66
RESULT 32
CD974061/c
LOCUS CD974061 638 bp mRNA linear EST 16-JUL-2003
DEFINITION QAE41c05.yg QAE Zea mays cDNA clone QAE41c05, mRNA sequence.
ACCESSION CD974061
VERSION CD974061.1 GI:32834383
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 638)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
FEATURES
source
1..638
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QAE41c05"
/tissue_type="pericarp"
/clone_lib="QAE"
ORIGIN
Query Match 56.1%; Score 23; DB 6; Length 638;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCG 39
||||| ||||| ||||| ||||| ||||| :|||
Db 41 AGGGCTCCAAATGCCAGTCCCTGCCGCGCGCGCTCG 3
RESULT 33
CC658573
LOCUS CC658573 643 bp DNA linear GSS 19-JUN-2003
DEFINITION OGUGT39TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0436H06,
genomic survey sequence.
ACCESSION CC658573
VERSION CC658573.1 GI:32062011
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 643)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfling,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUGT39TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
FEATURES
source
1..643
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0436H06"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
ORIGIN
Query Match 56.1%; Score 23; DB 9; Length 643;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||| ||||| ||||| ||||| ||||| :|||
Db 349 GCCTCCGCGAGAGACCCGCACTGTGTCTCGGCCGCG 387
RESULT 34
BZ539634/c
LOCUS BZ539634 704 bp DNA linear GSS 16-DEC-2002
DEFINITION OGAEW36TC ZM2_0.7_1.5_KB Zea mays genomic clone ZMMBma0045F23,
genomic survey sequence.
ACCESSION BZ539634
VERSION BZ539634.1 GI:27088070
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 704)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfling,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
FEATURES
source
1..704
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0045F23"

Db 641 AGCCCCAGGTGCGAGTCCCGCATCGCTCGCGCGCGCGC 603

CG447083 736 bp DNA linear GSS 17-SEP-2003
OGVGN54TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0477I12,
genomic survey sequence.

CG447083
CG447083.1 GI:34831290
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 736)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGVGN54TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.

Location/Qualifiers
1..736
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0477I12"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 10; Length 736;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157 GCCTTCGGCCACCAGTTCCTCGTCGCGCGGCGACGCG 195

RESULT 38
DR789445
LOCUS
DEFINITION
ZM BFB0008A01.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION
DR789445
VERSION
DR789445.1 GI:71306568
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 769)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA

CG447083 736 bp DNA linear GSS 17-SEP-2003
OGVGN54TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0477I12,
genomic survey sequence.

CG447083
CG447083.1 GI:34831290
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 736)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGVGN54TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.

Location/Qualifiers
1..736
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0477I12"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 56.1%; Score 23; DB 10; Length 736;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157 GCCTTCGGCCACCAGTTCCTCGTCGCGCGGCGACGCG 195

RESULT 38
DR789445
LOCUS
DEFINITION
ZM BFB0008A01.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION
DR789445
VERSION
DR789445.1 GI:71306568
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 769)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0008 row: A column: 01.
Location/Qualifiers
1..769
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"
/note="Vector: pCMV-SPORT 6.1; Site 1: EcorV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

ORIGIN

Query Match 56.1%; Score 23; DB 8; Length 769;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 405 GCCTTCGGCCACCAGTTCCTCGTCGCGGCGACGCG 443

RESULT 39
CC628013/c
LOCUS
DEFINITION
OGNAF67TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0325K14,
genomic survey sequence.
ACCESSION
CC628013
VERSION
CC628013.1 GI:31998986
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 794)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGNAF67TH
Contact: Cathy Whitelaw

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
1. .794
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0325K14"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES
source
Query Match 56.1%; Score 23; DB 9; Length 794;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 255 GCCTTCGGCCACCAGTTCCTCGTCGCGCGGACGACGCG 217

CC684604 808 bp DNA linear GSS 19-JUN-2003
OGUGA96TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0432023,
genomic survey sequence.
CC684604
CC684604.1 GI:32089380
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 808)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUGA96TV
Contact: Cathy Whitelaw

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. .808
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0432023"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES
source
Query Match 56.1%; Score 23; DB 9; Length 808;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41

Db 284 GCCTTCGGCCACCAGTTCCTCGTCGCGCGGACGACGCG 322
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 41
CG267676/c
LOCUS
DEFINITION
CG267676 816 bp DNA linear GSS 25-AUG-2003
OG2CD60TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0760J24,
genomic survey sequence.
ACCESSION
CG267676
VERSION
CG267676.1 GI:34179817
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 816)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OG2CD60TH
Contact: Cathy Whitelaw

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
Location/Qualifiers
1. .816
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0760J24"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 56.1%; Score 23; DB 10; Length 816;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 95 GCCTTCGGCCACCAGTTCCTCGTCGCGCGGACGACGCG 57

BZ733090 822 bp DNA linear GSS 03-MAR-2003
OGFAO64TM ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0240L07,
genomic survey sequence.
ACCESSION
BZ733090
VERSION
BZ733090.1 GI:28708619
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 822)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGFAO64TC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM10010 row: n column: 08
High quality sequence start: 3
High quality sequence stop: 577.

FEATURES

source

1. .995
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:4363975"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_85"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 56.1%; Score 23; DB 2; Length 995;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGNCGC 40

Db 366 AGGAGCAGGATGGCAGACACTGATCGCTGGCAGGTCTC 404

RESULT 49

CW932307/c

LOCUS

DEFINITION EDC65TR A. castellanii, 6-8 kb library from total genomic DNA
Acanthamoeba castellanii genomic clone EDC65, genomic survey
sequence.

ACCESSION

VERSION CW932307.1 GI:60248317

KEYWORDS

SOURCE

ORGANISM

Acanthamoeba castellanii

Eukaryota; Acanthamoebidae; Acanthamoeba.

1 (bases 1 to 1035)

Anderson, I.J. and Loftus, B.J.

Gene discovery in the Acanthamoeba castellanii genome

Unpublished (2004)

Contact: Iain Anderson

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-795-7949

Fax: 301-838-0208

Class: shotgun.

FEATURES

source

1. .1035
/organism="Acanthamoeba castellanii"
/mol_type="genomic DNA"
/strain="Neff"
/db_xref="taxon:5755"
/clone="EDCC65"
/clone_lib="A. castellanii, 6-8 kb library from total genomic DNA"
/note="Vector: pHOS2"

ORIGIN

Query Match 56.1%; Score 23; DB 10; Length 1035;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGNCGC 41

Db 84 GCCGCCAGCGGACGTCCTCATCGCGCGTGTGTC 46

RESULT 50

CNS02GX3

LOCUS

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
138D19 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

VERSION AL196896

KEYWORDS GSS; genome survey sequence.

SOURCE

ORGANISM

Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

1 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

2 Nat. Genet. 25 (2), 235-238 (2000)
10835645
Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A. and Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

3 (bases 1 to 1054)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES

Location/Qualifiers

1. .1054
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="138D19"
/clone_lib="G"
/note="Genoscope sequence ID : COAG138CB10SP1
end : PUC-Ori"

ORIGIN

Query Match 56.1%; Score 23; DB 10; Length 1054;
Best Local Similarity 71.8%; Pred. No. 3.5e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGNCGC 40

Db 33 AGCCTCCAGTGCCTGTCCTCCCGAGAGCTGCCCGACGGC 71

RESULT 51

BQ712863

LOCUS

BQ712863 1415 bp mRNA linear EST 16-JUL-2002

DEFINITION AGENCOURT 8468872 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6308419

5', mRNA sequence.

ACCESSION BQ712863

VERSION BQ712863.1 GI:21851762

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 1415)

NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1AM13727 row: h column: 20
High quality sequence start: 60
High quality sequence stop: 286.
High quality sequence stop: 286.

FEATURES

source Location/Qualifiers

1..1415

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:6308419"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_129"

/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 56.1%; Score 23; DB 5; Length 1415;
Best Local Similarity 71.8%; Pred. No. 3.6e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGGCG 41
||| |||| ||| || | ||||| ||: |||||

Db 677 GCCCCCGTCGCCGTTCTGTGTCGTGGCCGGGCGCG 715

RESULT 52

AQ581777/c

LOCUS AQ581777 112 bp DNA linear GSS 07-JUN-1999

DEFINITION RPCI-11-433H17.TJ RPCI-11 Homo sapiens genomic clone

RPCI-11-433H17, genomic survey sequence.

ACCESSION AQ581777

VERSION AQ581777.1 GI:5008887

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 112)

AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

JOURNAL Unpublished (1997)

COMMENT Other_GSSs: RPCI-11-433H17.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES

source Location/Qualifiers

1..112

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="GDB:7666072"

/db_xref="taxon:9606"

/clone="RPCI-11-433H17"

/sex="Male"

/cell_type="Lymphocytes"

/clone_lib="RPCI-11"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN

Query Match 55.6%; Score 22.8; DB 9; Length 112;
Best Local Similarity 79.4%; Pred. No. 3.7e+03;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCC 34
| |||| ||||| ||||| ||||| ||||| |||||

Db 34 AGGCCTCTGGATGCCTGTCCCAAGTCTCTGGCCCC 1

RESULT 53

BH229820

LOCUS BH229820 283 bp DNA linear GSS 08-NOV-2001

DEFINITION 1006154F07.x1 1006 - RescueMu Grid G Zea mays genomic, genomic survey sequence.

ACCESSION BH229820

VERSION BH229820.1 GI:16832264

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 283)

REFERENCE Walbot,V.

AUTHORS Maize genomic sequences found using engineered RescueMu transposon

TITLE Unpublished (2001)

JOURNAL Contact: Walbot V

COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
Plate: 1006154 row: 17
Class: transposon-tagged.

FEATURES

source Location/Qualifiers

1..283

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1006 - RescueMu Grid G"

/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription sites. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 55.1%; Score 22.6; DB 9; Length 283;
Best Local Similarity 73.0%; Pred. No. 4.5e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 4 CCTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
||||| ||| ||||| | ||||| ||||| ||||| :|||
Db 87 CCTCTGATCCAGATTGGCTCGCGGCGCCCGCGGC 123

RESULT 54

AU178502

LOCUS

DEFINITION

AU178502 291 bp mRNA linear EST 21-MAR-2001
AU178502 Medaka ovary cDNA library (OLD) from HNI Oryzias latipes
cDNA clone OLD04.07g similar to pir|I38029| matrix
metalloproteinase 15 (EC 3.4.24.-) membrane type precursor - human,
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryzias latipes (Japanese medaka)

Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 291)
Naruse,K., Mitani,H. and Tanaka,M.
Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)

Contact: Kiyoshi Naruse

Department of Biological Sciences

Graduate School of Science, University of Tokyo

Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan

Tel: 81-3-5841-4443

Fax: 81-3-5841-4410

Email: naruse@biol.s.u-tokyo.ac.jp

This clone was isolated from Medaka ovary cDNA library (OLD).

FEATURES

source

Location/Qualifiers

1..291
/organism="Oryzias latipes"
/mol_type="mRNA"
/strain="HNI"
/db_xref="taxon:8090"
/clone="OLD04.07g"
/tissue_type="ovary"
/dev_stage="adult"
/clone_lib="Medaka ovary cDNA library (OLD) from HNI"

ORIGIN

Query Match 55.1%; Score 22.6; DB 1; Length 291;
Best Local Similarity 73.0%; Pred. No. 4.5e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 AGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||| ||| ||||| ||| || ||||| ||||| :|

Db

2 AGCAGCCCGCTGCGCTCCGCCAACGCTGGCCCGGCC 38

RESULT 55

BI516993/c

LOCUS

DEFINITION

BI516993 351 bp mRNA linear EST 08-APR-2002
BB160024A10F04.5 Bee Brain Normalized Library, BB16 Apis mellifera
cDNA clone BB160024A10F04 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Apis mellifera (honey bee)

Apis mellifera

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 351)
Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee

JOURNAL

PUBMED

COMMENT

Genome Res. 12 (4), 555-566 (2002)

11932240

Contact: Gene E. Robinson

Department of Entomology

University of Illinois

505 S. Goodwin Ave., Urbana, IL 61801, USA

Tel: 217 265 0309

Fax: 217 244 3499

Email: generobi@life.uiuc.edu

This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

PCR Primers

FORWARD: TAATACGACTCACTATAGGG

BACKWARD: ATTAACCTCACTAAAG

Plate: BB160024A10 row: F column: 04

Seq primer: AGCGGATAACAATTTCACACAGGA

High quality sequence stop: 351.

FEATURES

source

1..351
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB160024A10F04"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized Library, BB16"
/note="Organ: brain; Vector: pT7T3-Pac; Site 1: EcoRI;
Site 2: NotI; The BB16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."

ORIGIN

Query Match 55.1%; Score 22.6; DB 3; Length 351;
Best Local Similarity 73.0%; Pred. No. 4.5e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||||| ||| || ||||| ||||| ||||| :|

Db 94 AGCCTGCGCCTGAAAGTCTCTCATCGCTGGCAAGAAC 58

RESULT 56

CB291106/c

LOCUS

DEFINITION

CB291106 358 bp mRNA linear EST 28-FEB-2003
UCRCS01_02be07 b1 Washington Navel orange cold acclimated flavedo &
albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02be07, mRNA
sequence.

DEFINITION UCRCS03_03I06_r Washington Navel Orange Shoot Meristem cDNA Library

ACCESSION Citrus sinensis cDNA clone CS_PEA03I06, mRNA sequence.

VERSION CF836754

KEYWORDS CF836754.1 GI:38052406

SOURCE EST.

ORGANISM Citrus sinensis

Citrus sinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE 1 (bases 1 to 361)

AUTHORS Close,T.J.,, Roose,M.L., Federici,C.F., Mu,L., Fenton,R.D., Wanamaker,S., Kim,H.R., Kudrna,D., Wing,R. and Yu,Y.

TITLE Development of EST Resources and New Genetic Markers for California Citrus - Washington Navel Orange Shoot Meristem

JOURNAL Unpublished (2003)

COMMENT Contact: Timothy Close

Department of Botany & Plant Sciences, University of California Riverside, CA, 92521-0124

Tel: 9097873318

Fax: 9097874437

Email: timothy.close@ucr.edu

Seq primer: T3.

Location/Qualifiers

1. .361

/organism="Citrus sinensis"

/mol_type="mRNA"

/cultivar="Parent Washington Navel"

/db_xref="taxon:2711"

/clone="CS_PEA03I06"

/tissue_type="Shoot meristem"

/dev_stage="10 year old trees"

/lab_host="E. coli TJCl21"

/clone_lib="Washington Navel Orange Shoot Meristem cDNA Library"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Parent Washington Navel Orange trees on Troyer rootstock (UCR 16K) were the source of tissue. Trees, at UC Riverside Agricultural Operations, were planted October 12, 1992. In each of 17 reps one tree on Troyer rootstock was initially treated with Enzone, one with Alliette and Nema cure, and one was left untreated. These treatments were discontinued in 1998. At the time of sampling, there were differences in the apparent health and size of the trees on Troyer rootstock. Fall-flush shoots were sampled in early November 2002 to minimize the number of floral shoot meristems. Federici and Mu (Roose lab) harvested meristems only from trees that appeared to be healthy and had a large number of young shoot tips on the day of collection. The average weight of a meristem was about 2 mg. Federici noted that there were quite a few insects and signs of insect damage to the shoot tips. Mealy bugs, thrips and aphids were observed, plus a few very tiny fast moving insects that may have been mites or crawler stage of scale (although Federici did not see any mature scale). It was not difficult to avoid collecting most of these because they were easy to see with the dissecting microscope. It was harder to exclude the frass. Some frass was definitely retained in the samples. Tissues were snap frozen and then stored at -80C until further processing. Fenton (Close lab) purified RNA by the phenol method described in J. Japanese Soc. Hort. Sci. 1996. 64 (4): 809-814, purified poly(A) mRNA using a PolyATtrack mRNA Isolation System IV (promega), produced a primary cDNA library using a lambda ZAP XR cDNA Synthesis Kit (Stratagene), then mass-excised one million pfu from the primary library to produce a phagemid population. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute, University of Arizona (Kim, Kudrna, Wing, Yu).

Chromatogram files were downloaded by FTP to UC Riverside (by Close), then processed at UC Riverside (by Wanamaker,

Close lab) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

ORIGIN

Query Match 55.1%; Score 22.6; DB 7; Length 361;

Best Local Similarity 73.0%; Pred. No. 4.5e+03;

Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 5 CTCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41

| | | | | | | | | | | | | | | | | | | | | |

Db 21 CACCGGATTCTTGTCTTCATCGGTGGCGCGCCTCG 57

| | | | | | | | | | | | | | | | | | | | | |

RESULT 61

DN957603

LOCUS DN957603 368 bp mRNA linear EST 09-MAY-2005

DEFINITION USDA-FP/ARO 13433 Star Ruby grapefruit hot water-treated flavedo Citrus x paradisi cDNA clone Hw-01_D05 5', mRNA sequence.

ACCESSION DN957603

VERSION DN957603.1 GI:63104337

KEYWORDS EST.

SOURCE Citrus x paradisi

ORGANISM Citrus x paradisi

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE 1 (bases 1 to 368)

AUTHORS McCollum,T.G., Maul,P. and Porat,R.

TITLE Expressed Sequence Tags (ESTs) from flavedo of Star Ruby grapefruit after hot water treatment

JOURNAL Unpublished (2005)

COMMENT Contact: McCollum, T.G.

US Horticultural Research Laboratory

USDA, ARS

2001 S. Rock Road, Ft. Pierce, FL 34945, USA

Tel: 561-462-5836

Fax: 561-462-5986

Email: gmccollum@ushrl.ars.usda.gov

Seq primer: T3 Primer.

Location/Qualifiers

1. .368

/organism="Citrus x paradisi"

/mol_type="mRNA"

/db_xref="taxon:37656"

/clone="Hw-01_D05"

/tissue_type="flavedo"

/dev_stage="mature fruit"

/lab_host="SOLR"

/clone_lib="Star Ruby grapefruit hot water-treated flavedo"

/note="Organ: fruit; Vector: pBluescript II SK+; Site_1: EcoRI; Site 2: XhoI; Standard library construction protocols from Stratagene cDNA synthesis kit (Cat No. 200401-5) and Uni-ZAP XR vector kit (Cat No. 237211)"

ORIGIN

Query Match 55.1%; Score 22.6; DB 8; Length 368;

Best Local Similarity 73.0%; Pred. No. 4.5e+03;

Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 5 CTCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41

| | | | | | | | | | | | | | | | | | | | | |

Db 242 CACCGGATTCTTGTCTTCATCGGTGGCGCGCCTCG 278

| | | | | | | | | | | | | | | | | | | | | |

RESULT 62

CO179529

LOCUS CO179529 369 bp mRNA linear EST 18-JUN-2004

DEFINITION EK059641.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila melanogaster cDNA clone EK059641 5', mRNA sequence.

ACCESSION CO179529
VERSION CO179529.1 GI:48952410
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 369)
AUTHORS Kopczynski,C., Platt,D., Campbell,J., Muzong,C., Laufer,A.,
Peterson,E. and Swimmer,C.
TITLE Exelixis FlyTag EST Project CK01 Library
JOURNAL Unpublished (2004)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: EK.596 row: D column: 5
High quality sequence stop: 368.
Location/Qualifiers
1. .369
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EK059641"
/clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
/note="Organ: mixed stage embryos, imaginal disks, and
adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
XhoI; Random primed, normalized library from mixed_stage
embryos, imaginal disks, and adult heads."

ORIGIN
Query Match 55.1%; Score 22.6; DB 7; Length 369;
Best Local Similarity 73.0%; Pred. No. 4.5e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGTGGCCCGNCG 39
|||||
105 GTCTCGGATGCCACACCCACAGCGTGGAGTGGCG 141

Db

RESULT 63
AQ191651/c
LOCUS
DEFINITION
HS_3225_B1_G10_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3225 Col=19 Row=N, genomic survey
sequence.
ACCESSION AQ191651
VERSION AQ191651.1 GI:3590273
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 379)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector

Plate: 3225 row: N column: 19
Class: BAC ends
High quality sequence stop: 379.
Location/Qualifiers
1. .379
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3225 Col=19 Row=N"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match 55.1%; Score 22.6; DB 9; Length 379;
Best Local Similarity 73.0%; Pred. No. 4.6e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGN 37
|||||
Db 113 AAGCCTCCGATGCCAGTCCCTCATCGTGGTCTTGAG 77

RESULT 64
AI711336/c
LOCUS
DEFINITION
AI711336 UI-R-AA1-zv-h-08-0-UI.s1 414 bp mRNA linear EST 04-JUN-1999
UI-R-AA1-zv-h-08-0-UI 3', mRNA sequence.
ACCESSION AI711336
VERSION AI711336.1 GI:5001112
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 414)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized atrium at 16.5 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1. .414
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AA1-zv-h-08-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-AA1"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AA1
library is a normalized library constructed from 16.5 dpc

rat atrium. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Jim Lin, Department of Biology, University of Iowa.

TAG_TISSUE=atrium at 16.5 dpc
TAG_LIB=UI-R-AA1
TAG_SEQ=GATTC"

ORIGIN

Query Match 55.1%; Score 22.6; DB 1; Length 414;
Best Local Similarity 73.0%; Pred. No. 4.6e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 AGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGNC 38
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 309 AGCCTACAGATGCCCTCCCCCAGCTCTGGCTGGCC 273

RESULT 65
CA728594
LOCUS
DEFINITION
604 bp mRNA linear EST 26-NOV-2002
wdilc.pk005.o7 wdilc Triticum aestivum cDNA clone wdilc.pk005.o7 5'
end, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA728594
CA728594.1 GI:25450584
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 604)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.

FEATURES
source
1..604
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wdilc.pk005.o7"
/tissue_type="inflorescence"
/lab_host="DH10B"
/clone_lib="wdilc"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum, Hi Line) developing
inflorescence +/- 4 cm"

ORIGIN

Query Match 55.1%; Score 22.6; DB 6; Length 604;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 4 CCTCCGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 207 CCTCCGATCCCGGCCACGTCGCCCGCGGTGCG 243

RESULT 66
CC763987/c
LOCUS
DEFINITION
624 bp DNA linear GSS 27-JUN-2003
CH240_41B8.TV CHORI-240 Bos taurus genomic clone CH240_41B8,

genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CC763987
CC763987.1 GI:32310485
GSS.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 624)
Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P.,
Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L.,
Womack,J.E., de Jong,P.J. and Lewin,H.A.
Bovine BAC end sequences from CHORI-240 library
Unpublished (2003)
Other_GSSs: CH240_41B8.TJ
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

TITLE
JOURNAL
COMMENT

1
1 (bases 1 to 624)
Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P.,
Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L.,
Womack,J.E., de Jong,P.J. and Lewin,H.A.
Bovine BAC end sequences from CHORI-240 library
Unpublished (2003)
Other_GSSs: CH240_41B8.TJ
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

FEATURES
source
1..624
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_41B8"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 55.1%; Score 22.6; DB 9; Length 624;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 AGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGNC 38
||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 478 AGCGCCACATTCAGAACCTCATCCCTGGCTGGGC 442

RESULT 67
BI765915/c
LOCUS
DEFINITION
625 bp mRNA linear EST 25-SEP-2001
603046189F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186231 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI765915
BI765915.1 GI:15757493
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

were still intact and were included in the sample. The pulp had color but the fruit rind was still green. The peel from each half fruit was bagged separately in foil packets, and pressed between sheets of dry ice to freeze. All packets were placed in a paper bag with the date and information about 'control' or 'infested' written on the bag, and then placed at -80oC. The second sampling date from the first infestation was 11 October. Paul brought 19 infested and 9 uninfested fruit to Claire. These were all set up on 30 August. The insects were at the late third instar. Mikeal Roose's advice was to prepare three bulks of each, 5 infested and 3 uninfested fruit per bulk. The remaining four infested fruit were infested to a lesser degree and were discarded. Washing was done as before and the peel from each fruit frozen between sheets of aluminum foil pressed between sheets of dry ice. There were quite a lot of adhering insects in the frozen rind. After it was frozen, the peel from 3 uninfested or 5 infested fruit were pooled in a foil packet, then stored at -80oC. The pulp had color but the rind was mostly green. However, there was a little color developing on some fruit around the insects. The third sampling date was 2 December. Paul brought the first fruit from the second infestation, which were set up on September 27 or 28. He brought 15 infested and 10 uninfested fruit. Claire cut and froze them as before, making three pools of 5 infested fruit and three pools of 3 uninfested fruit. The control fruit all had green at the stem end, mostly about 1/4 of the circumference from stem to blossom end, but one fruit was green all over. The infested fruit were almost fully orange, with only a small amount of the surface still green, approximately the size of a quarter coin. Paul said it would be at least a month, probably 6 weeks or even more before the insects reach the late third instar, so this was the final sample for the cDNA library due to time constraints for EST sequencing. Mandal and Fenton (Close lab) purified RNA by the phenol method described in J. Japanese Soc. Hort. Sci. 1996. 64 (4): 809-814, purified poly(A) mRNA using PolyAT Tract mRNA isolation kit (Promega), produced a primary cDNA library using a lambda ZAP XR cDNA Synthesis Kit (Stratagene), then mass-excised 1 million pfu from the primary library to produce a phagemid population. The library was made from a mixture of RNA from each of the three treatments such that approximately equal amounts of early second instar and late third instar RNA were used. Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute (Kim, Kudrna, Collura, Wissotski, Byrne, Stum, Smart, Muller, Wing). Chromatogram files were downloaded by FTP by Close, then processed by Wanamaker (Close lab) using the HarVEST pipeline (<http://harvest.ucr.edu>) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were assembled, then chimeras were removed following manual inspection of assemblies (Wanamaker, Close, Roose). Sequences that survived all removal steps were submitted to GenBank. Clones from this library are archived at the Arizona Genomics Institute (<http://www.genome.arizona.edu/orders/>)."

ORIGIN

Query Match	55.1%;	Score	22.6;	DB	8;	Length	658;
Best Local Similarity	73.0%;	Pred.	No. 4.7e+03;				
Matches	27;	Conservative	1;	Mismatches	9;	Indels	0;
				Gaps	0;		
QY	5	CTCCGGATGCCAGTCCTCATCGCTGGCCCGNCGCG	41				
Db	245	CACCGGATTCCTGCTTCATCGTGGCGCGCCTCG	209				

DN621130	DN621130	677 bp	mRNA	linear	EST 22-MAR-2005
LOCUS	UCRCS11_06E15_r	Parent Washington Navel Orange Scale-Infested Rind			
DEFINITION	cDNA Library UCRCS11 Citrus sinensis cDNA clone CS_WED0006E15, mRNA sequence.				
ACCESSION	DN621130				
VERSION	DN621130.1	GI:61690230			
KEYWORDS	EST.				
SOURCE	Citrus sinensis				
ORGANISM	Citrus sinensis				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Sapindales; Rutaceae; Citrus.				
REFERENCE	1 (bases 1 to 677)				
AUTHORS	Close,T.J., Roose,M.L., Federici,C.F., Mandal,J., Fenton,R.D., Luck,R., Forster,L., Morse,J., Flores,P., Wanamaker,S., Kim,H.R., Kudrna,D., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D., Muller,C. and Wing,R.				
	Development of EST Resources and New Genetic Markers for California Citrus - Parent Washington Navel Orange Scale-Infested Rind cDNA Library UCRCS11				
TITLE	Unpublished (2005)				
	Contact: Timothy J. Close				
JOURNAL	Department of Botany & Plant Sciences				
COMMENT	University of California				
	Riverside, CA 92521-0124, USA				
	Tel: 909-787-3318				
	Fax: 909-787-4437				
	Email: timothy.close@ucr.edu				
	Seq primer: T3.				
FEATURES	Location/Qualifiers				
	source				
	1..677				
	/organism="Citrus sinensis"				
	/mol_type="mRNA"				
	/cultivar="Parent Washington Navel"				
	/db_xref="taxon:2711"				
	/clone="CS_WED0006E15"				
	/tissue_type="Flavedo, albedo, some red scale"				
	/dev_stage="12 year old trees"				
	/lab_host="E. coli TJCl21"				
	/clone_lib="Parent Washington Navel Orange Scale-Infested Rind cDNA Library UCRCS11"				
	/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; In cooperation with Dr. Robert Luck and Dr. Joseph Morse, Department of Entomology, University of California Riverside, navel orange fruit was infested with red scale (Aonidiella aurantii [Maskell]). Dr. Luck's technician, Lisa Forster, maintained colonies of red scale. Dr. Morse's technician, Paul Flores, cleaned and infested the fruit, bagged the fruit after the crawlers had time to settle, then harvested the fruit at the early second instar and late third instar phases of the insect. Claire Federici (Dr. Mikeal Roose's lab) cleaned off most of the insects (some remained firmly attached), cut the peel, then froze and stored at -80oC. The trees used for this set of samples were growing in field 16K of the University of California Citrus Experiment Station. This was the same field from which the tissue was collected for the navel shoot meristems and the peel for citrus thrips, Scirtothrips citri [Moulton]. The trees were planted 12 October 1992. The scion was Parent navel. The trees used for infesting with red scale all had Troyer rootstock. Three different trees were used for each of the two infestations, a total of 6 trees. This experiment did not take place according to the original schedule because the red scale colony became infested with mites, so too few insects were available to infest the fruit on the date originally planned. The plan had been to infest on or about June 30 and August 13. Instead the infestation dates were August 30 and September 27, 2004. Because this took us into the cool weather of fall, the insects applied on the second infestation date took about three times as long to develop				

to the same stage as the insects applied on the first infestation date. The insects were reared on lemons. Before infesting the fruit on the trees, Paul Flores cleaned the peel and checked to make sure it was not already infested. He placed about 200 crawler stage insects on the fruit using a soft paintbrush. After the crawlers had a day to move around and find a spot to attach, Paul placed a very fine mesh drawstring bag over the fruit to exclude predators and parasitoids of the scale. Bags were left in place for the duration of the field development period and also covered control fruit. Paul Flores infested fruit on 30 August and 1 September 2004 after cleaning the fruit on August 27. On 21 September the first set of red scale infested fruit were sampled. He brought Claire Federici 15 infested fruit and 12 uninfested control fruit. The insects were at the early second instar. The controls had been cleaned and bagged at the same time as inoculated ones, but had no scale introduced. The infestation was heavy, so the insects were not well separated on the fruit. A razor blade was used to slice off the flavedo with about half the thickness of the albedo included. The peel from only the stem half of the fruit was used because that was where the insects were most concentrated. The insects were impossible to wash off without severely damaging the peel; each fruit was washed with water and a sponge or bottlebrush and wiped dry with a paper towel before cutting it, but many of the insects were still intact and were included in the sample. The pulp had color but the fruit rind was still green. The peel from each half fruit was bagged separately in foil packets, and pressed between sheets of dry ice to freeze. All packets were placed in a paper bag with the date and information about 'control' or 'infested' written on the bag, and then placed at -80oC. The second sampling date from the first infestation was 11 October. Paul brought 19 infested and 9 uninfested fruit to Claire. These were all set up on 30 August. The insects were at the late third instar. Mikeal Roose's advice was to prepare three bulks of each, 5 infested and 3 uninfested fruit per bulk. The remaining four infested fruit were infested to a lesser degree and were discarded. Washing was done as before and the peel from each fruit frozen between sheets of aluminum foil pressed between insects in the frozen rind. After it was frozen, the peel from 3 uninfested or 5 infested fruit were pooled in a foil packet, then stored at -80oC. The pulp had color but the rind was mostly green. However, there was a little color developing on some fruit around the insects. The third sampling date was 2 December. Paul brought the first fruit from the second infestation, which were set up on September 27 or 28. He brought 15 infested and 10 uninfested fruit. Claire cut and froze them as before, making three pools of 5 infested fruit and three pools of 3 uninfested fruit. The control fruit all had green at the stem end, mostly about 1/4 of the circumference from stem to blossom end, but one fruit was green all over. The infested fruit were almost fully orange, with only a small amount of the surface still green, approximately the size of a quarter coin. Paul said it would be at least a month, probably 6 weeks or even more before the insects reach the late third instar, so this was the final sample for the cDNA library due to time constraints for EST sequencing. Mandal and Fenton (Close lab) purified RNA by the phenol method described in J. Japanese Soc. Hort. Sci. 1996. 64 (4): 809-814, purified poly(A) mRNA using PolyAT Tract mRNA Isolation Kit (Promega), produced a primary cDNA library using a lambda ZAP XR cDNA Synthesis Kit (Stratagene), then mass-excised 1 million pfu from the primary library to produce a phagemid population. The library was made from a mixture of RNA from each of the three treatments such that approximately equal amounts of early second instar and late third instar RNA were used. Phagemids were plated,

plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI3730 at the Arizona Genomics Institute (Kim, Kudrna, Collura, Wissotski, Byrne, Stum, Smart, Muller, Wing). Chromatogram files were downloaded by FTP by Close, then processed by Wanamaker (Close lab) using the HarVEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were assembled, then chimeras were removed following manual inspection of assemblies (Wanamaker, Close, Roose). Sequences that survived all removal steps were submitted to GenBank. Clones from this library are archived at the Arizona Genomics Institute (http://www.genome.arizona.edu/orders/).

ORIGIN

Query Match 55.1%; Score 22.6; DB 8; Length 677;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 5 CTCGGATGCCAGTCCCTCATCGTCGCCCGGCGCG 41
| | | | | | | | | | | | | | | | | | | | | | | |
Db 640 CACCGGATCTTGTCCTTCATCGGTGGCGCGCCTCG 676

RESULT 70
BJ213473/c

LOCUS BJ213473 684 bp mRNA linear EST 04-APR-2002
DEFINITION BJ213473 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
cDNA clone wh22j06 5', mRNA sequence.

ACCESSION BJ213473
VERSION BJ213473.1 GI:19953031
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 684)
Ogihara,Y. and Murai,K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source

1..684
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wh22j06"
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh"

ORIGIN

Query Match 55.1%; Score 22.6; DB 3; Length 684;
Best Local Similarity 73.0%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGTCGGCCCGGN 37
| | | | | | | | | | | | | | | | | | | | | | | |
Db 217 AGGCCTCCGGTGGCACCACCGCCTCATCTGTGGCCGTGA 181

RESULT 71
CK193871

[illegible]

Plate: 1007083 column: 31
Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
1. .312
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcripion units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 54.6%; Score 22.4; DB 9; Length 312;
Best Local Similarity 70.0%; Pred. No. 5.2e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGCG 41
||||| | | | | | | | | | | | | | | | | | | | |
Db 209 AGCCTCCGGCTCCCGATCCTGCCTGATCGGCCGATCCG 170

RESULT 92
DN148717/c

LOCUS
DEFINITION

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM
Panicum virgatum (switchgrass)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Paniceae; Panicum.

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT
An EST survey of Switchgrass: a C4 perennial grass
Unpublished (2005)
Contact: Tobias CM
Genomics and Gene Discovery Unit
USDA, Agricultural Research Service, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510 559-6172
Fax: 510 559-5818
Email: ctobias@pw.usda.gov

The phred basecalling program was used to call bases and identify the high scoring region using the -trim_alt '', and trim_cutoff 0.01 options. Vector sequences have been removed using the program cross_match.

Seq primer: M13 reverse.
Location/Qualifiers
1. .373

FEATURES
source

/organism="Panicum virgatum"
/mol_type="mRNA"
/cultivar="Kanlow"
/db_xref="taxon:38727"
/clone="4936_G06_G06"

/dev_stage="immature tillers"
/lab_host="E. coli DH5alpha"
/clone_lib="Switchgrass leaf cDNA library"
/note="Organ: Leaf; Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Switchgrass cv. Kanlow plants were grown from seed in a greenhouse in potting soil. Immature tillers were collected randomly, leaf tissue was flash frozen in liquid nitrogen. The tissue was prepared by Gautam Sarath, USDA, ARS, Wheat Forage and Sorghum Research Unit, U. Nebraska, Lincoln. Total RNA and poly(A) RNA were prepared, cDNA synthesized, and directionally ligated into pSPORT1 by Paul Twigg, Biology Department, U. Nebraska Kearney, Kearney, NE. Plasmid DNA preparations and DNA sequencing were performed in the laboratory of CM Tobias."

ORIGIN

Query Match 54.6%; Score 22.4; DB 8; Length 373;
Best Local Similarity 70.0%; Pred. No. 5.3e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGCG 41
||||| | | | | | | | | | | | | | | | | | | | |
Db 254 AGTTCTCAGGCCAGTCTTTCTGTCGGAGGCCGAGGCGCG 215

RESULT 93
CF808758

LOCUS
DEFINITION

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM
Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT
Tyler B. Not Published
Unpublished (2003)
Contact: Tyler B
Tyler lab
VBI
1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyle@vt.edu

PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 039 row: D column: 06
Seq primer: BK reverse primer
High quality sequence stop: 382.

Location/Qualifiers
1. .382

FEATURES
source

/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Harosoy"
/db_xref="taxon:3847"
/clone="SHB039D06"
/tissue_type="Phytophthora sojae-infected hypocotyl"
/cell_line="Phytophthora sojae culture P6497"
/dev_stage="48 hr. post infection stage"
/clone_lib="USDA-IFAPS:Expression of Phytophthora sojae genes during infection and propagation"
/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI"

ORIGIN

Query Match 54.6%; Score 22.4; DB 6; Length 382;
Best Local Similarity 70.0%; Pred. No. 5.3e+03;

	Matches	28;	Conservative	1;	Mismatches	11;	Indels	0;	Gaps	0;
Qy	1	AAGCCTCCGGATGCCAGTCCCTCATCGTGCCGCGNCGC	40							
Dδ	302	AGGCCACCGATTCTCTCTCTTCCTCCGCGGCCCTGCGCG	341							

RESULT 94					
AU055771/c					
LOCUS	AU055771	409 bp	mRNA	linear	EST 01-APR-2002
DEFINITION	AU055771 Oryza sativa mature leaf Nipponbare Oryza sativa (japonica cultivar-group) cDNA clone S20046 1A, mRNA sequence.				

SOURCE	ORGANISM
Oryza sativa (japonica cultivar-group)	Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)	Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	Oryza sativa (japonica cultivar-group)

rice cDNA from mature leaf
Unpublished (1999)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL: <http://rgp.dna.affrc.go.jp/>
PROJECT = 'RGP'.

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mrna"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="S20046_1A"
/tissue_type="mature leaf"
/clone_lib="Oryza sativa mature leaf Nipponbare"

```

TITLE	McCann,R., Waterston,R. and Wilson,R.
JOURNAL	Public Soybean EST Project
COMMENT	Unpublished (1999) Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Putative full length read vector to vector length is 417 This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com).

Query Match	54.6%;	Score 22.4;	DB 2;	Length 414;
Best Local Similarity	70.0%;	Pred. No. 5.3e+03;		
Matches 28; Conservative		1; Mismatches 11;	Indels 0;	Gaps 0;
ORIGIN				

RESULT 96					
BM721516					
LOCUS	BM721516	415 bp	mRNA	linear	EST 01-MAR-2002
DEFINITION	UI-E-EO1-aic-o-13-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone UI-E-EO1-aic-o-13-0-UI 5', mRNA sequence.				

KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 415)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
PUBMED	8889548
COMMENT	Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES

source

1. .415
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-E01-aic-o-13-0-UI"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-E01"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site 2: Not I; UI-E-E01 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dfr)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Query Match 54.6%; Score 22.4; DB 3; Length 415;
Best Local Similarity 70.0%; Pred. No. 5.3e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 253 AAGACGACGACTGCCTGCCCTCTCGCTACCCCTGCCGC 292

RESULT 97

BG717495

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 482)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM10728 row: f column: 16

High quality sequence stop: 441.

FEATURES

source

Location/Qualifiers
1. .482
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4821519"
/lab_host="DH10B"
/clone_lib="NIH_MGC 97"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: Sali-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 54.6%; Score 22.4; DB 2; Length 482;
Best Local Similarity 70.0%; Pred. No. 5.4e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 270 AAGACGACGACTGCCTGCCCTCTCGCTACCCCTGCCGC 309

RESULT 98

BQ785316

LOCUS

DEFINITION

BQ785316 554 bp mRNA linear EST 02-JUL-2004
saq76a07.y1 Gm-cl076 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl076-5414 5' similar to TR:O80915 O80915 T19C21.15 PROTEIN. ;,
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 554)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 422.

FEATURES

Location/Qualifiers

```
source
1. .554
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl076-5414"
/tissue_type="wounded cotyledons"
/dev_stage="11 day old seedlings"
/lab_host="DH10B"
/clone_lib="Gm-cl076"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from 11 day old seedlings treated with that were treated
with 2 ugs/ml of a crude glucan elicitor preparation
isolated from the mycelial walls of Phytophthora sojae.
The library was prepared using the Stratagene pBluescript
II SK(+) library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an XhoI restriction site. EcoRI
adaptors were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into E.coli ElectroMax DH10B host cells. Plant
material was provided by Michael G. Hahn (Complex
Carbohydrate Research Center, University of Georgia) and
the library was constructed by Anu Khanna (Lila Vodkin
lab, University of Illinois)."
```

ORIGIN

Query Match 54.6%; Score 22.4; DB 5; Length 554;
Best Local Similarity 70.0%; Pred. No. 5.4e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
| ||| ||||| || ||||| || ||||| ||||| ||||| : |||
Db 238 AGGCCACCGGATTCTCTCTCTCTCCGCGCCCTGCCGC 277

RESULT 99
CW579372
LOCUS CW579372 638 bp DNA linear GSS 22-OCT-2004
DEFINITION OA_ABA0109B01.r OA_ABA Oryza australiensis genomic clone
OA_ABA0109B01 3', genomic survey sequence.
ACCESSION CW579372
VERSION CW579372.1 GI:54465170
KEYWORDS GSS.
SOURCE Oryza australiensis
ORGANISM Oryza australiensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 638)
AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0109 row: B column: 01
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
1. .638
/organism="Oryza australiensis"

```
/mol_type="genomic DNA"
/db_xref="taxon:4532"
/clone="OA_ABA0109B01"
/tissue_type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OA_ABA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 54.6%; Score 22.4; DB 10; Length 638;
Best Local Similarity 70.0%; Pred. No. 5.4e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 150 AAGCCTCCGCAAGCCTCTCTCCAGCGCCGCTCGGCCTC 189

RESULT 100
AG104213/c
LOCUS AG104213 680 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-108A23.F, genomic survey sequence.
ACCESSION AG104213
VERSION AG104213.1 GI:16724731
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 680)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsrumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKSI45
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. .680
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-108A23.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 54.6%; Score 22.4; DB 10; Length 680;
Best Local Similarity 70.0%; Pred. No. 5.4e+03;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
|| ||| || ||| ||| ||| ||| ||| ||| ||| : |||
Db 269 AAACCTGCTGCAGCAAAATCCCGCATCCCTGGCCTGGCCAC 230
```

Search completed: May 9, 2006, 22:55:13
Job time : 1917 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 22:18:30 ; Search time 144 Seconds
(without alignments)
506.111 Million cell updates/sec

Title: US-09-904-968A-1_N3336_COPY_3300_3340
Perfect score: 41
Sequence: 1 aagcctccgagtcagctcc.....tcatcgctggcccgncgcg 41

Scoring table: IDENTITY_NUCDX
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCrUS COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	41	100.0	31571	2	US-08-323-443B-1
c 2	41	100.0	53526	3	US-08-658-136-2
c 3	41	100.0	53577	3	US-08-658-136-1
c 4	41	100.0	53577	3	US-08-460-215A-1
c 5	24.6	60.0	1424	3	US-09-902-540-3125
c 6	24.6	60.0	15268	3	US-09-902-540-1142
c 7	22.6	55.1	369	3	US-09-270-767-7807
c 8	22.6	55.1	369	3	US-09-270-767-23089
c 9	22.4	54.6	1269	3	US-09-252-991A-3470
c 10	22.4	54.6	227390	3	US-09-949-016-12201
c 11	22.4	54.6	227391	3	US-09-949-016-13365
c 12	22	53.7	1281	3	US-09-902-540-7196
c 13	22	53.7	6430	3	US-09-902-540-669
c 14	22	53.7	8559	3	US-09-949-016-13412
c 15	22	53.7	59252	3	US-09-949-016-12150
c 16	22	53.7	59252	3	US-09-949-016-15374
c 17	21.8	53.2	289	3	US-09-313-294A-4625
c 18	21.8	53.2	687	3	US-09-902-540-8880
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c 20	21.6	52.7	230	3	US-09-060-756-422
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c 22	21.6	52.7	1689	3	US-09-902-540-3347
c 23	21.6	52.7	18537	3	US-09-902-540-1157
c 24	21.4	52.2	234	3	US-09-252-991A-4962
c 25	21.4	52.2	409	3	US-09-902-540-5238
c 26	21.4	52.2	444	3	US-09-252-991A-11328
c 27	21.4	52.2	501	3	US-09-252-991A-11294
c 28	21.4	52.2	654	3	US-09-252-991A-13109
c 29	21.4	52.2	738	3	US-09-252-991A-12833
c 30	21.4	52.2	816	3	US-09-252-991A-10112
c 31	21.4	52.2	834	3	US-09-252-991A-10044
c 32	21.4	52.2	909	3	US-09-252-991A-9793
c 33	21.4	52.2	966	3	US-09-252-991A-12948
c 34	21.4	52.2	1356	3	US-09-252-991A-4935
c 35	21.4	52.2	1532	3	US-09-270-767-12050
c 36	21.4	52.2	2046	3	US-09-252-991A-4982
c 37	21.4	52.2	4236	3	US-09-902-540-5367
c 38	21.4	52.2	11854	3	US-09-902-540-1037
c 39	21.4	52.2	34662	3	US-09-902-540-1261
c 40	21.2	51.7	4403765	3	US-09-103-840A-2
c 41	21.2	51.7	4411529	3	US-09-103-840A-1
c 42	21	51.2	420	3	US-09-252-991A-13290
c 43	21	51.2	624	3	US-09-252-991A-12674
c 44	21	51.2	747	3	US-09-758-759-112
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c 46	21	51.2	972	3	US-09-909-796-11
c 47	21	51.2	1139	3	US-09-909-796-1
c 48	21	51.2	1146	3	US-09-252-991A-12818
c 49	21	51.2	1362	3	US-09-902-540-8360
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c 56	21	51.2	29559	3	US-09-902-540-1254
c 57	21	51.2	41170	3	US-09-902-540-1267
c 58	21	51.2	67386	3	US-09-949-016-16519
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c 60	21	51.2	146095	3	US-09-949-016-12872
c 61	21	51.2	146104	3	US-09-949-016-13239
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c 63	20.8	50.7	682	3	US-08-796-792-1
c 64	20.8	50.7	682	3	US-09-491-795-1
c 65	20.8	50.7	958	3	US-09-902-540-194
c 66	20.8	50.7	1134	3	US-09-342-681C-15
c 67	20.8	50.7	1661	3	US-09-342-681C-3
c 68	20.8	50.7	15073	3	US-09-949-016-15673
c 69	20.8	50.7	97195	3	US-09-949-016-12212
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c 86	20.4	49.8	708	3	US-09-902-540-1910
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c 89	20.4	49.8	1410	3	US-09-252-991A-1239
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c 96	20.4	49.8	2263	3	US-09-595-549-1
c 97	20.4	49.8	2712	3	US-09-252-991A-1366

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c 442 19.2 46.8 22481 6 PCT-US95-07201-43 Sequence 43, Appl
c 443 19.2 46.8 22484 3 US-09-875-223-2 Sequence 2, Appli
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c 446 19.2 46.8 27463 3 US-09-949-016-11876 Sequence 11876, A
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448 19.2 46.8 44377 2 US-08-804-227C-7 Sequence 7, Appli
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c 462 19 46.3 322 3 US-09-513-999C-12600 Sequence 12600, A

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c 464 19 46.3 435 3 US-09-252-991A-5474 Sequence 5474, Ap
465 19 46.3 489 3 US-09-252-991A-452 Sequence 452, App
c 466 19 46.3 513 3 US-09-252-991A-411 Sequence 411, App
467 19 46.3 579 3 US-09-252-991A-2876 Sequence 2876, Ap
468 19 46.3 582 2 US-08-722-001-23 Sequence 23, Appl
469 19 46.3 601 3 US-09-949-016-76658 Sequence 76658, A
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475 19 46.3 966 3 US-09-252-991A-15974 Sequence 15974, A
476 19 46.3 981 3 US-09-252-991A-431 Sequence 431, App
477 19 46.3 984 3 US-09-489-039A-1470 Sequence 1470, Ap
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c 479 19 46.3 1059 3 US-09-252-991A-884 Sequence 884, App
480 19 46.3 1179 3 US-09-489-039A-1542 Sequence 1542, Ap
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482 19 46.3 1206 3 US-09-252-991A-801 Sequence 801, App
483 19 46.3 1257 3 US-09-252-991A-5429 Sequence 5429, Ap
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c 485 19 46.3 1302 3 US-09-252-991A-5460 Sequence 5460, Ap
c 486 19 46.3 1470 3 US-09-252-991A-369 Sequence 369, App
c 487 19 46.3 1536 3 US-09-252-991A-3182 Sequence 3182, Ap
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489 19 46.3 1578 3 US-09-489-039A-3846 Sequence 3846, Ap
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c 491 19 46.3 1632 3 US-09-902-540-3845 Sequence 3845, Ap
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c 494 19 46.3 1866 3 US-09-537-120-1 Sequence 1, Appli
c 495 19 46.3 1894 3 US-09-270-767-31098 Sequence 31098, A
c 496 19 46.3 1944 3 US-09-252-991A-16245 Sequence 16245, A
497 19 46.3 2070 3 US-09-252-991A-2687 Sequence 2687, Ap
498 19 46.3 2108 3 US-09-032-742-6 Sequence 6, Appli
c 499 19 46.3 2131 3 US-09-270-767-14846 Sequence 14846, A
c 500 19 46.3 2160 3 US-09-489-039A-6468 Sequence 6468, Ap

ALIGNMENTS

RESULT 1
US-08-323-443B-1/c
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/0A462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match 100.0%; Score 41; DB 2; Length 31571;
Best Local Similarity 97.6%; Pred. No. 6.7e-05;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
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Db 3633 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 3593

RESULT 2
US-08-658-136-2
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match 100.0%; Score 41; DB 3; Length 53526;
Best Local Similarity 97.6%; Pred. No. 6.9e-05;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
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Db 3300 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 3340

RESULT 3
US-08-658-136-1
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match 100.0%; Score 41; DB 3; Length 53577;
Best Local Similarity 97.6%; Pred. No. 6.9e-05;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 41
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Db 3300 AAGCTCCGGATGCCAGTCCCTCATCGTGGCCCGGCGG 3340

RESULT 4
US-08-460-215A-1
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23089
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23089

Query Match 55.1%; Score 22.6; DB 3; Length 369;
Best Local Similarity 73.0%; Pred. No. 97;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
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Db 105 GTCTCGGATGCCACCCACACGCGCTGGAGTGGCG 141

RESULT 9
US-09-252-991A-3470/c
; Sequence 3470, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3470
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3470

Query Match 54.6%; Score 22.4; DB 3; Length 1269;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGG 41
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Db 998 AGGCTCATGATGCCAGCCCCCGATGCCAGACCCGCTCGCG 959

RESULT 10
US-09-949-016-12201/c
; Sequence 12201, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12201
; LENGTH: 227390
; TYPE: DNA
; ORGANISM: Human

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(227390)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12201

Query Match 54.6%; Score 22.4; DB 3; Length 227390;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
||| ||||| ||| ||| ||||| |||
Db 80961 ATGCCACCTGATGCCTGTCTCCCTCCCTGGTCTGGAGGC 80922

RESULT 11
US-09-949-016-13365/c
; Sequence 13365, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13365
; LENGTH: 227391
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(227391)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13365

Query Match 54.6%; Score 22.4; DB 3; Length 227391;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
||| ||||| ||| ||| ||||| |||
Db 80961 ATGCCACCTGATGCCTGTCTCCCTCCCTGGTCTGGAGGC 80922

RESULT 12
US-09-902-540-7196
; Sequence 7196, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7196
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Myxococcus xanthus

US-09-902-540-7196

Query Match 53.7%; Score 22; DB 3; Length 1281;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 24; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 12 TGCCAGTCCCTCATCGCTGCCCGCGGCGG 41
| | | | | | | | | | | | | | | | | | | | | |
Db 742 TACAAGTACCTCAACGCCGCGCGCGCGGCGG 771

RESULT 13
US-09-902-540-669/c
; Sequence 669, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 669
; LENGTH: 6430
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(6430)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-669

Query Match 53.7%; Score 22; DB 3; Length 6430;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 24; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 12 TGCCAGTCCCTCATCGCTGCCCGCGGCGG 41
| | | | | | | | | | | | | | | | | | | | | |
Db 2916 TACAAGTACCTCAACGCCGCGCGCGGCGG 2887

RESULT 14
US-09-949-016-13412/c
; Sequence 13412, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13412
; LENGTH: 8559
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13412

Query Match 53.7%; Score 22; DB 3; Length 8559;
Best Local Similarity 71.1%; Pred. No. 1.9e+02;

Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGG 39
| | | | | | | | | | | | | | | | | | | | | |
Db 686 AGCCCCGGGATGCCGGGCGCGGAGCGCTGGGGGGCGG 649

RESULT 15
US-09-949-016-12150/c
; Sequence 12150, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12150
; LENGTH: 59252
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12150

Query Match 53.7%; Score 22; DB 3; Length 59252;
Best Local Similarity 71.1%; Pred. No. 2.1e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGG 40
| | | | | | | | | | | | | | | | | | | | | |
Db 42417 GGCCCTGGATGCCACACCCCTCATTCCTGCCCGGTTTAC 42380

RESULT 16
US-09-949-016-15374/c
; Sequence 15374, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15374
; LENGTH: 59252
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15374

Query Match 53.7%; Score 22; DB 3; Length 59252;
Best Local Similarity 71.1%; Pred. No. 2.1e+02;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCCCGGCGG 40
| | | | | | | | | | | | | | | | | | | | | |
Db 42417 GGCCCTGGATGCCACACCCCTCATTCCTGCCCGGTTTAC 42380

```

; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 945
; LENGTH: 10528
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-945

Query Match      53.2%; Score 21.8; DB 3; Length 10528;
Best Local Similarity 68.3%; Pred. No. 2.2e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      8588 ACGCCTCCGGCGCCAGGCCTTCATCAGCGCCCGCGCGTG 8548

RESULT 20
US-09-060-756-422
; Sequence 422, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 422
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-422

Query Match      52.7%; Score 21.6; DB 3; Length 230;
Best Local Similarity 72.2%; Pred. No. 2.1e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      6 TCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      33 TCCGGATTCTGGGCTTCATCGCTCGCGCCGTCGCG 68

RESULT 21
US-09-670-314-422
; Sequence 422, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
```

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; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 945
; LENGTH: 10528
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-945

Query Match      53.2%; Score 21.8; DB 3; Length 289;
Best Local Similarity 68.3%; Pred. No. 1.8e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      258 ACGCCTCTGGATGATTGCCCTCACCTCTGGACCTGATGGG 218

RESULT 18
US-09-902-540-8880
; Sequence 880, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 880
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8880

Query Match      53.2%; Score 21.8; DB 3; Length 687;
Best Local Similarity 68.3%; Pred. No. 1.9e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      110 ACGCCTCCGGCGCCAGGCCTTCATCAGCGCCCGCGCGTG 150

RESULT 19
US-09-902-540-945/c
; Sequence 945, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
```


RESULT 28
US-09-252-991A-13109/c
; Sequence 13109, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-10112

Query Match 52.2%; Score 21.4; DB 3; Length 816;
Best Local Similarity 69.2%; Pred. No. 2.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
||| || ||||| ||| | ||||| ||: |||||
Db 82 GCCACCTGATGCCAGGACAGCTTGACCGCCTGGGCGCG 44

RESULT 31

US-09-252-991A-10044/c
; Sequence 10044, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10044
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-10044

Query Match 52.2%; Score 21.4; DB 3; Length 834;
Best Local Similarity 69.2%; Pred. No. 2.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
||| || ||||| ||| | ||||| ||: |||||
Db 749 GCCACCTGATGCCAGGACAGCTTGACCGCCTGGGCGCG 711

RESULT 32

US-09-252-991A-9793
; Sequence 9793, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9793
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9793

Query Match 52.2%; Score 21.4; DB 3; Length 909;
Best Local Similarity 69.2%; Pred. No. 2.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
||| || ||||| ||| | ||||| ||: |||||
Db 275 GCCACCTGATGCCAGGACAGCTTGACCGCCTGGGCGCG 313

RESULT 33

US-09-252-991A-12948/c
; Sequence 12948, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12948
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-12948

Query Match 52.2%; Score 21.4; DB 3; Length 966;
Best Local Similarity 69.2%; Pred. No. 2.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
||| || ||||| ||||| ||||| ||||| : |||||
Db 604 GCAACCGCAGGCCAGTTCTCTCGTCGTCGGCCAGCCAGCG 566

RESULT 34

US-09-252-991A-4935
; Sequence 4935, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4935
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-4935

Query Match 52.2%; Score 21.4; DB 3; Length 1356;
Best Local Similarity 69.2%; Pred. No. 2.7e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
||| ||||| ||||| ||||| ||||| ||: |||||
Db 569 GCCGCCGAATCCACTCGCTCTTACCCCGCTTGGCGCG 607

RESULT 35

US-09-270-767-12050
; Sequence 12050, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517


```
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          51.7%; Score 21.2; DB 3; Length 4403765;
Best Local Similarity 73.5%; Pred. No. 2.8e+02;
Matches 25; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 8 CGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    |||| || |||| || |||| |||| |||| ||||
Db 2011537 CGGACGGCGTCCCGTAACGCCGGCCGACCGCG 2011570

RESULT 41
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          51.7%; Score 21.2; DB 3; Length 4411529;
Best Local Similarity 73.5%; Pred. No. 2.8e+02;
Matches 25; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 8 CGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    |||| || |||| || |||| |||| |||| ||||
Db 2014147 CGGACGGCGTCCCGTAACGCCGGCCGACCGCG 2014180

RESULT 42
US-09-252-991A-13290/c
; Sequence 13290, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13290
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13290

Query Match          51.2%; Score 21; DB 3; Length 420;
Best Local Similarity 70.3%; Pred. No. 3.4e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
    |||| |||| |||| || |||| |||| |||| ||
Db 110 GCCTTCGGTGCCTGGCGATCATCGCCGACCGGCG 74

RESULT 43
US-09-252-991A-12674
; Sequence 12674, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12674
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12674

Query Match          51.2%; Score 21; DB 3; Length 624;
Best Local Similarity 70.3%; Pred. No. 3.5e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
    |||| |||| |||| || |||| |||| |||| ||
Db 401 GCCTTCGGTGCCTGGCGATCATCGCCGACCGGCG 437

RESULT 44
US-09-758-759-112
; Sequence 112, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everninomicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(747)
```

```
; OTHER INFORMATION: evbL
US-09-758-759-112

Query Match          51.2%; Score 21; DB 3; Length 747;
Best Local Similarity 70.3%; Pred. No. 3.6e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      5 CTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      108 CTCGGCTGGGCTTCCACATCGCCGGCGGCGCGG 144

RESULT 45
US-09-533-559-7620
; Sequence 7620, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7620
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Tricoderma reesei
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(929)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-7620

Query Match          51.2%; Score 21; DB 3; Length 929;
Best Local Similarity 70.3%; Pred. No. 3.6e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      212 CGTCCGGGACCCAGTCGCTCAGCCCTGCCCGAGCCTC 248

RESULT 46
US-09-909-796-11
; Sequence 11, Application US/09909796
; Patent No. 6867237
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, Catherine, et al.
; TITLE OF INVENTION: DNA ENCODING APOPTOSIS-INDUCED EUCARYOTIC INITIATION FACTOR-5A AN
; TITLE OF INVENTION: DEOXYHYPUSINE SYNTHASE AND A METHOD FOR CONTROLLING APOPTOSIS IN
; TITLE OF INVENTION: HUMANS
; FILE REFERENCE: 10799/13
; CURRENT APPLICATION NUMBER: US/09/909,796
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Rodent
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(330)
US-09-909-796-11
```

```
Query Match          51.2%; Score 21; DB 3; Length 972;
Best Local Similarity 70.3%; Pred. No. 3.6e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
      ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      371 AGCTACAGAGGCCCTCCCCCAGCTCTGGCTGGGCC 407

RESULT 47
US-09-909-796-1
; Sequence 1, Application US/09909796
; Patent No. 6867237
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, Catherine, et al.
; TITLE OF INVENTION: DNA ENCODING APOPTOSIS-INDUCED EUCARYOTIC INITIATION FACTOR-5A A
; TITLE OF INVENTION: DEOXYHYPUSINE SYNTHASE AND A METHOD FOR CONTROLLING APOPTOSIS I
; TITLE OF INVENTION: HUMANS
; FILE REFERENCE: 10799/13
; CURRENT APPLICATION NUMBER: US/09/909,796
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Rodent
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)...(497)
US-09-909-796-1
```

```
Query Match          51.2%; Score 21; DB 3; Length 1139;
Best Local Similarity 70.3%; Pred. No. 3.6e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
      ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      538 AGCTACAGAGGCCCTCCCCCAGCTCTGGCTGGGCC 574
```

```
RESULT 48
US-09-252-991A-12818
; Sequence 12818, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12818
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12818
```

```
Query Match          51.2%; Score 21; DB 3; Length 1146;
Best Local Similarity 70.3%; Pred. No. 3.6e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
      ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      868 GCCTTCGGTCGCTGGCGATCATCGCCGACCGGCCG 904
```



```
RESULT 49
US-09-902-540-8360/c
; Sequence 8360, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8360
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8360

Query Match          51.2%; Score 21; DB 3; Length 1362;
Best Local Similarity 70.3%; Pred. No. 3.7e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
||||| ||| || ||||| ||| || ||: ||
Db 943 CCTCGGAGCCCGCTCCTCAGCGCACGGGTGGC 907

RESULT 50
US-09-902-540-5562
; Sequence 5562, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5562
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5562

Query Match          51.2%; Score 21; DB 3; Length 1737;
Best Local Similarity 70.3%; Pred. No. 3.7e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 39
||||| ||| || ||||| ||| ||||| ||| |||
Db 1147 GCCTCCGACGGCGAAATCCTCATCCGCGCCCGGCCG 1183

RESULT 51
US-09-252-991A-13124/c
; Sequence 13124, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```

```
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13124
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13124

Query Match          51.2%; Score 21; DB 3; Length 1845;
Best Local Similarity 70.3%; Pred. No. 3.7e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 39
||||| ||| ||| ||| ||| ||||| ||| |||: ||
Db 51 GCCTTCGGTCGCTGGCGATCATCGCCGACCGGCCG 15

RESULT 52
US-10-104-047-556/c
; Sequence 556, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 556
; LENGTH: 2185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-556

Query Match          51.2%; Score 21; DB 3; Length 2185;
Best Local Similarity 82.8%; Pred. No. 3.8e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTG 30
||||| ||||| ||||| ||||| |||||
Db 665 AGCCTCTCAATGCCTGTCCCTCATGTGCTG 637

RESULT 53
US-09-902-540-5156/c
; Sequence 5156, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5156
; LENGTH: 2421
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5156

Query Match          51.2%; Score 21; DB 3; Length 2421;
Best Local Similarity 70.3%; Pred. No. 3.8e+02;
```

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
Db 795 CTCGTCAGCCACTGCCGACCGTGGCCCCGGCGG 759

RESULT 54
US-09-902-540-875
; Sequence 875, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 875
; LENGTH: 7628
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-875

Query Match 51.2%; Score 21; DB 3; Length 7628;
Best Local Similarity 70.3%; Pred. No. 4e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
Db 422 CCTCGGAGCCCCGCTCCCTCAGCGCACGCGTGTGGC 458

RESULT 55
US-09-773-816-1/c
; Sequence 1, Application US/09773816
; Patent No. 6340774
; GENERAL INFORMATION:
; APPLICANT: Stanford University
; APPLICANT: Khosla, Chaitan
; TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; FILE REFERENCE: 28600-20210.00
; CURRENT APPLICATION NUMBER: US/09/773,816
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/243,458
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/179,305
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 23673
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(23623)
; OTHER INFORMATION: n = A,T,C or G
US-09-773-816-1

Query Match 51.2%; Score 21; DB 3; Length 23673;
Best Local Similarity 70.3%; Pred. No. 4.3e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGG 37
Db 1484 ACGCGTCCGGATTCCCGTCCCGACTCGCGGCCAGAT 1448

Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

RESULT 56
US-09-902-540-1254/c
; Sequence 1254, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1254
; LENGTH: 29559
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1254

Query Match 51.2%; Score 21; DB 3; Length 29559;
Best Local Similarity 70.3%; Pred. No. 4.4e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
Db 14752 CTCGTCAGCCACTGCCGACCGTGGCCCCGGCGG 14716

RESULT 57
US-09-902-540-1267/c
; Sequence 1267, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1267
; LENGTH: 41170
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(41170)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1267

Query Match 51.2%; Score 21; DB 3; Length 41170;
Best Local Similarity 70.3%; Pred. No. 4.4e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCG 39
Db 38840 GCCTCCGACGGCGAAATCCTCATCGCGGCCCGCGG 38804

RESULT 58
US-09-949-016-16519/c
; Sequence 16519, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16519
; LENGTH: 67386
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(67386)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16519

Query Match 51.2%; Score 21; DB 3; Length 67386;
Best Local Similarity 70.3%; Pred. No. 4.5e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AGCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||||| | | | | | | | | | | | | | | | | | | | |
Db 66734 AGCCTCTGAAGGCCCTCACTCATCCCTTTCCAGCC 66698

RESULT 59

US-09-758-759-1/c
; Sequence 1, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everninomicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 109519
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
US-09-758-759-1

Query Match 51.2%; Score 21; DB 3; Length 109519;
Best Local Similarity 70.3%; Pred. No. 4.6e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 5 CTCCGGATGCCAGTCCCTCATCGTGGCCCGGNCGG 41
||||| | | | | | | | | | | | | | | | | | | | |
Db 70252 CTCCGGCTGGGCCTTCCACATCGCCGGCGGCCGG 70216

RESULT 60

US-09-949-016-12872/c
; Sequence 12872, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12872
; LENGTH: 146095
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12872

Query Match 51.2%; Score 21; DB 3; Length 146095;
Best Local Similarity 82.8%; Pred. No. 4.7e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCGCTG 30
||||| | | | | | | | | | | | | | | | | | | | |
Db 94296 AGCCTCTCAATGCCTGTCCCTCATTGCTG 94268

RESULT 61

US-09-949-016-13239/c
; Sequence 13239, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13239
; LENGTH: 146104
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13239

Query Match 51.2%; Score 21; DB 3; Length 146104;
Best Local Similarity 82.8%; Pred. No. 4.7e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCGCTG 30
||||| | | | | | | | | | | | | | | | | | | | |
Db 94296 AGCCTCTCAATGCCTGTCCCTCATTGCTG 94268

RESULT 62

US-09-902-540-5941
; Sequence 5941, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

```

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5941
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5941

Query Match      50.7%; Score 20.8; DB 3; Length 570;
Best Local Similarity 67.5%; Pred. No. 4.1e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
Db 446 AGGCCACCGTGGACCTGTCCCGCCTCGATGGCCTGTCCGC 485

RESULT 63
US-08-796-792-1/c
; Sequence 1, Application US/08796792
; Patent No. 6087163
; GENERAL INFORMATION:
; APPLICANT: Gennaro, Maria L.
; APPLICANT: Lyashchenko, Konstantin P.
; APPLICANT: Manca, Claudia M.A.
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS
; TITLE OF INVENTION: SPECIFIC PROTEINS AND GENES, MIXTURES OF ANTIGENS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 45 Rockefeller Plaza, Suite 2800
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,792
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,364
; FILING DATE: 09-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hone, William J.
; REGISTRATION NUMBER: 26,739
; REFERENCE/DOCKET NUMBER: 07763/03301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-765-5070
; TELEFAX: 212-258-2291
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 682 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 109...585
US-08-796-792-1

Query Match      50.7%; Score 20.8; DB 3; Length 682;
Best Local Similarity 67.5%; Pred. No. 4.1e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 41
Db 641 AGCCTGCCGGCCCAATACCTCAGCGGTGCGCTGGCGTG 602
```

```

RESULT 64
US-09-491-795-1/c
; Sequence 1, Application US/09491795
; Patent No. 6596281
; GENERAL INFORMATION:
; APPLICANT: Gennaro, Maria L.
; APPLICANT: Lyashchenko, Konstantin P.
; APPLICANT: Manca, Claudia M.A.
; TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC PROTEINS AND GENES,
; TITLE OF INVENTION: MIXTURES OF ANTIGENS AND USES THEREOF
; FILE REFERENCE: 07763/028002
; CURRENT APPLICATION NUMBER: US/09/491,795
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: US 08/796,792
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/011,364
; PRIOR FILING DATE: 1996-02-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 682
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)...(585)
US-09-491-795-1

Query Match      50.7%; Score 20.8; DB 3; Length 682;
Best Local Similarity 67.5%; Pred. No. 4.1e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 41
Db 641 AGCCTGCCGGCCCAATACCTCAGCGGTGCGCTGGCGTG 602

RESULT 65
US-09-902-540-194/c
; Sequence 194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 194
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-194

Query Match      50.7%; Score 20.8; DB 3; Length 958;
Best Local Similarity 67.5%; Pred. No. 4.2e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
Db 127 AGGCCACCGTGGACCTGTCCCGCCTCGATGGCCTGTCCGC 88

RESULT 66
US-09-342-681C-15
; Sequence 15, Application US/09342681C
```



```
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; FILE REFERENCE: 52978
; CURRENT APPLICATION NUMBER: US/09/342,681C
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/092,279
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/112,366
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1134)
US-09-342-681C-15

Query Match          50.7%; Score 20.8; DB 3; Length 1134;
Best Local Similarity 75.0%; Pred. No. 4.3e+02;
Matches 24; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      9 GGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||| | ||||| | ||| |||||: ||
Db      217 GGAACCGAGTCCCGCCTCGGTGGCCCGGTGC 248

RESULT 67
US-09-342-681C-3
; Sequence 3, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; FILE REFERENCE: 52978
; CURRENT APPLICATION NUMBER: US/09/342,681C
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/092,279
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/112,366
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (142)..(1275)
US-09-342-681C-3

Query Match          50.7%; Score 20.8; DB 3; Length 1661;
Best Local Similarity 75.0%; Pred. No. 4.3e+02;
Matches 24; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      9 GGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||| | ||||| | ||| |||||: ||
Db      358 GGAACCGAGTCCCGCCTCGGTGGCCCGGTGC 389

RESULT 68
US-09-949-016-15673/c
; Sequence 15673, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
```

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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15673
; LENGTH: 15073
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-15673

Query Match          50.7%; Score 20.8; DB 3; Length 15073;
Best Local Similarity 67.5%; Pred. No. 4.9e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||| | ||||| ||| | ||||| | ||: |||
Db      4681 AGGCTCCGGAGGCCCGAAAGGATCGCTGCCTAGGGCGC 4642

RESULT 69
US-09-949-016-12212/c
; Sequence 12212, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12212
; LENGTH: 97195
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(97195)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12212

Query Match          50.7%; Score 20.8; DB 3; Length 97195;
Best Local Similarity 67.5%; Pred. No. 5.4e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
      ||| | ||||| ||| | ||||| | |||: |||
Db      79549 AGCCACCGGATGCACCTCCCTAAACACCCGCCCTTGCCCG 79510

RESULT 70
US-09-949-016-16971/c
; Sequence 16971, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16971
; LENGTH: 97196
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(97196)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16971

Query Match 50.7%; Score 20.8; DB 3; Length 97196;
Best Local Similarity 67.5%; Pred. No. 5.4e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41
|||||
Db 79549 AGCCACCGGATGCACCTCCCTAAACACCCGCCCTTGCCCG 79510

RESULT 71
US-09-949-016-16480
; Sequence 16480, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16480
; LENGTH: 225127
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(225127)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16480

Query Match 50.7%; Score 20.8; DB 3; Length 225127;
Best Local Similarity 67.5%; Pred. No. 5.5e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41
|||||
Db 1121 AGGCCCGGCGACGACAGATCCTCAGGCGCGGTCCGGCGGG 1160

RESULT 72
US-09-902-540-6444/c
; Sequence 6444, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6444
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6444

Query Match 50.2%; Score 20.6; DB 3; Length 744;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGATGCCAGTCCCTCATCGCTGCGCCCGN 37
|||||
Db 635 GCCTCGGGCGGAGGCCCTTCATCGCCTGCTCGGT 601

RESULT 73
US-09-902-540-3367/c
; Sequence 3367, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3367
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3367

Query Match 50.2%; Score 20.6; DB 3; Length 777;
Best Local Similarity 81.5%; Pred. No. 4.9e+02;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 13 GCCAGTCCCTCATCGCTGCGCCCGNCG 39
|||||
Db 236 GCCAGTCCCTCCTCGGTGCGCCCGGCG 210

RESULT 74
US-09-758-759-201/c
; Sequence 201, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everninomicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 201

```
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(927)
; OTHER INFORMATION: ORF10
US-09-758-759-201

Query Match          50.2%; Score 20.6; DB 3; Length 927;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 920 CCGGTTGCCGGGCGCCTCGCCGGCCCGGTAGAG 886

RESULT 75
US-09-724-797-43/c
; Sequence 43, Application US/09724797
; Patent No. 6733998
; GENERAL INFORMATION:
; APPLICANT: Jon S. THORSON
; TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES
; TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
; TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTANCE THERETO
; FILE REFERENCE: 2653-40
; CURRENT APPLICATION NUMBER: US/09/724,797
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/111,325
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1347
; TYPE: DNA
; ORGANISM:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1347)
US-09-724-797-43

Query Match          50.2%; Score 20.6; DB 3; Length 1347;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 94 CCGGCGGCCCGGCGTGACCGCTGGCCCGGCGGTG 60

RESULT 76
US-09-758-759-182/c
; Sequence 182, Application US/09758759
; Patent No. 6861513
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas J.
; APPLICANT: Wang, Tim X.
; APPLICANT: Horan, Ann C.
; TITLE OF INVENTION: Everninomicin Biosynthetic Genes
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 182
; LENGTH: 12152
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea
US-09-758-759-182
```

```
Query Match          50.2%; Score 20.6; DB 3; Length 12152;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10494 CCGGTTCCGGGGCGCCTCGCCGGCCCGGTAGAG 10460

RESULT 77
US-09-902-540-1048
; Sequence 1048, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1048
; LENGTH: 12865
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1048

Query Match          50.2%; Score 20.6; DB 3; Length 12865;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGG 37
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5531 GCCTCGGGGCGGAGGCCCTTCATCGCCTGCTCGGT 5565

RESULT 78
US-09-902-540-1158/c
; Sequence 1158, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1158
; LENGTH: 17125
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1158

Query Match          50.2%; Score 20.6; DB 3; Length 17125;
Best Local Similarity 81.5%; Pred. No. 5.8e+02;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 13 GCCAGTCCCTCATCGCTGGCCCGGNCG 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 13817 GCCAGTCTCTCCTCGGTGGCCCGGCGG 13791

RESULT 79
```

```
US-09-847-960-7/c
; Sequence 7, Application US/09847960
; Patent No. 6946247
; GENERAL INFORMATION:
; APPLICANT: Swift, Susan E.
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: RNase PROBE PROTECTION ASSAYS IN SCREENING FOR MODULATORS OF
; FILE REFERENCE: A-69332-1/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/847,960
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,333
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Germline Ig Alpha-1 proble
US-09-847-960-7

Query Match          49.8%; Score 20.4; DB 3; Length 399;
Best Local Similarity 68.4%; Pred. No. 5.5e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      102 GCCTCCGGCGTGCAGGCCCTCATGTGCAGGTCCACCCTC 65

RESULT 80
US-09-266-965-27
; Sequence 27, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/624,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Streptomyces lavendulae
US-09-266-965-27

Query Match          49.8%; Score 20.4; DB 3; Length 420;
Best Local Similarity 76.7%; Pred. No. 5.5e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      12 TGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
      ||||| ||||| ||||| ||||| ||||| |||||
Db      178 TCCCAGGACCTCGTCGGGTCCCGCGCG 207

RESULT 81
US-09-847-960-8/c
; Sequence 8, Application US/09847960
; Patent No. 6946247
```

```
; GENERAL INFORMATION:
; APPLICANT: Swift, Susan E.
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: RNase PROBE PROTECTION ASSAYS IN SCREENING FOR MODULATORS OF
; FILE REFERENCE: A-69332-1/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/847,960
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,333
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Germline Ig Alpha-2 probe
US-09-847-960-8

Query Match          49.8%; Score 20.4; DB 3; Length 430;
Best Local Similarity 68.4%; Pred. No. 5.5e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      133 GCCTCCGGCGTGCAGGCCCTCATGTGCAGGTCCACCCTC 96

RESULT 82
US-09-847-960-1/c
; Sequence 1, Application US/09847960
; Patent No. 6946247
; GENERAL INFORMATION:
; APPLICANT: Swift, Susan E.
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: RNase PROBE PROTECTION ASSAYS IN SCREENING FOR MODULATORS OF
; FILE REFERENCE: A-69332-1/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/847,960
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,333
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Germline Ig Alpha-2 probe
US-09-847-960-1

Query Match          49.8%; Score 20.4; DB 3; Length 533;
Best Local Similarity 68.4%; Pred. No. 5.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      133 GCCTCCGGCGTGCAGGCCCTCATGTGCAGGTCCACCCTC 96

RESULT 83
US-09-252-991A-1469
; Sequence 1469, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```



```
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1469
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1469

Query Match          49.8%; Score 20.4; DB 3; Length 549;
Best Local Similarity 68.4%; Pred. No. 5.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCCCCGCGCG 41
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 CCGCAGGGTGCCAGTACGGCGCGCGCGCGCGGAAGCG 96

RESULT 84
US-09-949-016-46393/c
; Sequence 46393, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46393
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-46393

Query Match          49.8%; Score 20.4; DB 3; Length 601;
Best Local Similarity 68.4%; Pred. No. 5.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCCCCGCGCG 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 488 GCCGGGGATGCCCTGCCCTCTCGCTGCCGGGTCCC 451

RESULT 85
US-09-902-540-8798
; Sequence 8798, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8798
; LENGTH: 672
; TYPE: DNA
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; ORGANISM: Myxococcus xanthus
US-09-902-540-8798

Query Match          49.8%; Score 20.4; DB 3; Length 672;
Best Local Similarity 68.4%; Pred. No. 5.7e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCCCCGCGCG 41
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 CCTCCGAGCCACGCCGCCGCTTGGACCTGACGCG 221

RESULT 86
US-09-902-540-1910
; Sequence 1910, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1910
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1910

Query Match          49.8%; Score 20.4; DB 3; Length 708;
Best Local Similarity 68.4%; Pred. No. 5.7e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCCCCGCGCG 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 432 GCCTCGAAGAGCCGCACCTCATCCATGCCATGACGC 469

RESULT 87
US-09-252-991A-1419
; Sequence 1419, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1419
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1419

Query Match          49.8%; Score 20.4; DB 3; Length 1056;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGCCCCGCGCG 41
   ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 993 CCGCAGGGTGCCAGTACGGCGCGCGCGCGCGGAAGCG 1030
```

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RESULT 88
US-09-902-540-9099/c
; Sequence 9099, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9099
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-9099

Query Match          49.8%; Score 20.4; DB 3; Length 1143;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
Db      282 GCCTCCGAAGAGCCGACCTCATCCATGGCCATGACGC 245

RESULT 89
US-09-252-991A-1239
; Sequence 1239, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1239
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1239

Query Match          49.8%; Score 20.4; DB 3; Length 1410;
Best Local Similarity 68.4%; Pred. No. 5.9e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
Db      584 GCCTCGGCGAGCCAGCGCGCTGCGCCGCGCGGGCGC 621

RESULT 90
US-09-199-737-3/c
; Sequence 3, Application US/09199737A
; Patent No. 6287788
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E.
; APPLICANT: Brancheck, Theresa A.
; APPLICANT: Gerald, Christophe P.G.
```

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; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding Galanin GALR3 Receptors And Uses Thereof
; FILE REFERENCE: 52241-D-PCT-US
; CURRENT APPLICATION NUMBER: US/09/199,737A
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-199-737-3

Query Match          49.8%; Score 20.4; DB 3; Length 1417;
Best Local Similarity 76.7%; Pred. No. 5.9e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      12 TGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
Db      1375 TGGCATTGCCCCATCCCTGGCCCGGTGGCG 1346

RESULT 91
US-09-058-333A-3/c
; Sequence 3, Application US/09058333A
; Patent No. 6368812
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A
; APPLICANT: Borowsky, Beth
; APPLICANT: Smith, Kelli E
; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,333A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52241-E/JPW/KOB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0525
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1281
US-09-058-333A-3

Query Match          49.8%; Score 20.4; DB 3; Length 1417;
Best Local Similarity 76.7%; Pred. No. 5.9e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      12 TGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
```



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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: human
US-09-595-549-1

Query Match          49.8%; Score 20.4; DB 3; Length 2263;
Best Local Similarity 76.7%; Pred. No. 6e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      12 TGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
Db      2256 TGGCATTGCCCCATCCCTGGCCCGGTGGCG 2227

RESULT 97
US-09-252-991A-1366/c
; Sequence 1366, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1366
; LENGTH: 2712
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1366

Query Match          49.8%; Score 20.4; DB 3; Length 2712;
Best Local Similarity 68.4%; Pred. No. 6.1e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 40
Db      2606 GCCTCGGAGCCAGCGCGGTGCGCCCGCGGGCGC 2569

RESULT 98
US-09-799-451-480
; Sequence 480, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
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; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 480
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)..(2730)
US-09-799-451-480

Query Match          49.8%; Score 20.4; DB 3; Length 2733;
Best Local Similarity 68.4%; Pred. No. 6.1e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 40
Db      1993 GCCTTCGAGTGCCAGTCCCTCCCTGCAGCTGCTGCCGC 2030

RESULT 99
US-09-016-434-1326
; Sequence 1326, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1326:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g33950
US-09-016-434-1326

Query Match          49.8%; Score 20.4; DB 3; Length 4080;
Best Local Similarity 68.4%; Pred. No. 6.2e+02;
```


Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGATGCCAGTCCCTCATCGCTGGCCCCGNCGC 40
||| ||| | | | | | | | | | | | | | | |
Db 2936 GCCCCCGGTACTACACCCTCACTGCAGACCAGGACGC 2973
||||| | | | | | | | | | : | | |

RESULT 100

US-09-023-655-1319
; Sequence 1319, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1319:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g33910
US-09-023-655-1319

Query Match	49.8%	Score 20.4;	DB 3;	Length 5645;
Best Local Similarity	68.4%	Pred. No. 6.4e+02;		
Matches 26;	Conservative	1;	Mismatches 11;	Indels 0;
				Gaps 0;

Qy

3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGNCGC 40
||| |||| | | | | | | | :
Dd

2875 GCCCCCGGTACTACACCCTCACTGCAGACCCAGGACGC 2912
|||| | | | | | | | :

Search completed: May 9, 2006, 22:59:00
Job time : 174 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 22:19:18 ; Search time 438 Seconds
(without alignments)
774.074 Million cell updates/sec

Title: US-09-904-968A-1_N3336_COPY_3300_3340

Perfect score: 41

Sequence: 1 aagcctccggtgccagtc.....tcatcgctggcccggnccgcg 41

Scoring table: IDENTITY_NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications NA_Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	29.8	72.7	623	8	US-10-363-345A-2651
3	29.8	72.7	623	8	US-10-363-345A-2652
C 4	29.8	72.7	623	9	US-10-363-483A-2651
5	29.8	72.7	623	9	US-10-363-483A-2652
C 6	29.8	72.7	6423	6	US-10-240-485-122
7	24.2	59.0	2202	10	US-11-097-143-42776
8	24.2	59.0	5083	10	US-11-097-143-42775
9	24	58.5	303	6	US-10-156-761-438
10	24	58.5	378	7	US-10-437-963-12669
11	24	58.5	9025608	6	US-10-156-761-1
C 12	23	56.1	413	3	US-09-983-965-1143
13	23	56.1	677	8	US-10-425-115-65882
14	22.6	55.1	400	4	US-09-925-065A-243582
15	22.6	55.1	400	4	US-09-925-065A-243583
C 16	22.6	55.1	768	6	US-10-369-493-42308
17	22.6	55.1	1992	7	US-10-437-963-73709
18	22.6	55.1	22715	3	US-09-997-722-118
C 19	22.4	54.6	622	9	US-10-487-901-5013
20	22.4	54.6	1758	8	US-10-425-115-72983
21	22.4	54.6	2940	9	US-10-496-905-631
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23	22.4	54.6	3723	7	US-10-467-434-32

C 24	22.4	54.6	243390	7	US-10-322-281-462	Sequence 462, App
C 25	22.4	54.6	3186778	5	US-10-027-632-174961	Sequence 174961,
C 26	22.4	54.6	3186778	6	US-10-027-632-174961	Sequence 174961,
27	22	53.7	279	8	US-10-211-028-38	Sequence 38, Appl
C 28	22	53.7	548	7	US-10-767-701-23293	Sequence 23293, A
C 29	22	53.7	918	3	US-09-770-445-425	Sequence 425, App
30	22	53.7	1497	7	US-10-437-963-94320	Sequence 94320, A
C 31	22	53.7	2145	7	US-10-282-122A-31337	Sequence 31337, A
32	22	53.7	2979	3	US-09-938-842A-48	Sequence 48, Appl
33	22	53.7	2979	3	US-09-938-842A-48	Sequence 48, Appl
34	22	53.7	4257	6	US-10-369-493-24352	Sequence 24352, A
35	22	53.7	4959	7	US-10-437-963-42040	Sequence 42040, A
36	22	53.7	5946	7	US-10-437-963-42038	Sequence 42038, A
C 37	22	53.7	75252	5	US-10-087-192-904	Sequence 904, App
38	22	53.7	90597	8	US-10-211-028-1	Sequence 1, Appli
39	21.8	53.2	564	6	US-10-156-761-7469	Sequence 7469, Ap
40	21.8	53.2	623	8	US-10-363-345A-2649	Sequence 2649, Ap
C 41	21.8	53.2	623	8	US-10-363-345A-2650	Sequence 2650, Ap
42	21.8	53.2	623	9	US-10-363-483A-2649	Sequence 2649, Ap
C 43	21.8	53.2	623	9	US-10-363-483A-2650	Sequence 2650, Ap
C 44	21.8	53.2	963	7	US-10-425-114-36530	Sequence 36530, A
C 45	21.8	53.2	995	8	US-10-425-115-87792	Sequence 87792, A
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56	21.6	52.7	230	6	US-10-259-678-422	Sequence 422, App
57	21.6	52.7	633	5	US-10-027-632-127507	Sequence 127507,
58	21.6	52.7	633	6	US-10-027-632-127507	Sequence 127507,
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C 64	21.6	52.7	2256646	7	US-10-470-565-1	Sequence 1, Appli
C 65	21.6	52.7	9025608	6	US-10-156-761-1	Sequence 1, Appli
C 66	21.4	52.2	183	6	US-10-156-761-6408	Sequence 6408, Ap
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70	21.4	52.2	381	3	US-09-983-965-1105	Sequence 1105, Ap
C 71	21.4	52.2	395	3	US-09-983-965-837	Sequence 837, App
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C 76	21.4	52.2	484	5	US-10-027-632-184352	Sequence 184352,
C 77	21.4	52.2	484	5	US-10-027-632-184353	Sequence 184353,
C 78	21.4	52.2	484	6	US-10-027-632-184352	Sequence 184352,
C 79	21.4	52.2	484	6	US-10-027-632-184353	Sequence 184353,
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82	21.4	52.2	712	7	US-10-767-701-5397	Sequence 5397, Ap
C 83	21.4	52.2	765	8	US-10-425-115-118915	Sequence 118915,
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85	21.4	52.2	1071	6	US-10-156-761-7131	Sequence 7131, Ap
C 86	21.4	52.2	1236	6	US-10-369-493-45519	Sequence 45519, A
C 87	21.4	52.2	1329	8	US-10-128-558-37	Sequence 37, Appl
C 88	21.4	52.2	1500	8	US-10-425-115-84915	Sequence 84915, A
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C 92	21.4	52.2	2435	8	US-10-425-115-119462	Sequence 119462,
C 93	21.4	52.2	2751	6	US-10-369-493-34212	Sequence 34212, A
94	21.4	52.2	2847	6	US-10-156-761-923	Sequence 923, App
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497	20.6	50.2	3233	6	US-10-157-781-81	Sequence 81, Appl
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499	20.6	50.2	3233	6	US-10-147-491-81	Sequence 81, Appl
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ALIGNMENTS

RESULT 1

US-09-904-968A-1

Sequence 1, Application US/09904968A

Publication No. US20030008288A1

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

APPLICANT: GERMINO, Gregory

APPLICANT: WATNICK, Terry

APPLICANT: PHAKDEEKITCHAROEN, Bunyong

TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE

FILE REFERENCE: JHU1680-2

CURRENT APPLICATION NUMBER: US/09/904,968A

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/283,691

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/218,261

PRIOR FILING DATE: 2000-07-13

NUMBER OF SEQ ID NOS: 113

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 53522

TYPE: DNA

ORGANISM: Homo sapiens

US-09-904-968A-1

Query Match 100.0%; Score 41; DB 3; Length 53522;

Best Local Similarity 97.6%; Pred. No. 5.4e-06;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
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Db 3300 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGTCGCG 3340

RESULT 2

US-10-363-345A-2651/c
; Sequence 2651, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2651
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2651
US-10-363-345A-2651

Query Match 72.7%; Score 29.8; DB 8; Length 623;
Best Local Similarity 80.5%; Pred. No. 0.14;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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RESULT 3

US-10-363-345A-2652
; Sequence 2652, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2652
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2652
US-10-363-345A-2652

Query Match 72.7%; Score 29.8; DB 8; Length 623;
Best Local Similarity 80.5%; Pred. No. 0.14;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
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Db 162 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 202

RESULT 4

US-10-363-483A-2651/c
; Sequence 2651, Application US/10363483A
; Publication No. US20050064401A1

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2651
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2651
US-10-363-483A-2651

Query Match 72.7%; Score 29.8; DB 9; Length 623;
Best Local Similarity 80.5%; Pred. No. 0.14;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
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RESULT 5

US-10-363-483A-2652
; Sequence 2652, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2652
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2652
US-10-363-483A-2652

Query Match 72.7%; Score 29.8; DB 9; Length 623;
Best Local Similarity 80.5%; Pred. No. 0.14;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
|||
Db 162 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGCG 202

RESULT 6

US-10-240-485-122/c
; Sequence 122, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02

; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 122
; LENGTH: 6423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-122

Query Match 72.7%; Score 29.8; DB 6; Length 6423;
Best Local Similarity 80.5%; Pred. No. 0.1;
Matches 33; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCGC 41
||| ||||| || ||| ||||| ||||| ||||| :|||
Db 1563 AAACCTCCGAATACCAATCCCTCATCGCTAACCCGATCGC 1523

RESULT 7
US-11-097-143-42776
; Sequence 42776, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42776
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-42776

Query Match 59.0%; Score 24.2; DB 10; Length 2202;
Best Local Similarity 75.7%; Pred. No. 14;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCG 39
||| ||||| ||||| ||| ||||| ||||| :|||
Db 80 GTCTCCGATGCCACACCCACAGCGCTGGAGTGGCG 116

RESULT 8
US-11-097-143-42775
; Sequence 42775, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42775
; LENGTH: 5083
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-42775

Query Match 59.0%; Score 24.2; DB 10; Length 5083;
Best Local Similarity 75.7%; Pred. No. 13;
Matches 28; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GCCTCCGATGCCAGTCCCTCATCGTGGCCCGNCG 39
||| ||||| ||||| ||| ||||| ||||| :|||
Db 1080 GTCTCCGATGCCACACCCACAGCGCTGGAGTGGCG 1116

RESULT 9
US-10-156-761-438
; Sequence 438, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 438
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:

```
; NAME/KEY: CDS
; LOCATION: (1)..(303)
US-10-156-761-438

Query Match      58.5%; Score 24; DB 6; Length 303;
Best Local Similarity 72.5%; Pred. No. 23;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
   ||||||| ||||| ||||| ||||| ||||| ||||| : ||
Db 179 ACGTCTCCGGACGCCAGGCCACCTCGCAGGCCGGCTGGC 218

RESULT 10
US-10-437-963-12669
; Sequence 12669, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 12669
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18776C.1
US-10-437-963-12669

Query Match      58.5%; Score 24; DB 7; Length 378;
Best Local Similarity 72.5%; Pred. No. 22;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
   ||||||| ||||| ||||| ||||| ||||| ||||| : ||
Db 284 AAGCCGCGGCTGCCCGCCCTCCGTGCTGCCCGGCCTC 323

RESULT 11
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
```

```
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      58.5%; Score 24; DB 6; Length 9025608;
Best Local Similarity 72.5%; Pred. No. 5.3;
Matches 29; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
   ||||||| ||||| ||||| ||||| ||||| ||||| : ||
Db 596716 ACGTCTCCGGACGCCAGGCCACCTCGCAGGCCGGCTGGC 596755

RESULT 12
US-09-983-965-1143/c
; Sequence 1143, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 1143
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 64-LIB188-019-Q1-E1-H8
US-09-983-965-1143

Query Match      56.1%; Score 23; DB 3; Length 413;
Best Local Similarity 71.8%; Pred. No. 51;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
   ||| |||| ||||||| ||||| ||||| ||||| : ||
Db 267 AACCAGCGGAGACCAGTCCCAATGGCAGGCCCTGAAGC 229

RESULT 13
US-10-425-115-65882
; Sequence 65882, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 65882
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_160086C.1
```



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US-10-425-115-65882
Query Match          56.1%; Score 23; DB 8; Length 677;
Best Local Similarity 71.8%; Pred. No. 48;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
   ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 396 GCCTTCGGCCACCAGTTCCTCGTCGCCGGCGACGACGCG 434

RESULT 14
US-09-925-065A-243582
; Sequence 243582, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 243582
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-243582

Query Match          55.1%; Score 22.6; DB 4; Length 400;
Best Local Similarity 73.0%; Pred. No. 72;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29 CGCCGGTTGCCTGGCTCTGGTGGGTGGCCCGCGCGCG 65

RESULT 15
US-09-925-065A-243583
; Sequence 243583, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 243583
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; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-243583

Query Match          55.1%; Score 22.6; DB 4; Length 400;
Best Local Similarity 73.0%; Pred. No. 72;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29 CGCCGGTTGCCTGGCTCTGGTGGGTGGCCCGCGCGCG 65

RESULT 16
US-10-369-493-42308/c
; Sequence 42308, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42308
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Halobacterium sp. NRC-1
US-10-369-493-42308

Query Match          55.1%; Score 22.6; DB 6; Length 768;
Best Local Similarity 73.0%; Pred. No. 66;
Matches 27; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 96 GCCGTGGCGCCAGTCGCTCGGCGGTGCGCCGCGCG 60

RESULT 17
US-10-437-963-73709
; Sequence 73709, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 73709
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73965C.1
US-10-437-963-73709
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; PRIOR APPLICATION NUMBER: US 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/04098
; PRIOR FILING DATE: 2001-02-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 631
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-496-905-631

Query Match      54.6%; Score 22.4; DB 9; Length 2940;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      1538 AAGACGACGACTGCCTGCCCTCTCGCTACCCCTGCCGC 1577

RESULT 22
US-10-496-905-629
; Sequence 629, Application US/10496905
; Publication No. US20050192215A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhao, Qing
; APPLICANT: Xu, Chongjun
; APPLICANT: Mulero, Julio J
; APPLICANT: Boyle, Bryan J.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCL
; FILE REFERENCE: HYS-BICIP/US
; CURRENT APPLICATION NUMBER: US/10/496,905
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: PCT/US00/34263
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/04098
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 629
; LENGTH: 3568
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2940)
US-10-496-905-629

Query Match      54.6%; Score 22.4; DB 9; Length 3568;
Best Local Similarity 70.0%; Pred. No. 63;

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Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      1538 AAGACGACGACTGCCTGCCCTCTCGCTACCCCTGCCGC 1577

RESULT 23
US-10-467-434-32
; Sequence 32, Application US/10467434
; Publication No. US20040092715A1
; GENERAL INFORMATION:
; APPLICANT: DING, Li; WARREN, Bridget A.;
; APPLICANT: ELLIOTT, Vicki S.; TANG, Y. Tom;
; APPLICANT: YUE, Henry; BURFORD, Neil;
; APPLICANT: LEE, Sally; RICHARDSON, Thomas W.;
; APPLICANT: LAL, Preeti G.; NGUYEN, Danniel B.;
; APPLICANT: YONG, Junming; HAFALIA, April J.A.;
; APPLICANT: ISON, Craig H.; GURURAJAN, Rajagopal;
; APPLICANT: BAUGHN, Mariah R.; WANG, Yumei E.;
; APPLICANT: YAO, Monique G.; THANGAVELU, Kavitha;
; APPLICANT: SWARNAKAR, Anita; GRIFFIN, Jennifer A.;
; APPLICANT: FORSYTHE, Ian J.; EMERLING, Brooke M.;
; APPLICANT: CHAWLA, Narinder K.;
; TITLE OF INVENTION: Intracellular Signaling Molecules
; FILE REFERENCE: PF-0897 USN
; CURRENT APPLICATION NUMBER: US/10/467,434
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03966
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/267,925
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/274,435
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/277,819
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/281,326
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/291,195
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/291,550
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/293,591
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/295,348
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 3723
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7193277CB1
US-10-467-434-32

Query Match      54.6%; Score 22.4; DB 7; Length 3723;
Best Local Similarity 70.0%; Pred. No. 62;
Matches 28; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
      ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      1714 AAGACGACGACTGCCTGCCCTCTCGCTACCCCTGCCGC 1753

RESULT 24
US-10-322-281-462/c
; Sequence 462, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro

```



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; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31337
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Pseudomonas putida
US-10-282-122A-31337

Query Match      53.7%; Score 22; DB 7; Length 2145;
Best Local Similarity 71.1%; Pred. No. 95;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
      ||| |||| ||| ||| ||| ||| ||| ||| ||| |||
Db      985 AGGCATCGGAGGCGAGCCGCTCACGGCGGCCGCGCG 948

RESULT 32
US-09-938-842A-48
; Sequence 48, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 48
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-48

Query Match      53.7%; Score 22; DB 3; Length 2979;
Best Local Similarity 71.1%; Pred. No. 90;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
      ||| |||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2598 AGCTTCCGAGTGCGATGCTCCTCGATCGCTGGCTCGTACG 2635

RESULT 33
US-09-938-842A-48
; Sequence 48, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 48
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-48

Query Match      53.7%; Score 22; DB 6; Length 4257;
Best Local Similarity 71.1%; Pred. No. 86;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 40
      ||| |||| ||| |||| |||| |||| |||| |||| |||
Db      126 GCGCTGGCGGCCAGTCCCTCTTCCCGTCCCGCCGC 163

RESULT 34
US-10-369-493-24352
; Sequence 24352, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 24352
; LENGTH: 4257
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans
US-10-369-493-24352

Query Match      53.7%; Score 22; DB 6; Length 4257;
Best Local Similarity 71.1%; Pred. No. 86;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 40
      ||| |||| ||| |||| |||| |||| |||| |||| |||
Db      126 GCGCTGGCGGCCAGTCCCTCTTCCCGTCCCGCCGC 163

RESULT 35
US-10-437-963-42040
```

```

; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31337
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Pseudomonas putida
US-10-282-122A-31337

Query Match      53.7%; Score 22; DB 7; Length 2145;
Best Local Similarity 71.1%; Pred. No. 95;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
      ||| |||| ||| ||| ||| ||| ||| ||| ||| |||
Db      985 AGGCATCGGAGGCGAGCCGCTCACGGCGGCCGCGCG 948

RESULT 32
US-09-938-842A-48
; Sequence 48, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 48
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-48

Query Match      53.7%; Score 22; DB 3; Length 2979;
Best Local Similarity 71.1%; Pred. No. 90;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
      ||| |||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2598 AGCTTCCGAGTGCGATGCTCCTCGATCGCTGGCTCGTACG 2635

RESULT 33
US-09-938-842A-48
; Sequence 48, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 48
; LENGTH: 2979
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-48

Query Match      53.7%; Score 22; DB 6; Length 4257;
Best Local Similarity 71.1%; Pred. No. 86;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 40
      ||| |||| ||| |||| |||| |||| |||| |||| |||
Db      126 GCGCTGGCGGCCAGTCCCTCTTCCCGTCCCGCCGC 163

RESULT 34
US-10-369-493-24352
; Sequence 24352, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 24352
; LENGTH: 4257
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans
US-10-369-493-24352

Query Match      53.7%; Score 22; DB 6; Length 4257;
Best Local Similarity 71.1%; Pred. No. 86;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 40
      ||| |||| ||| |||| |||| |||| |||| |||| |||
Db      126 GCGCTGGCGGCCAGTCCCTCTTCCCGTCCCGCCGC 163

RESULT 35
US-10-437-963-42040
```

; Sequence 42040, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 42040
; LENGTH: 4959
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45328C.1
US-10-437-963-42040

Query Match 53.7%; Score 22; DB 7; Length 4959;
Best Local Similarity 71.1%; Pred. No. 84;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
Db 463 CATTCGGTGCCACTCCCTCATCGGCGCCTCCGACTCG 500

RESULT 36

US-10-437-963-42038
; Sequence 42038, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 42038
; LENGTH: 5946
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45326C.1
US-10-437-963-42038

Query Match 53.7%; Score 22; DB 7; Length 5946;
Best Local Similarity 71.1%; Pred. No. 82;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
Db 463 CATTCGGTGCCACTCCCTCATCGGCGCCTCCGACTCG 500

RESULT 37

US-10-087-192-904/c
; Sequence 904, Application US/10087192

; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 904
; LENGTH: 75252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-904

Query Match 53.7%; Score 22; DB 5; Length 75252;
Best Local Similarity 71.1%; Pred. No. 57;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
Db 50417 GGCCTGGATGCCACACCTCATTCCTGCCCGTTTCC 50380

RESULT 38

US-10-211-028-1
; Sequence 1, Application US/10211028
; Publication No. US20050027113A1
; GENERAL INFORMATION:
; APPLICANT: CUBIST PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: CUB-12 PCT CIP
; CURRENT APPLICATION NUMBER: US/10/211,028
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: PCT/US02/24310
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US01/32354
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/310,385
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 60/379,866
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 90597
; TYPE: DNA
; ORGANISM: Streptomyces roseosporus
US-10-211-028-1

Query Match 53.7%; Score 22; DB 8; Length 90597;
Best Local Similarity 71.1%; Pred. No. 56;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
Db 14303 CCTCCGATGGTGGCCACCAGCGGGTCCCGGCCCG 14340

RESULT 39

US-10-156-761-7469
; Sequence 7469, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO

```
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7469
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(564)
US-10-156-761-7469

Query Match      53.2%; Score 21.8; DB 6; Length 564;
Best Local Similarity 68.3%; Pred. No. 1.4e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
   ||||| ||||| ||| | ||||| ||||| |||||
Db 404 ACGCCGCCGATGGGAGGTCTGCTCGCCGCCCTGGACGCG 444

RESULT 40
US-10-363-345A-2649
; Sequence 2649, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2649
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2649
US-10-363-345A-2649

Query Match      53.2%; Score 21.8; DB 8; Length 623;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
   ||||| ||||| ||| | ||||| ||||| |||||
Db 162 AAGTTTCGGATGTTAGTTTTTTATCGTTGGTTCGGTCGCG 202

RESULT 41
US-10-363-345A-2650/c
; Sequence 2650, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
```

```
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2650
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2650
US-10-363-345A-2650

Query Match      53.2%; Score 21.8; DB 8; Length 623;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
   ||||| ||||| ||| | ||||| ||||| |||||
Db 462 AAGTTTCGGATGTTAGTTTTTTATCGTTGGTTCGGTCGCG 422

RESULT 42
US-10-363-483A-2649
; Sequence 2649, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2649
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2649
US-10-363-483A-2649

Query Match      53.2%; Score 21.8; DB 9; Length 623;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
   ||||| ||||| ||| | ||||| ||||| |||||
Db 162 AAGTTTCGGATGTTAGTTTTTTATCGTTGGTTCGGTCGCG 202

RESULT 43
US-10-363-483A-2650/c
; Sequence 2650, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2650
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
```



```
;
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 2650
US-10-363-483A-2650

Query Match          53.2%; Score 21.8; DB 9; Length 623;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    ||| | ||||| ||| | ||||| ||| | ||||| ||| | |||||
Db 462 AAGTTTCGGATGTTAGTTTTTTATCGTTGGTTCGGTCGCG 422

RESULT 44
US-10-425-114-36530/c
; Sequence 36530, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36530
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MRPTEOSINTE117E11_FLI
US-10-425-114-36530

Query Match          53.2%; Score 21.8; DB 7; Length 963;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    | ||||| ||||| | ||||| ||||| ||||| ||||| |||||
Db 566 ACGCCTCTGGATGATTGCCCCCTCACCTCTGGACCTGATGGG 526

RESULT 45
US-10-425-115-87792/c
; Sequence 87792, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 87792
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_180064C.1
US-10-425-115-87792

Query Match          53.2%; Score 21.8; DB 8; Length 995;
Best Local Similarity 68.3%; Pred. No. 1.3e+02;
```

```
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    | ||||| ||||| | ||||| ||||| ||||| ||||| |||||
Db 566 ACGCCTCTGGATGATTGCCCCCTCACCTCTGGACCTGATGGG 526

RESULT 46
US-10-156-761-6527
; Sequence 6527, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6527
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1383)
US-10-156-761-6527

Query Match          53.2%; Score 21.8; DB 6; Length 1383;
Best Local Similarity 68.3%; Pred. No. 1.2e+02;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    | || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1133 AGCGACCGGACGCGCAGTCCTTCGTACGCGGAGGCG 1173

RESULT 47
US-10-437-963-45894
; Sequence 45894, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45894
; LENGTH: 1891
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48814C.1
US-10-437-963-45894
```



```
Best Local Similarity 68.3%; Pred. No. 96;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      ||||| | ||||| ||| | ||||| ||| ||||| |||||
Db      4861 AAGTTTTCGGATGTTAGTTTTTATCGTTGGTTCGGTCGCG 4901

RESULT 52
US-11-097-143-1121
; Sequence 1121, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1121
; LENGTH: 6492
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-1121

Query Match      53.2%; Score 21.8; DB 10; Length 6492;
Best Local Similarity 68.3%; Pred. No. 96;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      ||||| | ||||| ||| | ||||| ||| ||||| |||||
Db      238 AAGTCGGGATGCCCTCACCTCCTCGTGGTGGCCCGGAAGAG 278

RESULT 53
US-10-915-740A-9
; Sequence 9, Application US/10915740A
; Publication No. US20050191316A1
; GENERAL INFORMATION:
; APPLICANT: Frazer, Claire M.
; APPLICANT: Hickey, Erin
; APPLICANT: Peterson, Jeremy
; APPLICANT: Tettelin, Herve
; APPLICANT: Venter, J. Craig
; APPLICANT: Maignani, Vega
; APPLICANT: Galeotti, Cesira
; APPLICANT: Mora, Manrosa
; APPLICANT: Ratti, Giulio
; APPLICANT: Scarselli, Maria
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagratia
; APPLICANT: Grandi, Guido
```

```
; TITLE OF INVENTION: Neisseria Genomic Sequences And Methods Of Their Use
; FILE REFERENCE: 002441.00090
; CURRENT APPLICATION NUMBER: US/10/915,740A
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 09/806,866
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: USSN 60/103,794
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: USSN 60/132,068
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/US99/25373
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 1068
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 9941
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-915-740A-9

Query Match      53.2%; Score 21.8; DB 9; Length 9941;
Best Local Similarity 68.3%; Pred. No. 90;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1752 AAGCCGCCCTGCGAGTACGTATGGCGGGCGCGGATGCG 1792

RESULT 54
US-11-097-143-1120
; Sequence 1120, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1120
; LENGTH: 16105
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-1120

Query Match      53.2%; Score 21.8; DB 10; Length 16105;
Best Local Similarity 68.3%; Pred. No. 85;
Matches 28; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
      |||| | ||||| ||| ||| ||||| ||| ||||| |||
Db      1238 AAGTCGGGATGCCCTCACCTCCTCGTGGTGGCCCGGAAGAG 1278
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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 127507
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-127507

Query Match          52.7%; Score 21.6; DB 6; Length 633;
Best Local Similarity 72.2%; Pred. No. 1.6e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      394 GCCCCTGGATCCAGTCCCTCGCTGGTGGTCTGGTC 429

RESULT 59
US-10-027-632-166051/c
; Sequence 166051, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166051
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-166051

Query Match          52.7%; Score 21.6; DB 5; Length 831;
Best Local Similarity 72.2%; Pred. No. 1.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      454 CCTCTGCACTCCAGACCCCATCTCTGGCTCTGGCG 419

RESULT 60
US-10-027-632-166051/c
; Sequence 166051, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166051
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-166051

Query Match          52.7%; Score 21.6; DB 6; Length 831;
Best Local Similarity 72.2%; Pred. No. 1.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      454 CCTCTGCACTCCAGACCCCATCTCTGGCTCTGGCG 419

RESULT 61
US-10-425-115-113559
; Sequence 113559, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 113559
; LENGTH: 835
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_35046C.1
US-10-425-115-113559

Query Match          52.7%; Score 21.6; DB 8; Length 835;
Best Local Similarity 72.2%; Pred. No. 1.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      188 CCTTCGTCTGCCAGCCGCTACCGCGCCACGGACG 223

RESULT 62
US-10-156-761-774
; Sequence 774, Application US/10156761
; Publication No. US20030119018A1
```

```
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 774
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2772)
US-10-156-761-774

Query Match          52.7%; Score 21.6; DB 6; Length 2772;
Best Local Similarity 72.2%; Pred. No. 1.3e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
Db 1387 GACTACGGCATCCATTCCCTCATCGCCGCCCGGATC 1422

RESULT 63
US-10-322-281-1
; Sequence 1, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 24883
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(24883)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-1

Query Match          52.7%; Score 21.6; DB 7; Length 24883;
Best Local Similarity 72.2%; Pred. No. 94;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 39
Db 6088 CCTCAGGATGACTGTCACTTAAGGCTGCCCGGTACG 6123

RESULT 64
US-10-470-565-1/c
; Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
```

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; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium
; FILE REFERENCE: 80290/WO
; CURRENT APPLICATION NUMBER: US/10/470,565
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: EP 01102050.0
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-470-565-1
```

Query Match 52.7%; Score 21.6; DB 7; Length 2256646;
Best Local Similarity 72.2%; Pred. No. 49;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 39
Db 1095460 CCTCCGAAGCCACAGCCTGATCGCCGCTGTCCG 1095425

```
RESULT 65
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
```

Query Match 52.7%; Score 21.6; DB 6; Length 9025608;
Best Local Similarity 72.2%; Pred. No. 40;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
Db 937341 GACTACGGCATCCATTCCCTCATCGCCGCCCGGATC 937306

```
RESULT 66
US-10-156-761-6408/c
; Sequence 6408, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
```

```
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6408
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(183)
US-10-156-761-6408

Query Match          52.2%; Score 21.4; DB 6; Length 183;
Best Local Similarity 69.2%; Pred. No. 2.2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCG 39
    ||||| ||||| ||||| ||||| ||||| |||||: ||
Db 155 AAGTCGCGGAAGTCCAGGTCCCTCGATGACCCGGCG 117

RESULT 67
US-09-867-550-1859/c
; Sequence 1859, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1859
; LENGTH: 292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-550-1859

Query Match          52.2%; Score 21.4; DB 3; Length 292;
Best Local Similarity 69.2%; Pred. No. 2.1e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| |||||
Db 288 GCCCCCGCGCGCGCGCCCTCGCGCGCGCGGGGCG 250

RESULT 68
US-09-983-965-719
; Sequence 719, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 719
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 17-LfB188-005-Q1-E1-E1
US-09-983-965-719

Query Match          52.2%; Score 21.4; DB 3; Length 381;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
    ||||| ||||| ||||| ||||| ||||| |||||: ||
Db 121 AACCAGCGGAGACCAGTCCCGCTTGGCAGGCCCTGAAGC 159

RESULT 69
US-09-983-965-1061/c
; Sequence 1061, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 1061
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 55-LfB188-019-Q1-E1-F12
US-09-983-965-1061

Query Match          52.2%; Score 21.4; DB 3; Length 381;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
    ||||| ||||| ||||| ||||| ||||| |||||: ||
Db 261 AACCAGCGGAGACCAGTCCCACTTGGCAGGCCCTGAAGC 223

RESULT 70
US-09-983-965-1105
; Sequence 1105, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 1105
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 60-LIB188-013-Q1-E1-H1
US-09-983-965-1105

Query Match      52.2%; Score 21.4; DB 3; Length 381;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
      ||| ||||| ||||| ||| ||||| |||
Db      121 AACCAGCGGAGACCACTGGCAGGCCCTGAAGC 159

RESULT 71
US-09-983-965-837/c
; Sequence 837, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 837
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (358)
; OTHER INFORMATION:
; OTHER INFORMATION: Clone ID: 29-LIB188-023-Q1-E1-H1
US-09-983-965-837

Query Match      52.2%; Score 21.4; DB 3; Length 395;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
      ||| ||||| ||||| ||| ||||| |||
Db      275 AACCAGCGGAGACCACTGGCAGGCCCTGAAGC 237

RESULT 72
US-10-437-963-89803
; Sequence 89803, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
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; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 89803
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_88528C.1
US-10-437-963-89803

Query Match      52.2%; Score 21.4; DB 7; Length 405;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
      ||| ||||| ||||| ||| ||||| |||
Db      339 GCCGCTTGATGCCTCTCCCTCACCGTCGCCATGGCCGCG 377

RESULT 73
US-09-983-965-852
; Sequence 852, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 852
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 31-LIB188-011-Q1-E1-H11
US-09-983-965-852

Query Match      52.2%; Score 21.4; DB 3; Length 419;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
      ||| ||||| ||||| ||| ||||| |||
Db      159 AACCAGCGGAGACCACTGGCAGGCCCTGAAGC 197

RESULT 74
US-10-156-761-2289/c
; Sequence 2289, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
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; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2289
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(429)
US-10-156-761-2289

Query Match          52.2%; Score 21.4; DB 6; Length 429;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 GCCGCCGACAGTCCGGCCGTCGTCGGGGCGGGCCGAG 18

RESULT 75
US-10-425-115-3328/c
; Sequence 3328, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 3328
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_103036C.1
US-10-425-115-3328

Query Match          52.2%; Score 21.4; DB 8; Length 477;
Best Local Similarity 69.2%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 98 GCCGCCGCGCGCGTCCCTCGTCGCGTCTCGATGGCG 60

RESULT 76
US-10-027-632-184352/c
; Sequence 184352, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; NUMBER OF SEQ ID NOS: 2002-04-30
; SEQ ID NO 184352
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-184352

Query Match          52.2%; Score 21.4; DB 5; Length 484;
Best Local Similarity 77.4%; Pred. No. 2e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184352
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-184352

Query Match          52.2%; Score 21.4; DB 5; Length 484;
Best Local Similarity 77.4%; Pred. No. 2e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 9 GGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 GGAGGCGCGTCCCTCACCGCTGGCCCGAGG 286

RESULT 77
US-10-027-632-184353/c
; Sequence 184353, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184353
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-184353

Query Match          52.2%; Score 21.4; DB 5; Length 484;
Best Local Similarity 77.4%; Pred. No. 2e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 9 GGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 GGAGGCGCGTCCCTCACCGCTGGCCCGAGG 286

RESULT 78
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Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    ||| ||| ||| ||| ||| ||| ||| ||| ||| :|||
Db 45 GCCGCGCCTGCCGTACCTCCGGGCTGGCCGGCTCGG 7

RESULT 89
US-11-097-143-26600
; Sequence 26600, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26600
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-26600

Query Match 52.2%; Score 21.4; DB 10; Length 1861;
Best Local Similarity 69.2%; Pred. No. 1.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
    ||| | ||| ||| ||| ||| ||| ||| ||| :|
Db 1589 AACCACGAGTGCAGTTCCTCAAGGTGGCCCAATTG 1627

RESULT 90
US-10-437-963-32570/c
; Sequence 32570, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 32570
```

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; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36766C.1
US-10-437-963-32570

Query Match 52.2%; Score 21.4; DB 7; Length 2070;
Best Local Similarity 69.2%; Pred. No. 1.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
    ||| | ||| ||| ||| ||| ||| ||| ||| :|||
Db 1844 GCCGCTGGATTGTCGGCCCTTGTGCGCGGCCGCTCTCG 1806

RESULT 91
US-11-097-143-1040
; Sequence 1040, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1040
; LENGTH: 2266
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-1040

Query Match 52.2%; Score 21.4; DB 10; Length 2266;
Best Local Similarity 69.2%; Pred. No. 1.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCTTCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
    ||| | ||| ||| ||| ||| ||| ||| ||| :|
Db 1589 AACCACGAGTGCAGTTCCTCAAGGTGGCCCAATTG 1627

RESULT 92
US-10-425-115-119462/c
; Sequence 119462, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
```

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; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 119462
; LENGTH: 2435
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40432C.1
US-10-425-115-119462

Query Match          52.2%; Score 21.4; DB 8; Length 2435;
Best Local Similarity 69.2%; Pred. No. 1.6e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
Db      2287 GCGTTCGGATCCAGACCCCTCACCTGGGTGCGGACGCG 2249

RESULT 93
US-10-369-493-34212/c
; Sequence 34212, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 34212
; LENGTH: 2751
; TYPE: DNA
; ORGANISM: Sphingomonas aromaticivorans
US-10-369-493-34212

Query Match          52.2%; Score 21.4; DB 6; Length 2751;
Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCG 39
Db      1763 AGGCTGCCGAACGCCAGTGCTCGCCGGTCGCCCAGTCG 1725

RESULT 94
US-10-156-761-923
; Sequence 923, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
```

```
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 923
; LENGTH: 2847
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2847)
US-10-156-761-923

Query Match          52.2%; Score 21.4; DB 6; Length 2847;
Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
Db      2173 GCCGCCGTCCGCGACTTCTCTACCCGCCGCCGGGTGGCG 2211

RESULT 95
US-10-739-930-1807
; Sequence 1807, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 1807
; LENGTH: 2886
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEAMA-23APR03-CLUSTER13300_1
US-10-739-930-1807

Query Match          52.2%; Score 21.4; DB 8; Length 2886;
Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
Db      600 GCGTTCGGATCCAGACCCCTCACCTGGGTGCGGACGCG 638

RESULT 96
US-10-027-632-114768
; Sequence 114768, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
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; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114768
; LENGTH: 3110
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114768

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Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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; Sequence 114768, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114768
; LENGTH: 3110
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-114768

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Best Local Similarity 69.2%; Pred. No. 1.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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; Sequence 2415, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
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; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 3548
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US-10-128-714-2415

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; Publication No. US20030119013A1
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; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
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; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
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; LENGTH: 3642
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-7415

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; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
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; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-1415

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Best Local Similarity 77.4%; Pred. No. 1.5e+02;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Listing first 500 summaries

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C 239	19.4	47.3	1191	18	US-11-096-568A-19966	Sequence 19966, A	C 312	19.2	46.8	86	10	US-10-310-914A-4203	Sequence 4203, Ap
C 240	19.4	47.3	1206	16	US-11-082-389-63	Sequence 63, Appl	C 313	19.2	46.8	201	17	US-11-124-367A-25367	Sequence 25367, A
C 241	19.4	47.3	1251	7	US-09-925-065A-2773	Sequence 2773, Ap	C 314	19.2	46.8	201	17	US-11-124-367A-26146	Sequence 26146, A
C 242	19.4	47.3	1251	7	US-09-925-065A-2774	Sequence 2774, Ap	C 315	19.2	46.8	385	7	US-09-925-065A-469722	Sequence 469722,
C 243	19.4	47.3	1251	11	US-10-301-480-104010	Sequence 104010,	C 316	19.2	46.8	385	7	US-09-925-065A-469723	Sequence 469723,
C 244	19.4	47.3	1251	11	US-10-301-480-104011	Sequence 104011,	C 317	19.2	46.8	385	7	US-09-925-065A-469724	Sequence 469724,
C 245	19.4	47.3	1251	12	US-10-301-480-717419	Sequence 717419,	C 318	19.2	46.8	385	7	US-09-925-065A-469725	Sequence 469725,
C 246	19.4	47.3	1251	12	US-10-301-480-717420	Sequence 717420,	C 319	19.2	46.8	398	7	US-09-925-065A-468648	Sequence 468648,
C 247	19.4	47.3	1284	11	US-10-297-341-10	Sequence 10, Appl	C 320	19.2	46.8	403	17	US-11-055-822-271	Sequence 271, App
C 248	19.4	47.3	1374	18	US-11-096-568A-2065	Sequence 2065, Ap	C 321	19.2	46.8	417	7	US-09-925-065A-501351	Sequence 501351,
C 249	19.4	47.3	1432	7	US-09-925-065A-69293	Sequence 69293, A	C 322	19.2	46.8	452	7	US-09-925-065A-790392	Sequence 790392,
C 250	19.4	47.3	1432	11	US-10-301-480-170532	Sequence 170532,	C 323	19.2	46.8	491	7	US-09-925-065A-537194	Sequence 537194,
C 251	19.4	47.3	1432	12	US-10-301-480-783941	Sequence 783941,	C 324	19.2	46.8	505	7	US-09-925-065A-513645	Sequence 513645,
C 252	19.4	47.3	1553	17	US-11-105-864-1	Sequence 1, Appli	C 325	19.2	46.8	521	18	US-11-021-492-104	Sequence 104, App
C 253	19.4	47.3	1618	18	US-11-072-512-1463	Sequence 1463, Ap	C 326	19.2	46.8	530	7	US-09-925-065A-500354	Sequence 500354,
C 254	19.4	47.3	1698	18	US-11-096-568A-9856	Sequence 9856, Ap	C 327	19.2	46.8	543	7	US-09-925-065A-16197	Sequence 16197, A
C 255	19.4	47.3	1751	7	US-09-925-065A-69096	Sequence 69096, A	C 328	19.2	46.8	543	11	US-10-301-480-117434	Sequence 117434,
C 256	19.4	47.3	1751	11	US-10-301-480-170335	Sequence 170335,	C 329	19.2	46.8	543	12	US-10-301-480-730843	Sequence 730843,
C 257	19.4	47.3	1751	12	US-10-301-480-783744	Sequence 783744,	C 330	19.2	46.8	574	11	US-10-301-480-47004	Sequence 47004, A
C 258	19.4	47.3	1914	17	US-11-105-864-7	Sequence 7, Appli	C 331	19.2	46.8	574	12	US-10-301-480-660413	Sequence 660413,
C 259	19.4	47.3	1934	10	US-10-750-185-50132	Sequence 50132, A	C 332	19.2	46.8	598	7	US-09-925-065A-34030	Sequence 34030, A
C 260	19.4	47.3	1934	10	US-10-750-623-50132	Sequence 50132, A	C 333	19.2	46.8	598	7	US-09-925-065A-34031	Sequence 34031, A
C 261	19.4	47.3	2000	7	US-09-925-065A-679193	Sequence 679193,	C 334	19.2	46.8	598	11	US-10-301-480-135268	Sequence 135268,
C 262	19.4	47.3	2000	7	US-09-925-065A-679194	Sequence 679194,	C 335	19.2	46.8	598	11	US-10-301-480-135269	Sequence 135269,
C 263	19.4	47.3	2000	7	US-09-925-065A-679195	Sequence 679195,	C 336	19.2	46.8	598	12	US-10-301-480-748677	Sequence 748677,
C 264	19.4	47.3	2000	7	US-09-925-065A-679196	Sequence 679196,	C 337	19.2	46.8	598	12	US-10-301-480-748678	Sequence 748678,
C 265	19.4	47.3	2067	10	US-10-750-185-33091	Sequence 33091, A	C 338	19.2	46.8	623	11	US-10-301-480-52983	Sequence 52983, A
C 266	19.4	47.3	2067	10	US-10-750-623-33091	Sequence 33091, A	C 339	19.2	46.8	623	12	US-10-301-480-666392	Sequence 666392,
C 267	19.4	47.3	2346	17	US-11-136-527-129	Sequence 129, App	C 340	19.2	46.8	631	7	US-09-925-065A-542928	Sequence 542928,
C 268	19.4	47.3	2537	18	US-11-072-512-1255	Sequence 1255, Ap	C 341	19.2	46.8	661	7	US-09-925-065A-814548	Sequence 814548,
C 269	19.4	47.3	3153	18	US-11-072-512-1302	Sequence 1302, Ap	C 342	19.2	46.8	666	7	US-09-925-065A-710183	Sequence 710183,
C 270	19.4	47.3	3236	11	US-10-501-035-79	Sequence 79, Appl	C 343	19.2	46.8	739	7	US-09-925-065A-9164	Sequence 9164, Ap
C 271	19.4	47.3	3419	18	US-11-228-659-17	Sequence 17, Appl	C 344	19.2	46.8	739	7	US-09-925-065A-9165	Sequence 9165, Ap
C 272	19.4	47.3	3579	10	US-10-858-730-143	Sequence 143, App	C 345	19.2	46.8	739	7	US-09-925-065A-9166	Sequence 9166, Ap
C 273	19.4	47.3	3624	9	US-10-370-959-79	Sequence 79, Appl	C 346	19.2	46.8	739	7	US-09-925-065A-9167	Sequence 9167, Ap
C 274	19.4	47.3	4098	9	US-10-510-508-2	Sequence 2, Appli	C 347	19.2	46.8	739	11	US-10-301-480-110401	Sequence 110401,
C 275	19.4	47.3	4098	17	US-11-000-688-433	Sequence 433, App	C 348	19.2	46.8	739	11	US-10-301-480-110402	Sequence 110402,
C 276	19.4	47.3	4204	9	US-10-505-928-760	Sequence 760, App	C 349	19.2	46.8	739	11	US-10-301-480-110403	Sequence 110403,
C 277	19.4	47.3	4392	17	US-11-080-991-73	Sequence 73, Appl	C 350	19.2	46.8	739	11	US-10-301-480-110404	Sequence 110404,
C 278	19.4	47.3	4510	17	US-11-136-527-1828	Sequence 1828, Ap	C 351	19.2	46.8	739	12	US-10-301-480-723810	Sequence 723810,
C 279	19.4	47.3	4873	17	US-11-091-883-479	Sequence 479, App	C 352	19.2	46.8	739	12	US-10-301-480-723811	Sequence 723811,
C 280	19.4	47.3	6377	10	US-10-995-561-401	Sequence 401, App	C 353	19.2	46.8	739	12	US-10-301-480-723812	Sequence 723812,
C 281	19.4	47.3	6868	17	US-11-186-284-190	Sequence 190, App	C 354	19.2	46.8	739	12	US-10-301-480-723813	Sequence 723813,
C 282	19.4	47.3	6891	14	US-11-251-724-2	Sequence 2, Appli	C 355	19.2	46.8	849	18	US-11-096-568A-15643	Sequence 15643, A
C 283	19.4	47.3	6891	17	US-11-101-000-2	Sequence 2, Appli	C 356	19.2	46.8	1143	17	US-11-055-822-269	Sequence 269, App
C 284	19.4	47.3	6891	17	US-11-130-945-2	Sequence 2, Appli	C 357	19.2	46.8	1203	18	US-11-096-568A-22714	Sequence 22714, A
C 285	19.4	47.3	9724	17	US-11-128-061-857	Sequence 857, App	C 358	19.2	46.8	1303	11	US-10-301-480-31025	Sequence 31025, A
C 286	19.4	47.3	9724	17	US-11-128-049-857	Sequence 857, App	C 359	19.2	46.8	1303	11	US-10-301-480-31026	Sequence 31026, A
C 287	19.4	47.3	14172	10	US-10-995-561-13226	Sequence 13226, A	C 360	19.2	46.8	1303	11	US-10-301-480-31027	Sequence 31027, A
C 288	19.4	47.3	14196	10	US-10-995-561-13429	Sequence 13429, A	C 361	19.2	46.8	1303	12	US-10-301-480-644434	Sequence 644434,
C 289	19.4	47.3	15118	17	US-11-124-367A-5029	Sequence 5029, Ap	C 362	19.2	46.8	1303	12	US-10-301-480-644435	Sequence 644435,
C 290	19.4	47.3	15876	17	US-11-052-554A-660	Sequence 660, App	C 363	19.2	46.8	1303	12	US-10-301-480-644436	Sequence 644436,
C 291	19.4	47.3	19691	17	US-11-124-367A-5034	Sequence 5034, Ap	C 364	19.2	46.8	1470	10	US-10-750-185-48974	Sequence 48974, A
C 292	19.4	47.3	60729	11	US-10-330-773-841	Sequence 841, App	C 365	19.2	46.8	1470	10	US-10-750-623-48974	Sequence 48974, A
C 293	19.4	47.3	88892	11	US-10-330-773-672	Sequence 672, App	C 366	19.2	46.8	1500	17	US-11-087-100-7	Sequence 7, Appli
C 294	19.4	47.3	100000	17	US-11-124-367A-5004	Sequence 5004, Ap	C 367	19.2	46.8	1500	17	US-11-087-084-7	Sequence 7, Appli
C 295	19.4	47.3	101046	10	US-10-995-561-13330	Sequence 13330, A	C 368	19.2	46.8	1500	17	US-11-087-085-7	Sequence 7, Appli
C 296	19.4	47.3	159781	17	US-11-121-086-932	Sequence 92, Appl	C 369	19.2	46.8	1720	10	US-10-750-185-24896	Sequence 24896, A
C 297	19.4	47.3	185750	18	US-11-114-798-56	Sequence 56, Appl	C 370	19.2	46.8	1720	10	US-10-750-623-24896	Sequence 24896, A
C 298	19.4	47.3	212716	17	US-11-121-086-95	Sequence 95, Appl	C 371	19.2	46.8	1802	7	US-09-925-065A-78109	Sequence 78109, A
C 299	19.4	47.3	220895	10	US-10-775-169-88	Sequence 88, Appl	C 372	19.2	46.8	1802	7	US-09-925-065A-78110	Sequence 78110, A
C 300	19.4	47.3	1080000	10	US-10-928-446A-1	Sequence 1, Appli	C 373	19.2	46.8	1802	11	US-10-301-480-179348	Sequence 179348,
C 301	19.4	47.3	1080000	10	US-10-928-446A-181	Sequence 181, App	C 374	19.2	46.8	1802	11	US-10-301-480-179349	Sequence 179349,
C 302	19.4	47.3	1080000	10	US-10-928-446A-183	Sequence 183, App	C 375	19.2	46.8	1802	12	US-10-301-480-792757	Sequence 792757,
C 303	19.4	47.3	1080000	10	US-10-928-446A-185	Sequence 185, App	C 376	19.2	46.8	1802	12	US-10-301-480-792758	Sequence 792758,
C 304	19.4	47.3	1080000	10	US-10-928-446A-187	Sequence 187, App	C 377	19.2	46.8	1814	10	US-10-750-185-51922	Sequence 51922, A
C 305	19.4	47.3	1080000	10	US-10-928-446A-189	Sequence 189, App	C 378	19.2	46.8	1814	10	US-10-750-623-51922	Sequence 51922, A
C 306	19.4	47.3	1080000	10	US-10-928-446A-191	Sequence 191, App	C 379	19.2	46.8	2001	17	US-11-043-752-2129	Sequence 2129, Ap

Query Match 53.7%; Score 22; DB 17; Length 23704;
Best Local Similarity 71.1%; Pred. No. 91;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
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Db 6147 GCCTGGGGTGCCAGGCTCCCATCCATGCGCCAGCCCC 6110

RESULT 9
US-10-802-796-422
; Sequence 422, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 422
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (145)
; OTHER INFORMATION: a, t, c or g
; NAME/KEY: modified_base
; LOCATION: (230)
; OTHER INFORMATION: a, t, c or g
US-10-802-796-422

Query Match 52.7%; Score 21.6; DB 10; Length 230;
Best Local Similarity 72.2%; Pred. No. 2.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 TCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
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Db 33 TCCGGATTCTGGGCTTCATCGCTCGCGCGCGTCGCG 68

RESULT 10
US-11-221-284-422
; Sequence 422, Application US/11221284
; Publication No. US20060063182A1
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/11/221,284
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: US/09/060,756

; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 422
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-11-221-284-422

Query Match 52.7%; Score 21.6; DB 18; Length 230;
Best Local Similarity 72.2%; Pred. No. 2.5e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 6 TCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 41
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Db 33 TCCGGATTCTGGGCTTCATCGCTCGCGCGCGTCGCG 68

RESULT 11
US-10-750-185-41952
; Sequence 41952, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41952
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Bovine 19866881725438
US-10-750-185-41952

Query Match 52.7%; Score 21.6; DB 10; Length 777;
Best Local Similarity 72.2%; Pred. No. 2.1e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGN 37
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Db 433 AGCTCCGCATGCCTGTCCCTCTCTGCGCAGTCTCTGT 468

RESULT 12
US-10-750-623-41952
; Sequence 41952, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31


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; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41952
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Bovine 19866881725438
US-10-750-623-41952

Query Match      52.7%; Score 21.6; DB 10; Length 777;
Best Local Similarity 72.2%; Pred. No. 2.1e+02;
Matches 26; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGN 37
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Db      433 AGGCTCCGATGCCTGTCTCCCTCCTGGCAGTCTCTGT 468

RESULT 13
US-11-136-527-6815/c
; Sequence 6815, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6815
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6815

Query Match      52.2%; Score 21.4; DB 17; Length 600;
Best Local Similarity 69.2%; Pred. No. 2.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGG 41
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Db      292 GCCTACGGAAGCGGGACCTCATCCCTCCAGGCCCG 254

RESULT 14
US-11-285-798-28/c
; Sequence 28, Application US/11285798
; Publication No. US20060079451A1
; GENERAL INFORMATION:
; APPLICANT: Imamura, Toru
; APPLICANT: Asada, Masahiro
; APPLICANT: Oka, Syuichi
; APPLICANT: Suzuki, Masashi
; APPLICANT: Yoneda, Atsuko
; APPLICANT: Ota, Keiko
; APPLICANT: Oda, Yuko
; APPLICANT: Miyakawa, Kazuko
; APPLICANT: Orikasa, Noriko
; APPLICANT: Asada, Chie
; APPLICANT: Kojima, Tetsuhito
; TITLE OF INVENTION: HEPARIN-BINDING PROTEINS MODIFIED WITH SUGAR CHAINS,
; TITLE OF INVENTION: METHOD OF PRODUCING THE SAME AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS CONTAINING THE SAME
; FILE REFERENCE: 382.1019
; CURRENT APPLICATION NUMBER: US/11/285,798
; CURRENT FILING DATE: 2005-11-23
; PRIOR APPLICATION NUMBER: US/09/121,017
; PRIOR FILING DATE: 1998-07-22
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; PRIOR APPLICATION NUMBER: 307721/1997
; PRIOR FILING DATE: 1997-11-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion of
; OTHER INFORMATION: sequence for a part of mouse fibroblast growth factor 6 and
; OTHER INFORMATION: a part of human fibroblast growth 1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(630)
US-11-285-798-28

Query Match      52.2%; Score 21.4; DB 18; Length 630;
Best Local Similarity 69.2%; Pred. No. 2.5e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGC 40
      ||||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      130 AGCCTCTGGAGTCCAGTAGCTGCGCTTGGCGCGGCGC 92

RESULT 15
US-11-096-568A-21580
; Sequence 21580, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 21580
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1222)
; OTHER INFORMATION: Ceres Seq. ID no. 12405362
US-11-096-568A-21580

Query Match      52.2%; Score 21.4; DB 18; Length 1222;
Best Local Similarity 69.2%; Pred. No. 2.3e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY      3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      600 GCGTTCGGATCCAAGACCCTCACCTGGGTGCGGACGCG 638

RESULT 16
US-11-136-527-2719/c
; Sequence 2719, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2719
```

```
; LENGTH: 6683
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2719

Query Match      52.2%; Score 21.4; DB 17; Length 6683;
Best Local Similarity 69.2%; Pred. No. 1.8e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
Db 6375 GCCTACGAAGCGGACCTCATCCCTTCCAGGCCCG 6337

RESULT 17
US-11-121-086-9
; Sequence 9, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 196200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-9

Query Match      52.2%; Score 21.4; DB 17; Length 196200;
Best Local Similarity 69.2%; Pred. No. 1.1e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCG 39
Db 142580 AGGCTCCGCGGAGAGTCCCCCAGAGCGCGCGGGG 142618

RESULT 18
US-11-121-086-8
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: POULSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-8

Query Match      52.2%; Score 21.4; DB 17; Length 246960;
Best Local Similarity 69.2%; Pred. No. 1e+02;
Matches 27; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCG 39
Db 17716 AGGCTCCGCGGAGAGTCCCCCAGAGCGCGCGGGG 17754
```

```
RESULT 19
US-09-925-065A-404740/c
; Sequence 404740, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 404740
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-404740

Query Match      51.2%; Score 21; DB 7; Length 617;
Best Local Similarity 70.3%; Pred. No. 3.5e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGG 37
Db 547 AAGTCTCTGATGCCACACCTCATCCCTGCCCTGA 511

RESULT 20
US-09-925-065A-23066/c
; Sequence 23066, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23066
; LENGTH: 1025
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-23066

Query Match      51.2%; Score 21; DB 7; Length 1025;
Best Local Similarity 70.3%; Pred. No. 3.2e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
```

```
Db      37 AGCCCCGGGATGCCGGGCCCGGAGCGCTGGGGGGGCC 1
||||| | ||||| | ||| | ||||| ||:|
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124303
; LENGTH: 1025
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-124303

Query Match      51.2%; Score 21; DB 11; Length 1025;
Best Local Similarity 70.3%; Pred. No. 3.2e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||||| | ||||| | ||| | ||||| ||:|
Db      37 AGCCCCGGGATGCCGGGCCCGGAGCGCTGGGGGGGCC 1

RESULT 22
US-10-301-480-737712/c
; Sequence 737712, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 737712
; LENGTH: 1025
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-737712

Query Match      51.2%; Score 21; DB 12; Length 1025;
Best Local Similarity 70.3%; Pred. No. 3.2e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||||| | ||||| | ||| | ||||| ||:|
Db      37 AGCCCCGGGATGCCGGGCCCGGAGCGCTGGGGGGGCC 1

RESULT 23
US-09-925-065A-8417/c
; Sequence 8417, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8417
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-8417

Query Match      51.2%; Score 21; DB 7; Length 1623;
Best Local Similarity 82.8%; Pred. No. 3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTG 30
||||| | ||||| | ||| | ||||| ||||
Db      235 AGCCTCTCAATGCCTGTCCTCATTTGCTG 207

RESULT 24
US-10-301-480-109654/c
; Sequence 109654, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109654
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-109654

Query Match      51.2%; Score 21; DB 11; Length 1623;
Best Local Similarity 82.8%; Pred. No. 3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AGCCTCCGGATGCCAGTCCCTCATCGCTG 30
||||| | ||||| | ||| | ||||| ||||
Db      235 AGCCTCTCAATGCCTGTCCTCATTTGCTG 207

RESULT 25
US-10-301-480-723063/c
; Sequence 723063, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
```

```

; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 723063
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-723063

Query Match          51.2%; Score 21; DB 12; Length 1623;
Best Local Similarity 82.8%; Pred. No. 3e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTG 30
    ||||| ||||| ||||| ||||| |||||
Db 235 AGCCTCTCAATGCCTGTCCCTCATTTGCTG 207

RESULT 26
US-11-072-512-556/c
; Sequence 556, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 556
; LENGTH: 2185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-556

Query Match          51.2%; Score 21; DB 18; Length 2185;
Best Local Similarity 82.8%; Pred. No. 2.9e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTG 30
    ||||| ||||| ||||| ||||| |||||
Db 665 AGCCTCTCAATGCCTGTCCCTCATTTGCTG 637

RESULT 27
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US-11-052-554A-523/c
; Sequence 523, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 523
; LENGTH: 3921
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-523

Query Match          51.2%; Score 21; DB 17; Length 3921;
Best Local Similarity 70.3%; Pred. No. 2.7e+02;
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGCTGGCCCGGCGG 41
    ||||| ||||| ||||| ||||| |||||
Db 1375 CTTGGATCCAAATCCGAGACCGCGCCCGCGCGG 1339

RESULT 28
US-09-925-065A-748954
; Sequence 748954, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 748954
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-748954

Query Match          50.7%; Score 20.8; DB 7; Length 518;
Best Local Similarity 67.5%; Pred. No. 4.2e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGCGC 40
    ||||| ||||| ||||| ||||| |||||
Db 204 AAGTCTACAGCTTCCAGTCCCTCATGGCATGAGCAGTGGC 243

RESULT 29
US-10-517-696-5
; Sequence 5, Application US/10517696
; Publication No. US20060051759A1
```



```
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto A.
; APPLICANT: Turner, Leah R.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Peptides
; FILE REFERENCE: DEX-0432
; CURRENT APPLICATION NUMBER: US/10/517,696
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/389,327
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-517-696-5

Query Match      50.7%; Score 20.8; DB 11; Length 891;
Best Local Similarity 67.5%; Pred. No. 3.9e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGC 40
Db 706 AATCCTCCGCCCCCAGTCTTCGACCCAGGCACGAGCGC 745

RESULT 30
US-10-517-696-6
; Sequence 6, Application US/10517696
; Publication No. US20060051759A1
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto A.
; APPLICANT: Turner, Leah R.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Peptides
; FILE REFERENCE: DEX-0432
; CURRENT APPLICATION NUMBER: US/10/517,696
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/389,327
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-517-696-6

Query Match      50.7%; Score 20.8; DB 11; Length 1253;
Best Local Similarity 67.5%; Pred. No. 3.7e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGC 40
Db 706 AATCCTCCGCCCCCAGTCTTCGACCCAGGCACGAGCGC 745

RESULT 31
US-11-096-568A-22339
; Sequence 22339, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
```

```
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22339
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1440)
; OTHER INFORMATION: Ceres Seq. ID no. 12408549
US-11-096-568A-22339

Query Match      50.7%; Score 20.8; DB 18; Length 1440;
Best Local Similarity 67.5%; Pred. No. 3.6e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41
Db 146 AACACCAGACGCCAGTCCACCCGCTTCCCGTGCAGCG 185

RESULT 32
US-11-096-568A-19669
; Sequence 19669, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19669
; LENGTH: 1477
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1477)
; OTHER INFORMATION: Ceres Seq. ID no. 12374112
US-11-096-568A-19669

Query Match      50.7%; Score 20.8; DB 18; Length 1477;
Best Local Similarity 67.5%; Pred. No. 3.6e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCCCGNCGCG 41
Db 167 AACACCAGACGCCAGTCCACCCGCTTCCCGTGCAGCG 206

RESULT 33
US-11-124-367A-5047
; Sequence 5047, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 5047
; LENGTH: 54985
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 48521, 48522, 48523, 48524, 48525, 48526, 48527, 48528, 48529,
; LOCATION: 48530, 48531, 48532, 48533, 48534, 48535, 48536, 48537,
; LOCATION: 48538, 48539, 48540, 48541, 48542, 48543, 48544, 48545,
; LOCATION: 48546, 48547, 48548, 48549, 48550, 48551, 48552, 48553
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 48554, 48555, 48556, 48557, 48558, 48559, 48560, 48561, 48562,
; LOCATION: 48563, 48564, 48565, 48566, 48567, 48568, 48569, 48570,
; LOCATION: 48571, 48572, 48573, 48574, 48575, 48576, 48577, 48578,
; LOCATION: 48579, 48580, 48581, 48582, 48583, 48584, 48585, 48586
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 48587, 48588, 48589, 48590, 48591, 48592, 48593, 48594, 48595,
; LOCATION: 48596, 48597, 48598, 48599, 48600, 48601, 48602, 48603,
; LOCATION: 48604, 48605, 48606, 48607, 48608, 48609, 48610, 48611,
; LOCATION: 48612, 48613, 48614, 48615, 48616, 48617, 48618, 48619
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 48620, 48621, 48622, 48623, 48624, 48625, 48626, 48627, 48628,
; LOCATION: 48629, 48630, 48631, 48632, 48633, 48634, 48635, 48636,
; LOCATION: 48637, 48638, 48639, 48640, 48641, 48642, 48643, 48644,
; LOCATION: 48645, 48646, 48647, 48648, 48649, 48650, 48651, 48652
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 48653, 48654, 48655, 48656, 48657, 48658, 48659, 48660, 48661,
; LOCATION: 48662, 48663, 48664, 48665, 48666, 48667, 48668, 48669,
; LOCATION: 48670, 48671, 48672, 48673, 48674, 48675, 48676, 48677,
; LOCATION: 48678, 48679, 48680, 48681, 48682, 48683, 48684, 48685
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 48686, 48687, 48688, 48689, 48690, 48691, 48692, 48693, 48694,
; LOCATION: 48695, 48696, 48697, 48698, 48699, 48700, 48701, 48702,
; LOCATION: 48703, 48704, 48705, 48706, 48707, 48708, 48709, 48710,
; LOCATION: 48711, 48712, 48713, 48714, 48715, 48716, 48717, 48718
; OTHER INFORMATION: n = A,T,C or G
US-11-124-367A-5047

Query Match          50.7%; Score 20.8; DB 17; Length 54985;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 24; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 7 CCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 17389 CTGGAACCAAGCCCTCATGGCAGGCCAGGCC 17420

RESULT 34
US-10-478-943D-1
; Sequence 1, Application US/10478943D
; Publication No. US20060073574A1
; GENERAL INFORMATION:
; APPLICANT: University College Dublin, National University of Ireland
; TITLE OF INVENTION: Engineered biosynthesis of novel polyenes
; FILE REFERENCE: PC-1636US
; CURRENT APPLICATION NUMBER: US/10/478,943D
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: S2001/0527
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 113193
```

```
; TYPE: DNA
; ORGANISM: Streptomyces nodosus
US-10-478-943D-1

Query Match          50.7%; Score 20.8; DB 13; Length 113193;
Best Local Similarity 67.5%; Pred. No. 1.9e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70159 ACGACCCCGGACGCCAGGCCGTCGCCGACCGCCTGGACGC 70198

RESULT 35
US-11-121-086-66
; Sequence 66, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 163162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-66

Query Match          50.7%; Score 20.8; DB 17; Length 163162;
Best Local Similarity 67.5%; Pred. No. 1.8e+02;
Matches 27; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AAGCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61548 AATCCTCCAGATCCCGCCCTCAAATCTAGACCCCAACC 61587

RESULT 36
US-11-052-554A-450/c
; Sequence 450, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 450
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-450

Query Match          50.2%; Score 20.6; DB 17; Length 1206;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNC 37
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 984 GCCTCCGGATGCCAGACCTTCGTTGTTGGCAAGT 950
```

```
RESULT 37
US-11-052-554A-567/c
; Sequence 567, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 567
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Shigella flexneri 2a str. 2457T
US-11-052-554A-567

Query Match          50.2%; Score 20.6; DB 17; Length 1209;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGN 37
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 987 GCCTTCGGATGCCAGACCTTCGTTGTTGGCAAGT 953

RESULT 38
US-11-096-568A-25599/c
; Sequence 25599, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25599
; LENGTH: 1297
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1297)
; OTHER INFORMATION: Ceres Seq. ID no. 13492533
US-11-096-568A-25599

Query Match          50.2%; Score 20.6; DB 18; Length 1297;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGN 37
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 99 GCCTCCAGCTGCCGGTGCCTCACCGCCGCATGGC 65

RESULT 39
US-09-925-065A-70542
; Sequence 70542, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
```

```
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70542
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-70542

Query Match          50.2%; Score 20.6; DB 7; Length 1947;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12 CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46

RESULT 40
US-09-925-065A-70543
; Sequence 70543, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70543
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-70543

Query Match          50.2%; Score 20.6; DB 7; Length 1947;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 CCGATGCCAGTCCCTCATCGCTGGCCCGNCGCG 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12 CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46

RESULT 41
US-10-301-480-171781
; Sequence 171781, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 171781
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-171781
```

```
Query Match          50.2%;   Score 20.6;   DB 11;   Length 1947;
Best Local Similarity 71.4%;   Pred. No. 4.1e+02;
Matches 25;   Conservative 1;   Mismatches 9;   Indels 0;   Gaps 0;
```

```
QY      7  CCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
      |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      12  CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46
```

```
RESULT 42
US-10-301-480-171782
; Sequence 171782, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 171782
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-171782
```

```
Query Match          50.2%;   Score 20.6;   DB 11;   Length 1947;
Best Local Similarity 71.4%;   Pred. No. 4.1e+02;
Matches 25;   Conservative 1;   Mismatches 9;   Indels 0;   Gaps 0;
```

```
QY      7  CCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
      |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      12  CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46
```

```
RESULT 43
US-10-301-480-785190
; Sequence 785190, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
```

```
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 785190
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-785190

Query Match          50.2%;   Score 20.6;   DB 12;   Length 1947;
Best Local Similarity 71.4%;   Pred. No. 4.1e+02;
Matches 25;   Conservative 1;   Mismatches 9;   Indels 0;   Gaps 0;
```

```
QY      7  CCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
      |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      12  CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46
```

```
RESULT 44
US-10-301-480-785191
; Sequence 785191, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 785191
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-785191
```

```
Query Match          50.2%;   Score 20.6;   DB 12;   Length 1947;
Best Local Similarity 71.4%;   Pred. No. 4.1e+02;
Matches 25;   Conservative 1;   Mismatches 9;   Indels 0;   Gaps 0;
```

```
QY      7  CCGGATGCCAGTCCCTCATCGTGGCCCGGNCGCG 41
      |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      12  CCGGGGGCCAGGGCCTCATCGCAGGACGGGAAGAG 46
```

```
RESULT 45
US-10-131-826A-81
; Sequence 81, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```



```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19

```

Query Match	50.2%	Score 20.6;	DB 10;	Length 3233;
Best Local Similarity	71.4%	Pred. No. 3.8e+02;		
Matches 25;	Conservative	1;	Mismatches 9;	Indels 0;
				Gaps 0;

Qy 4 CCTCGGATGCCAGTCCCTCATCGCTGGCCCCGNC 38
 || | | | | | | | | | | | |
Db 823 CCCGGTATGCCAGGCCTCCTGGGCAGCCC GGCC 857
 | | | | | | | | | | | |

RESULT 46

US-10-973-115B-81

; Sequence 81, Application US/10973115B

; Publication No. US20060040351A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Quiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING

; TITLE OF INVENTION: SAME

; FILE REFERENCE: 39870-3330R1C300C1

; CURRENT APPLICATION NUMBER: US/10/973,115B

; CURRENT FILING DATE: 2004-10-22

; PRIOR APPLICATION NUMBER: US 10/145,747

; PRIOR FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: US 10/028,072

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: PCT/US00/32678

```

; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 81
; LENGTH: 3233
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-973-115B-81

```

Query Match 50.2%; Score 20.6; DB 11; Length 3233;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0;

Qy 4 CCTCGGATGCCAGTCCCTCATCGCTGGCCCCGNC 38
 |||||
Db 823 CCCGGTATGCCAGGCCCTCCTGGGCAGCCC GGCC 857
 :|||:

RESULT 47

US-10-137-873A-81

; Sequence 81, Application US/10137873A

; Publication No. US20060084138A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin


```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5108

Query Match          50.2%; Score 20.6; DB 17; Length 13310;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGN 37
| | | | | | | | | | | | | | | | | | | | |
Db 5399 GGCTCCTTAGCCATTCCCTGTCTCCCTGGCCCGGG 5365

RESULT 51
US-11-114-798-54/c
; Sequence 54, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; FILE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn ver. 3.3
; SEQ ID NO 54
; LENGTH: 198977
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-54

Query Match          50.2%; Score 20.6; DB 18; Length 198977;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 4 CCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNC 38
| | | | | | | | | | | | | | | | | | | | |
Db 25857 CCCC GTATGCCAGGCCCTCTCTGGG CAGCCCGGCC 25823

RESULT 52
US-10-995-561-57494/c
; Sequence 57494, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57494
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-57494

Query Match          49.8%; Score 20.4; DB 10; Length 201;
Best Local Similarity 65.0%; Pred. No. 6.7e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
```

```

QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
| | | | | | | | | | | | | | | | | | | | |
Db 137 AGGCTCCGGCGGCAAGTCCCGCGCAGGTGGCAGCGCGCG 98

RESULT 53
US-10-995-561-74443
; Sequence 74443, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74443
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-74443

Query Match          49.8%; Score 20.4; DB 10; Length 201;
Best Local Similarity 65.0%; Pred. No. 6.7e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
| | | | | | | | | | | | | | | | | | | | |
Db 65 AGGCTCCGGCGGCAAGTCCCGCGCAGGTGGCAGCGCGCG 104

RESULT 54
US-10-995-561-75232
; Sequence 75232, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75232
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-75232

Query Match          49.8%; Score 20.4; DB 10; Length 201;
Best Local Similarity 65.0%; Pred. No. 6.7e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 AGCTCCGGATGCCAGTCCCTCATCGCTGGCCCCGGNCGCG 41
| | | | | | | | | | | | | | | | | | | | |
Db 65 AGGCTCCGGCGGCAAGTCCCGCGCAGGTGGCAGCGCGCG 104

RESULT 55
US-09-925-065A-777593
; Sequence 777593, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
```


RESULT 63
US-10-750-185-35711
; Sequence 35711, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 35711
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Bovine 19866880855790
US-10-750-185-35711

Query Match 49.8%; Score 20.4; DB 10; Length 558;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
||| || |||| |||| |||| | || || || ||
Db 155 GCCTTTGGCTGCCCGTCCCTGCCCCAGGTCCAGCCGC 192

RESULT 64
US-10-750-623-35711
; Sequence 35711, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 35711
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Bovine 19866880855790
US-10-750-623-35711

Query Match 49.8%; Score 20.4; DB 10; Length 558;
Best Local Similarity 68.4%; Pred. No. 5.8e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGC 40
||| || |||| |||| |||| | || || || ||
Db 155 GCCTTTGGCTGCCCGTCCCTGCCCCAGGTCCAGCCGC 192

RESULT 65
US-09-925-065A-778479/c
; Sequence 778479, Application US/09925065A

; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 778479
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-778479

Query Match 49.8%; Score 20.4; DB 7; Length 626;
Best Local Similarity 76.7%; Pred. No. 5.7e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 9 GGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||| |||| |||| |||| |||| | || || ||
Db 68 GGAAGCCAGTCCCTCATGGCTTCCCTTGGC 39

RESULT 66
US-09-925-065A-795922/c
; Sequence 795922, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 795922
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-795922

Query Match 49.8%; Score 20.4; DB 7; Length 632;
Best Local Similarity 76.7%; Pred. No. 5.7e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 9 GGATGCCAGTCCCTCATCGCTGGCCCGGNC 38
||| |||| |||| |||| |||| | || || ||
Db 68 GGAAGCCAGTCCCTCATGGCTTCCCTTGGC 39

;
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 771
; LENGTH: 2180
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-771

Query Match 49.8%; Score 20.4; DB 9; Length 2180;
Best Local Similarity 68.4%; Pred. No. 4.7e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCGGNC 38
||||| | | | | | | | | | | | | | | | | |
Db 896 AAGCCAGCACACTCCAGGCCACATAGCTGGCCCGAC 859

RESULT 72

US-11-147-047-5
; Sequence 5, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-147-047-5

Query Match 49.8%; Score 20.4; DB 17; Length 2463;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
||||| | | | | | | | | | | | | | | | | |
Db 1723 GCCTTCGAGTGCAGTCCCTCCCTGCAGTGTGTGCCGC 1760

RESULT 73

US-10-370-959-151
; Sequence 151, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar

;
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0170MNIM
; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 2625
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)...(2151)
US-10-370-959-151

Query Match 49.8%; Score 20.4; DB 9; Length 2625;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 3 GCCTCCGGATGCCAGTCCCTCATCGCTGGCCCGNCGC 40
| | | | | | | | | | | | | | | | | |
Db 87 GGCCCTGGTCCCGAGCCCTCGTCGCAGCCCCGGCGC 124

RESULT 74

US-11-036-196-1453/c
; Sequence 1453, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-10-995-561-13457)

Query Match 49.8%; Score 20.4; DB 10; Length 23082;
Best Local Similarity 65.0%; Pred. No. 3.3e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCGGCGCG 41
DB 4610 AGGCTCCGGCGCAAGTCCCGCGCAGGTGGCAGCGCGCG 4649

RESULT 79
US-10-276-233A-6/c
; Sequence 6, Application US/10276233A
; Publication No. US20050260572A1
; GENERAL INFORMATION:
; APPLICANT: DNA Chip Research Inc.
; TITLE OF INVENTION: Hitachi Software Engineering Co., Ltd.
; FILE REFERENCE: PH-1533-PCT
; CURRENT APPLICATION NUMBER: US/10/276,233A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: JP 2001-73063
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: JP 2001-108503
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: JP 2001-234807
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 79528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-233A-6

Query Match 49.8%; Score 20.4; DB 10; Length 79528;
Best Local Similarity 76.7%; Pred. No. 2.8e+02;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 12 TGCCAGTCCCTCATCGCTGCGCGGCGCG 41
DB 33430 TGGCATGCCCATCCCTGCGCGGCGCG 33401

RESULT 80
US-10-995-561-13332/c
; Sequence 13332, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13332
; LENGTH: 94510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1).... (94510)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-10-995-561-13332)

Query Match 49.8%; Score 20.4; DB 10; Length 94510;
Best Local Similarity 65.0%; Pred. No. 2.7e+02;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 2 AGCCTCCGGATGCCAGTCCCTCATCGCTGCGCGGCGCG 41
DB 7309 AGGCTCCGGCGCAAGTCCCGCGCAGGTGGCAGCGCGCG 7270

RESULT 81
US-11-112-908-19
; Sequence 19, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 212805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-19

Query Match 49.8%; Score 20.4; DB 17; Length 212805;
Best Local Similarity 68.4%; Pred. No. 2.4e+02;
Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 3 GCCTCCGGATGCCAGTCCCTCATCGCTGCGCGGCGCG 40
DB 75342 GCCTCTCAAGTGGTCCCTGACCCCTGGCCTGGAGC 75379

RESULT 82
US-09-925-065A-546446
; Sequence 546446, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 546446
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-546446

Query Match 49.3%; Score 20.2; DB 7; Length 553;
Best Local Similarity 65.9%; Pred. No. 6.8e+02;

Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Qy 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGCCCGGNCGCG 41
||| | ||| | ||| | ||| | ||| | ||| | ||| : |||
Db 462 AAGACCCGGCGGCCACTCCCTCCGCGGCCCACTCCCTCG 502

RESULT 83

US-10-301-480-524396
; Sequence 524396, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 524396
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-524396

Query Match 49.3%; Score 20.2; DB 12; Length 553;
Best Local Similarity 65.9%; Pred. No. 6.8e+02;
Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Qy 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGCCCGGNCGCG 41
||| | ||| | ||| | ||| | ||| | ||| | ||| : |||
Db 462 AAGACCCGGCGGCCACTCCCTCCGCGGCCCACTCCCTCG 502

RESULT 84

US-10-301-480-1137805
; Sequence 1137805, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1137805
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1137805

Query Match 49.3%; Score 20.2; DB 12; Length 553;
Best Local Similarity 65.9%; Pred. No. 6.8e+02;
Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Qy 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGCCCGGNCGCG 41
||| | ||| | ||| | ||| | ||| | ||| | ||| : |||
Db 462 AAGACCCGGCGGCCACTCCCTCCGCGGCCCACTCCCTCG 502

RESULT 85

US-09-925-065A-717469

; Sequence 717469, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 717469
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-717469

Query Match 49.3%; Score 20.2; DB 7; Length 628;
Best Local Similarity 75.8%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AGCCTCGGATGCCAGTCCCTCATCGCTGGCCC 34
||||| | ||| | ||| | ||| | ||| | |||
Db 318 AGCCTACTGATTCCACCTCCTCATCTTGCCC 350

RESULT 86

US-09-925-065A-354974/c
; Sequence 354974, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 354974
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-354974

Query Match 49.3%; Score 20.2; DB 7; Length 658;
Best Local Similarity 72.7%; Pred. No. 6.6e+02;
Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 5 CTCGGATGCCAGTCCCTCATCGCTGGCCCCG 37
||| | ||| | ||| | ||| | ||| | ||| : |||
Db 269 CTGAGTTTCCAGTCCCATCAGCACTGGCCCCGA 237

RESULT 87
US-09-925-065A-354975/c
; Sequence 354975, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 354975
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-354975

Query Match 49.3%; Score 20.2; DB 7; Length 658;
Best Local Similarity 72.7%; Pred. No. 6.6e+02;
Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTGGCCCGGN 37
||| ||||||| ||| |||||||:
Db 269 CTTGAGTTTCCAGTCCATCAGCACTGGCCCGGA 237

RESULT 88
US-10-301-480-426502/c
; Sequence 426502, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 426502
; LENGTH: 659
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-426502

Query Match 49.3%; Score 20.2; DB 12; Length 659;
Best Local Similarity 72.7%; Pred. No. 6.6e+02;
Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTGGCCCGGN 37
||| ||||||| ||| |||||||:
Db 269 CTTGAGTTTCCAGTCCATCAGCACTGGCCCGGA 237

RESULT 89
US-10-301-480-426503/c

; Sequence 426503, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 426503
; LENGTH: 659
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-426503

Query Match 49.3%; Score 20.2; DB 12; Length 659;
Best Local Similarity 72.7%; Pred. No. 6.6e+02;
Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTGGCCCGGN 37
||| ||||||| ||| |||||||:
Db 269 CTTGAGTTTCCAGTCCATCAGCACTGGCCCGGA 237

RESULT 90
US-10-301-480-1039911/c
; Sequence 1039911, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1039911
; LENGTH: 659
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1039911

Query Match 49.3%; Score 20.2; DB 12; Length 659;
Best Local Similarity 72.7%; Pred. No. 6.6e+02;
Matches 24; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 5 CTCGGATGCCAGTCCCTCATCGTGGCCCGGN 37
||| ||||||| ||| |||||||:
Db 269 CTTGAGTTTCCAGTCCATCAGCACTGGCCCGGA 237

RESULT 91
US-10-301-480-1039912/c
; Sequence 1039912, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21


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; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1039912
; LENGTH: 659
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-1039912

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Query Match	49.3%	Score 20.2;	DB 12;	Length 659;
Best Local Similarity	72.7%	Pred. No. 6.6e+02;		
Matches 24;	Conservative	1;	Mismatches 8;	Indels 0;
				Gaps 0;

Qy 5 CTCCGATGCCAGTCCCTCATCGCTGGCCCGG 37
Db 269 CTTGAGTTTCCAGTCCATCAGCACTGGCCCGGA 237

RESULT 92
US-10-750-185-24911/c
; Sequence 24911, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR I
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,48
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24911
; LENGTH: 1331
; TYPE: DNA
; ORGANISM: Bovine 19866880925243
US-10-750-185-24911

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Query Match      49.3%; Score 20.2; DB 10; Length 1331;
Best Local Similarity 84.0%; Pred. No. 6e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Qy 16 AGTCCCTCATCGTGGCCCGGCGC 40
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 Db 1308 AGTCCCTCTCTCCCTGGCCCGGGCCC 1284

RESULT 93
US-10-750-623-24911/c
; Sequence 24911, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482

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; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 24911
; LENGTH: 1331
; TYPE: DNA
; ORGANISM: Bovine 19866880925243
US-10-750-623-24911

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Query Match      49.3%; Score 20.2; DB 10; Length 1331;
Best Local Similarity 84.0%; Pred. No. 6e+02;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Qy 16 AGTCCCTCATCGTGGCCGNCGC 40
||| ||| ||| ||| ||| : ||
Db 1308 AGTCCCTCCTCCTGGCCCGGCC 1284

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RESULT 94
US-10-750-185-34602
; Sequence 34602, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34602
; LENGTH: 1348
; TYPE: DNA
; ORGANISM: Bovine 19866880447689
US-10-750-185-34602

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Query Match 49.3%; Score 20.2; DB 10; Length 1348;
Best Local Similarity 65.9%; Pred. No. 6e+02;
Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Qy

1 AAGCTCCGGATGCCAGTCCCTCATCGCTGGCCGCGNCGGC 41
|| || || || || || || || || || : ||
Dβ

194 AACCTTCGGTATGCCAGTGACTCATAGCTCCCGGGAGGGG 234

RESULT 95
US-10-750-623-34602
; Sequence 34602, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS F
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1

QY 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
Db 63891 AAGCCTCGTAATGGCAGTCGTTCTCCCTCCACCAGGCTCG 63931

RESULT 100
US-10-506-454-1690/c
; Sequence 1690, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1690
; LENGTH: 1694969
; TYPE: DNA
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1690

Query Match 49.3%; Score 20.2; DB 13; Length 1694969;
Best Local Similarity 65.9%; Pred. No. 2e+02;
Matches 27; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

QY 1 AAGCCTCGGATGCCAGTCCCTCATCGCTGGCCCGGNCGCG 41
Db 360812 AGGACGCGCAATCGAGTCCCTCACAGCTGATCCGTGCGCG 360772

Search completed: May 9, 2006, 23:00:25
Job time : 346 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:42:48 ; Search time 0.001 Seconds
(without alignments)
3.570 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336
Perfect score: 21
Sequence: 1 gctggccggcgctgtggc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 85 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 8 summaries

Database : estdb1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	38.1	11	1	DN756222	ACCESSION:DN756222
2	7.8	37.1	11	1	AJ679435	ACCESSION:AJ679435
3	7.8	37.1	11	1	AJ681247	ACCESSION:AJ681247
4	7.8	37.1	11	1	AJ683713	ACCESSION:AJ683713
5	7.8	37.1	11	1	AJ686459	ACCESSION:AJ686459
6	7.4	35.2	10	1	BM396011	ACCESSION:BM396011
7	7.4	35.2	10	1	BM398849	ACCESSION:BM398849
8	7	33.3	10	1	AJ599908	ACCESSION:AJ599908

ALIGNMENTS

RESULT 1
DN756222/c
LOCUS DN756222 11 bp mRNA linear EST 01-APR-2005
DEFINITION GL-CF-13018 GLGC-LIB0001-cf Canis familiaris Normalized Mixed
Tissue cDNA Library Canis familiaris cDNA, mRNA sequence.

ACCESSION DN756222 GI:62145335
VERSION DN756222.1
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 11)
AUTHORS Liu,Q.
TITLE Direct Submission Gene Logic Inc
JOURNAL Unpublished (2005)
COMMENT Contact: Qing Liu
Gene Logic Inc.

610 Professional Drive, Gaithersburg, MD 20879, USA

FEATURES
source
1..11
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/lab_host="EMDH10B"
/clone_lib="GLGC-LIB0001-cf Canis familiaris Normalized
Mixed Tissue cDNA Library"
/note="Organ: heart, liver, kidney, testis, and brain;
Vector: pCMVSPORT6.0; Site_1: NotI; Site_2: SalI"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTGGCCCG 9
|||||||
Db 9 CTGGCCCG 2

RESULT 2
AJ679435
LOCUS AJ679435 11 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ679435 CSEQRAN04 Sus scrofa cDNA clone C0001779_B18, mRNA
sequence.

ACCESSION AJ679435 GI:49412022
VERSION AJ679435
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 11)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle

JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.

FEATURES
source
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001779_B18"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 CGCGCTGTGGC 21
|||||||
Db 1 CCCGCGGTGGC 11


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RESULT 3
AJ681247
LOCUS
DEFINITION
AJ681247 CSEQRAN04 Sus scrofa cDNA clone C0001795_I24, mRNA
sequence.
AJ681247
VERSION
AJ681247.1 GI:49413837
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
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Location/Qualifiers
1..11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001795_I24"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
| | | | |
Db 1 CCCGCGGTGGC 11

RESULT 4
AJ683713
LOCUS
DEFINITION
AJ683713 CSEQRAN04 Sus scrofa cDNA clone C0001802_O06, mRNA
sequence.
AJ683713
VERSION
AJ683713.1 GI:49416303
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
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v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
source
Location/Qualifiers
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001802_O06"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
| | | | |
Db 1 CCCGCGGTGGC 11

RESULT 5
AJ686459
LOCUS
DEFINITION
AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811_K23, mRNA
sequence.
AJ686459
VERSION
AJ686459.1 GI:49419049
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
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Location/Qualifiers
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001811_K23"
/tissue_type="uterus"
/clone_lib="CSEQRAN04"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
| | | | |
Db 1 CCCGCGGTGGC 21

RESULT 6
AJ686459
LOCUS
DEFINITION
AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811_K23, mRNA
sequence.
AJ686459
VERSION
AJ686459.1 GI:49419049
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 11)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
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Db 1 CCGCGGTGGC 11
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5009-0-15-E12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM396011
BM396011.1 GI:18196064
EST.
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."
FEATURES
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Db 2 CGCGGTGGC 10
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5009-0-5-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM398849
BM398849.1 GI:18198902
EST.
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
RESULT 6
BM396011
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Best Local Similarity 88.9%; Pred. No. 3.1;
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Tetrahymena thermophila cDNA, mRNA sequence.
BM398849
BM398849.1 GI:18198902
EST.
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
RESULT 7
BM398849
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Best Local Similarity 88.9%; Pred. No. 3.1;
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| ||| |||||
Db 2 CGCGGTGGC 10
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5009-0-5-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM398849
BM398849.1 GI:18198902
EST.
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 10)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
RESULT 8
AJ599908
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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source
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Db 2 CGCGGTGGC 10
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
496D12, genomic survey sequence.
AJ599908
AJ599908.1 GI:37949536
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1
Brunaud,V., Balzerue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
2 (bases 1 to 10)
Balzerue,S.
Direct Submission
Submitted (23-OCT-2003) Balzerue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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FEATURES
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 2 CGCGGTGGC 10
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
496D12, genomic survey sequence.
AJ599908
AJ599908.1 GI:37949536
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1
Brunaud,V., Balzerue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
2 (bases 1 to 10)
Balzerue,S.
Direct Submission
Submitted (23-OCT-2003) Balzerue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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left border"
misc_feature
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGCCCGG 10
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Db 4 GGCCCGG 10

Search completed: May 10, 2006, 10:42:48
Job time : 0.001 secs



GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 10, 2006, 10:45:14 ; Search time 0.001 Seconds
(without alignments)
44.394 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336
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Sequence: 1 gctggcccggcgctgtggc 21
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5
Searched: 100 seqs, 1057 residues
Total number of hits satisfying chosen parameters: 200

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 110 summaries
Database : issdb1:*

Issued - Patents - NA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	14.4	68.6	20	1	US-09-364-416-40
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C 4	10.8	51.4	15	1	US-08-861-096A-42
C 5	9.8	46.7	14	1	US-08-964-877-7
C 6	9.4	44.8	12	1	US-09-724-028A-20
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8	9.4	44.8	13	1	US-09-476-387-161
9	9.2	43.8	15	1	US-07-626-923A-11
10	9	42.9	10	1	US-09-875-453B-199
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C 12	8.8	41.9	12	1	US-10-053-526B-9
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C 16	8.4	40.0	12	1	US-09-949-041A-50
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C 18	8	38.1	10	1	US-09-720-201A-24
C 19	8	38.1	10	1	US-09-613-298-4
C 20	8	38.1	10	1	US-09-875-453B-200
C 21	8	38.1	10	1	PCT-US95-04971-4
22	8	38.1	11	1	US-09-249-155A-6
23	8	38.1	11	1	US-09-249-155A-170
24	8	38.1	11	1	US-09-249-155A-305
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C 37	7.4	35.2	10	1	US-08-388-353-387	Sequence 387, App
C 38	7.4	35.2	10	1	US-08-488-551B-386	Sequence 386, App
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42	7.4	35.2	10	1	US-08-358-928-43	Sequence 43, Appl
43	7.4	35.2	10	1	US-08-899-241-240	Sequence 240, App
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62	7.2	34.3	20	1	US-09-364-416-40	Sequence 40, Appl
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C 66	7	33.3	10	1	US-08-171-718-36	Sequence 36, Appl
67	7	33.3	10	1	US-08-477-396A-12	Sequence 12, Appl
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83	7	33.3	10	1	US-08-488-551B-581	Sequence 581, App
84	7	33.3	10	1	US-08-488-551B-582	Sequence 582, App
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C 87	7	33.3	10	1	US-08-765-257A-30	Sequence 30, Appl
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93	7	33.3	10	1	US-09-535-754-6	Sequence 6, Appli
C 94	7	33.3	10	1	US-09-336-946B-13	Sequence 13, Appl
C 95	7	33.3	10	1	US-09-508-753B-72	Sequence 72, Appl
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C 97	7	33.3	10	1	US-10-042-111-23	Sequence 23, Appl
C 98	7	33.3	10	1	US-09-769-482-54	Sequence 54, Appl
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101	7	33.3	10	1	US-10-087-426-6	Sequence 6, Appli
102	7	33.3	10	1	US-09-498-557-10	Sequence 10, Appl
103	7	33.3	10	1	US-09-885-551A-6	Sequence 6, Appli
104	7	33.3	10	1	US-09-875-453B-197	Sequence 197, App
C 105	7	33.3	10	1	US-09-875-453B-203	Sequence 203, App
C 106	7	33.3	10	1	US-09-479-608A-29	Sequence 29, Appl

c 107 7 33.3 10 1 US-09-479-608A-30 Sequence 30, Appl
c 108 7 33.3 10 1 US-09-479-608A-31 Sequence 31, Appl
c 109 7 33.3 10 1 US-09-479-608A-32 Sequence 32, Appl
110 7 33.3 10 1 US-10-029-221C-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-837-201C-40/c
; Sequence 40, Application US/08837201C
; Patent No. 5985558
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201C
; FILING DATE: April 14, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-837-201C-40

Query Match 68.6%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 4.7;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCTGTGC 21
| | | | | | | | | | | | | | | | | |
Db 16 CCCGGCGCGCTGTGC 1

RESULT 2
US-09-364-416-40/c
; Sequence 40, Application US/09364416
; Patent No. 6312900
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of

; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,416
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201
; FILING DATE: April 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-364-416-40

Query Match 68.6%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 4.7;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCTGTGC 21
| | | | | | | | | | | | | | | | | |
Db 16 CCCGGCGCGCTGTGC 1

RESULT 3
US-07-626-923A-11/c
; Sequence 11, Application US/07626923A
; GENERAL INFORMATION:
; APPLICANT: Yoshimura, Akihiko
; APPLICANT: Longmore, Gregory D.
; APPLICANT: Lodish, Harvey
; TITLE OF INVENTION: MUTANT EPO RECEPTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/626,923A
; FILING DATE: 13 December 1990
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI90-08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; OTHER INFORMATION: /product= "Internal portion of
; OTHER INFORMATION: wild-type murine EPOR"
US-07-626-923A-11

Query Match 52.4%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGCGCGC 15
Db 14 GCCCGGCGCGC 4

RESULT 4
US-08-861-096A-42/c
; Sequence 42, Application US/08861096A
; Patent No. 5958689
; GENERAL INFORMATION:
; APPLICANT: Scholin, Christopher A.
; APPLICANT: Cangelosi, Gerard A.
; APPLICANT: Haydock, Paul V.
; TITLE OF INVENTION: Detection of Toxigenic Marine Diatoms of
; TITLE OF INVENTION: the Genus Pseudo-nitzschia
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,096A
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/018,143
; FILING DATE: 22-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 017748-000110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
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```

US-08-861-096A-42

Query Match 51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CCGGCGCGCTGTGG 20
Db 15 CCTGGGCGCTGTGG 2

RESULT 5
US-08-964-877-7/c
; Sequence 7, Application US/08964877
; Patent No. 6204026
; GENERAL INFORMATION:
; APPLICANT: DesJardins et al.
; TITLE OF INVENTION: Detection of M. tuberculosis Complex via
; TITLE OF INVENTION: Reverse Transcriptase SDA
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,877
; FILING DATE: 05 NOV 97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D6006.B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 777-2321
; TELEFAX: (713) 777-6908
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bp
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; US-08-964-877-7

Query Match 46.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CGGCGCGCTGTGG 20
Db 14 CGGCTCGCTGTGC 2

RESULT 6
```

US-09-724-028A-20/c
; Sequence 20, Application US/09724028A
; Patent No. 6777180
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; TITLE OF INVENTION: METHOD FOR FULL-LENGTH CDNA CLONING
; TITLE OF INVENTION: USING DEGENERATE STEM LOOP ANNEALING PRIMERS
; FILE REFERENCE: A34701 (070050.1728)
; CURRENT APPLICATION NUMBER: US/09/724,028A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the 5' end of the C-ORF product of
; Patent No. 6777180
; OTHER INFORMATION: mda-5
US-09-724-028A-20

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGCGCGGC 15
| |||||
Db 11 GGCCGCGCGGC 1

RESULT 7
US-09-474-432B-161
; Sequence 161, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 161
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-161

Query Match 44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGGC 11
| | | | |
Db 3 GCUGGCUCCGC 13

RESULT 8
US-09-476-387-161
; Sequence 161, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MBHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 161
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-161

Query Match 44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 23;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGGC 11
| | | | |
Db 3 GCUGGCUCCGC 13

RESULT 9
US-07-626-923A-11
; Sequence 11, Application US/07626923A
; GENERAL INFORMATION:
; APPLICANT: Yoshimura, Akihiko
; APPLICANT: Longmore, Gregory D.
; APPLICANT: Lodish, Harvey
; TITLE OF INVENTION: MUTANT EPO RECEPTOR AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/626,923A
; FILING DATE: 13 December 1990
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: WHI90-08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
; OTHER INFORMATION: /product= "Internal portion of
; OTHER INFORMATION: wild-type murine EPOR"
US-07-626-923A-11

Query Match 43.8%; Score 9.2; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 39;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGCGC 15
||||| |||||
Db 1 CTGGCGCGCGCGGC 14

RESULT 10

US-09-875-453B-199
; Sequence 199, Application US/09875453B
; Patent No. 6838556

GENERAL INFORMATION:

; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875.453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-199

Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
||||| |||||
Db 1 GGCGCGCTG 9

RESULT 11

US-09-875-453B-145/c
; Sequence 145, Application US/09875453B
; Patent No. 6838556

; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875.453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-145

Query Match 42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCGCGCTGT 18
||||| |||||
Db 9 GCGCGCTGT 1

RESULT 12

US-10-053-526B-9/c
; Sequence 9, Application US/10053526B
; Patent No. 6936418

GENERAL INFORMATION:

; APPLICANT: Dutreix, Marie
; APPLICANT: Sun, Jian-Sheng
; APPLICANT: Biet, Elodie
; APPLICANT: Maurisse, Rosalie
; APPLICANT: Feugeas, Jean-Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EFFECTING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 03754/000K213-USO
; CURRENT APPLICATION NUMBER: US/10/053.526B
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/IB01/00749
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: EP 00401218.3
; PRIOR FILING DATE: 2000-03-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-053-526B-9

Query Match 41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGC 12
||||| |||||
Db 12 GCTGGCCACGCG 1


```
RESULT 13
US-10-053-526B-15/c
; Sequence 15, Application US/10053526B
; Patent No. 6936418
; GENERAL INFORMATION:
; APPLICANT: Dutreix, Marie
; APPLICANT: Sun, Jian-Sheng
; APPLICANT: Biet, Elodie
; APPLICANT: Maurisse, Rosalie
; APPLICANT: Feugeas, Jean-Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EFFECTING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 03754/000K213-US0
; CURRENT APPLICATION NUMBER: US/10/053,526B
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/IB01/00749
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: EP 00401218.3
; PRIOR FILING DATE: 2000-03-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-053-526B-15

Query Match          41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGGCG 12
Db 12 GCTGGCCACGCG 1

RESULT 14
US-08-441-887A-183
; Sequence 183, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-183

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGCCCGGCGC 13
Db 1 GGCCCGGAGC 10

RESULT 15
US-09-875-453B-195/c
; Sequence 195, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-195

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCCGGCGCGC 15
Db 10 CCGGCGCGC 1
```


;
; FILING DATE: 10-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Oligomer DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-613-298-4

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CGGCGCGC 15
|||
Db 10 CGGCGCGC 3

RESULT 20

US-09-875-453B-200/c
; Sequence 200, Application US/09875453B
; Patent No. 6838556

GENERAL INFORMATION:

; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: mutated sequence

US-09-875-453B-200

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCGCGCTG 17
|||
Db 9 GCGCGCTG 2

RESULT 21

PCT-US95-04971-4/c

; Sequence 4, Application PC/TUS9504971
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A Novel VZV Gene, Mutant VZV and Immunogenic
; TITLE OF INVENTION: Compositions
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04971
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,406
; FILING DATE: APRIL 28, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Oligomer DNA
; PCT-US95-04971-4

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CGGCGCGC 15
|||
Db 10 CGGCGCGC 3

RESULT 22

US-09-249-155A-6

; Sequence 6, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-6

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
| | | | |
Db 1 GCTGGCCC 8

RESULT 23

US-09-249-155A-170
; Sequence 170, Application US/09249155A
; Patent No. 6538173

GENERAL INFORMATION:

; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus

US-09-249-155A-170

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
| | | | |
Db 1 GCTGGCCC 8

RESULT 24

US-09-249-155A-305
; Sequence 305, Application US/09249155A
; Patent No. 6538173

GENERAL INFORMATION:

; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus

US-09-249-155A-305

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
| | | | |
Db 1 GCTGTGGC 8

RESULT 25

US-09-984-292-42/c
; Sequence 42, Application US/09984292
; Patent No. 6818747

GENERAL INFORMATION:

; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide

US-09-984-292-42

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCGCGC 15
| | | | |
Db 9 CGGCGCGC 2

RESULT 26

US-09-040-025-51
; Sequence 51, Application US/09040025
; Patent No. 6117637

GENERAL INFORMATION:

; APPLICANT: Borchert, Torben
; APPLICANT: Kretzschmar, Titus
; APPLICANT: Cherry, Joel
; TITLE OF INVENTION: Shuffling of Heterologous DNA Sequences
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117637o No. 6117637disk of No. 6117637th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,025
; FILING DATE: 17-MAR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A


```

;
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5113.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-040-025-51
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCCGGCGCGCT 16
Db 1 CCCGACGCGTT 11

RESULT 27
US-09-040-025-51
; Sequence 51, Application US/09040025
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben
; Kretzschmar, Titus
; Cherry, Joel
; TITLE OF INVENTION: Shuffling of Heterologous DNA Sequences
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10017
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,025
; FILING DATE: 17-Mar-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta A
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 5113.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
;
US-09-040-025-51
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCCGGCGCGCT 16
Db 1 CCCGACGCGTT 11
```

```

RESULT 28
US-09-291-129-16/c
; Sequence 16, Application US/09291129
; Patent No. 6468742
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Canter, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; TITLE OF INVENTION: BIOELECTRIC MICROCHIP
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/09/291,129
; CURRENT FILING DATE: 1999-04-12
; EARLIER APPLICATION NUMBER: US 09/030,156
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: US 08/986,065
; EARLIER FILING DATE: 1997-12-05
; EARLIER APPLICATION NUMBER: US 08/859,644
; EARLIER FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US 08/725,976
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: US 08/708,262
; EARLIER FILING DATE: 1996-09-06
; EARLIER APPLICATION NUMBER: US 08/534,454
; EARLIER FILING DATE: 1995-09-27
; EARLIER APPLICATION NUMBER: US 08/304,657
; EARLIER FILING DATE: 1994-09-09
; EARLIER APPLICATION NUMBER: US 08/271,882
; EARLIER FILING DATE: 1994-07-07
; EARLIER APPLICATION NUMBER: US 08/146,504
; EARLIER FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
;
US-09-291-129-16
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTGGCCCGCGC 12
Db 11 CTGGACAGGCG 1

RESULT 29
US-08-857-534-4
; Sequence 4, Application US/08857534
; Patent No. 6087170
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A No. 6087170el VZV Gene, Mutant VZV and Immunogenic
; TITLE OF INVENTION: Compositions
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,534
```

```

;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/235,406
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Oligomer DNA
; US-08-857-534-4

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 GGCGCGCTG 17
        |||||
Db      2 GGCGCGCCG 10

RESULT 30
US-09-613-298-4
; Sequence 4, Application US/09613298
; Patent No. 6713296
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A No. 6713296el VZV Gene, Mutant VZV and Immunogenic
;
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/613,298
; FILING DATE: 10-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown

```

```

;
; MOLECULE TYPE: Oligomer DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-613-298-4

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 GGCGCGCTG 17
        |||||
Db      2 GGCGCGCCG 10

RESULT 31
PCT-US95-04971-4
; Sequence 4, Application PC/TUS9504971
; GENERAL INFORMATION:
; APPLICANT: George W. Kemble
; TITLE OF INVENTION: A Novel VZV Gene, Mutant VZV and Immunogenic
; TITLE OF INVENTION: Compositions
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04971
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,406
; FILING DATE: APRIL 28, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-004/00WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Oligomer DNA
; PCT-US95-04971-4

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 GGCGCGCTG 17
        |||||
Db      2 GGCGCGCCG 10

RESULT 32
US-08-753-829A-4/c
; Sequence 4, Application US/08753829A
; Patent No. 5869250
; GENERAL INFORMATION:
; APPLICANT: Juliano, Rudolph L.
; APPLICANT: Cheng, Xiaojun

```

```

; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: PEPTIDES THAT RECOGNIZE SPECIFIC DNA SEQUENCES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: No. 5869250th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,829A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-134
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-520-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-753-829A-4

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGCCGCGC 12
Db 9 GCGCCGCGC 1

RESULT 33
US-08-734-973-10/c
; Sequence 10, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 15 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
;
US-08-734-973-15

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGT 18
Db 2 GCGCGCGGT 10
```

```

; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 10 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
;
US-08-734-973-10

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGCGCGC 15
Db 10 CCGCGCGC 2

RESULT 34
US-08-734-973-15
; Sequence 15, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 15 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
;
US-08-734-973-15

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGT 18
Db 2 GCGCGCGGT 10
```

RESULT 35
US-08-734-973-16
; Sequence 16, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 16 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
US-08-734-973-16

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 77.8%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGT 18
|||||:
Db 2 GCGCGCGGU 10

RESULT 36
US-08-388-353-386/c
; Sequence 386, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 386:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-386

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
|||||:
Db 10 CTGGCCCTG 2

RESULT 37
US-08-388-353-387/c
; Sequence 387, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 387:
; SEQUENCE CHARACTERISTICS:


```

; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-387

Query Match          35.2%;      Score 7.4;  DB 1;  Length 10;
Best Local Similarity 88.9%;      Pred. No. 33;
Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

RESULT 38
US-08-488-551B-386/C
; Sequence 386, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 386:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-386

```

```

Db          10 CTGGCCCTG 2

RESULT 39
US-08-488-551B-387/c
; Sequence 387, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 387:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-387

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels

QY      2 CTGGCCCGG 10
        |||||
Db      9 CTGGCCCTG 1

RESULT 40
US-08-651-472-43
; Sequence 43, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC

```

RESULT 40
US-08-651-472-43
; Sequence 43, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC

;; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
;; TITLE OF INVENTION: (HIV-1) ANTIGENS
;; NUMBER OF SEQUENCES: 95
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/651,472
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/914,738
;; FILING DATE: 20-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/750,080
;; FILING DATE: 26-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Other nucleic acid;
;; DESCRIPTION: Synthetic DNA oligonucleotide
US-08-651-472-43

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCCG 10
|||
Db 1 CTAGCCCCG 9

RESULT 41
US-08-522-384-42
; Sequence 42, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-42

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCCG 10
|||
Db 1 CTGGCCCTG 9

RESULT 42
US-08-358-928-43
; Sequence 43, Application US/08358928
; Patent No. 6265183
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: PFLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; TITLE OF INVENTION: (HIV-1) ANTIGENS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,928
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
US-08-358-928-43

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCCG 10
|||
Db 1 CTAGCCCCG 9

RESULT 43

```
US-08-899-241-240
; Sequence 240, Application US/08899241A
; Patent No. 6322995
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Huembelin, Markus
; APPLICANT: van Loon, Adolphus
; APPLICANT: Schurter, Walter
; TITLE OF INVENTION: Improved Riboflavin Production
; FILE REFERENCE: Improved Riboflavin Prod
; CURRENT APPLICATION NUMBER: US/08/899,241A
; CURRENT FILING DATE: 1997-07-23
; EARLIER APPLICATION NUMBER: 96111905.4
; EARLIER FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ac# J01749
US-08-899-241-240

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      6 CCCGCGCGC 14
      ||| |||||
Db      1 CCCAGCGCG 9

RESULT 44
US-08-899-241-240/c
; Sequence 240, Application US/08899241A
; Patent No. 6322995
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Huembelin, Markus
; APPLICANT: van Loon, Adolphus
; APPLICANT: Schurter, Walter
; TITLE OF INVENTION: Improved Riboflavin Production
; FILE REFERENCE: Improved Riboflavin Prod
; CURRENT APPLICATION NUMBER: US/08/899,241A
; CURRENT FILING DATE: 1997-07-23
; EARLIER APPLICATION NUMBER: 96111905.4
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Ac# J01749
US-08-899-241-240

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      6 CCCGCGCGC 14
      ||| |||||
Db      1 CCCAGCGCG 9

US-08-899-241-240/c
; Sequence 12, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      5 GCCCGCGCG 13
      ||||| |||
Db      2 GCCCGCGCG 10

RESULT 46
US-09-154-750A-12/c
; Sequence 12, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      8 CGGCGCGCT 16
      ||||| |||
Db      9 CGGCGGGCT 1

RESULT 47
US-09-475-947A-36/c
; Sequence 36, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: human
US-09-475-947A-36

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCCCGGCGC 13
Db      9 GCCCGGCCC 1

RESULT 48
US-09-475-947A-159/c
; Sequence 159, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-159

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCCCGGCGC 13
Db      9 GCCCGGCCC 1

RESULT 49
US-09-537-186-5/c
; Sequence 5, Application US/09537186
; Patent No. 6534696
; GENERAL INFORMATION:
; APPLICANT: COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
; TITLE OF INVENTION: A disease resistant high yielding variety Papaver somniferum call
; TITLE OF INVENTION: Rakshit
; FILE REFERENCE: Q58615
; CURRENT APPLICATION NUMBER: US/09/537,186
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: : Primer for generating random
; OTHER INFORMATION: m amplified polymorphic DNA profile of claimed plant
US-09-537-186-5

Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 CCGGCGCGC 15
Db      9 CCGGCGTGC 1

RESULT 50
US-09-537-186-5
```

```
US-09-538-456-3/c
; Sequence 3, Application US/09538456
; Patent No. 6558940
; GENERAL INFORMATION:
; APPLICANT: Alam, Mansoor
; APPLICANT: Sattar, Abdul
; APPLICANT: Kumar, Sushil
; APPLICANT: Samad, Abdul
; APPLICANT: Dhawan, Om Prakash
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Singh, Seema
; APPLICANT: Kumar, Poovappallivadakethil Viswanathan Nair Ajay
; APPLICANT: Khaliq, Abdul
; APPLICANT: Zaim, Mohammad
; APPLICANT: Shahabuddin, Saba
; APPLICANT: Trivedi, Mala
; TITLE OF INVENTION: A novel Streptomyces strain with potential anti-microbial
; TITLE OF INVENTION: activity against phytopathogenic fungi
; FILE REFERENCE: 148920.00003
; CURRENT APPLICATION NUMBER: US/09/538,456
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Word-97
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-538-456-3
```

```
Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 CCGGCGCGC 15
Db      9 CCGGCGTGC 1
```

```
RESULT 51
US-09-769-482-63/c
; Sequence 63, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-63
```

```
Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



```
QY      3 TGGCCCGGC 11
      |||||
Db     10 TGGCCCGGC 2
      |||||

RESULT 52
US-09-875-453B-194
; Sequence 194, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-194

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      9 GCGCGCGCTG 17
      |||||
Db     1 GCGCGCGCG 9
      |||||

RESULT 53
US-09-875-453B-204
; Sequence 204, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-204

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
; SEQ ID NO 204
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-204

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      8 CCGCGCGCT 16
      |||||
Db     2 CCGCGCGCT 10
      |||||

RESULT 54
US-09-875-453B-207/c
; Sequence 207, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-207

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY     10 GCGCGCTGT 18
      |||||
Db      9 GCGCGCTTT 1
      |||||

RESULT 55
US-09-263-790-6/c
; Sequence 6, Application US/09263790
; Patent No. PP12997
; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
```

; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAP 06 Primer - Primer used in RAPD analysis comparing Jal Pallav
; OTHER INFORMATION: with Jorlab-2, Manjusha, Mandakini, Bio-13, and Ceylon.
US-09-263-790-6

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
|||||
Db 9 CCGGCGTGC 1

RESULT 56

US-09-538-341-4/c
; Sequence 4, Application US/09538341
; Patent No. PPI3110
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Bahl, Janak Faj
; APPLICANT: Bansal, Ravi Prakash
; APPLICANT: Niwas, Shri
; APPLICANT: Naqvi, Arif Ali
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Singh, Vikram
; APPLICANT: Sinha, Shweta

; TITLE OF INVENTION: Lippia alba plant named 'Bhurakshak'

; FILE REFERENCE: U-012701-4

; CURRENT APPLICATION NUMBER: US/09/538,341

; CURRENT FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 13

; SEQ ID NO 4

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer for generating random amplified polymorphic DNA profile of
; OTHER INFORMATION: plant

US-09-538-341-4

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
|||||
Db 9 CCGGCGTGC 1

RESULT 57

US-09-785-716A-6/c
; Sequence 6, Application US/09785716A
; Patent No. PPI4090
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Singh, Maneesha
; APPLICANT: Singh, Ajay Pratap
; APPLICANT: Singh, Vandana
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Kuman, Sushil

; TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'

; FILE REFERENCE: 41799/VGG/K375

; CURRENT APPLICATION NUMBER: US/09/785,716A

; CURRENT FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for RAPD profile
US-09-785-716A-6

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
|||||
Db 9 CCGGCGTGC 1

RESULT 58

US-09-799-880-6/c
; Sequence 6, Application US/09799880
; Patent No. PPI4400
; GENERAL INFORMATION:

; APPLICANT: Kumar, Sushil
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastri, Kakaraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
; APPLICANT: Shasany, Ajit
; APPLICANT: Darokar, Mahendra
; APPLICANT: Khanuja, Suman

; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAFAI'

; FILE REFERENCE: 2734-102

; CURRENT APPLICATION NUMBER: US/09/799,880

; CURRENT FILING DATE: 2001-03-07

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-09-799-880-6

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
|||||
Db 9 CCGGCGTGC 1

RESULT 59

US-09-482-645A-6/c
; Sequence 6, Application US/09482645A
; Patent No. PPI4538
; GENERAL INFORMATION:
; APPLICANT: KHANUJA, Suman Preet Singh
; APPLICANT: SHASANY, Ajit Kumar
; APPLICANT: DHAWAN, Sunita
; APPLICANT: DAROKAR, Mahendra Pandurang
; APPLICANT: SATAPATHY, Sarita
; APPLICANT: KUMAR, Tiruppadiripuliyur Ranganathan Santha
; APPLICANT: SAIKIA, Dharmendra
; APPLICANT: PATRA, Nirmal Kumar
; APPLICANT: BAHL, Janak Raj
; APPLICANT: TRIPATHY, Arun Kumar
; TITLE OF INVENTION: Mint Plant Named ?Sambhav?
; FILE REFERENCE: U 012566-4
; CURRENT APPLICATION NUMBER: US/09/482,645A
; CURRENT FILING DATE: 2000-01-18


```
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
;   ANTI-SENSE: Yes
US-09-364-416-40

Query Match      34.3%; Score 7.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      8 CCGCGCGCTGTG 19
Db      5 CAGCGCGCCGGG 16

RESULT 63
US-07-627-538-5/c
; Sequence 5, Application US/07627538
; Patent No. 5248600
; GENERAL INFORMATION:
; APPLICANT: Topal, Michael D.
; APPLICANT: Conrad, Michael
; TITLE OF INVENTION: Method of Cleaving DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5248600th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/627,538
; FILING DATE: 19901214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5052-24
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 base pairs
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-07-627-538-5

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CCGCGCGC 13
Db      7 CCGCGCGC 1

RESULT 64
US-08-128-369-5/c
; Sequence 5, Application US/08128369
; Patent No. 5418150
; GENERAL INFORMATION:
; APPLICANT: Topal, Michael D.
; APPLICANT: Conrad, Michael J.
; TITLE OF INVENTION: METHOD OF CLEAVING DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
; ADDRESSEE: Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 5418150th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/128,369
; FILING DATE: 21-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-128-369-5

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CCGCGCGC 13
Db      7 CCGCGCGC 1

RESULT 65
US-08-170-290A-1/c
; Sequence 1, Application US/08170290A
; Patent No. 5702931
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Morser, Michael J.
; APPLICANT: Zielander, Laura R.
; TITLE OF INVENTION: No. 5702931el Mutagenesis Methods and
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James M. Heslin
; STREET: 379 Lytton Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```


;; APPLICATION NUMBER: US/08/170,290A
;; FILING DATE: 28-DEC-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA: PCT/US92/05573
;; FILING DATE: 01-JUL-1992
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/724,237
;; FILING DATE: 01-JUL-1991
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Heslin, James M.
;; REGISTRATION NUMBER: 29,541
;; REFERENCE/DOCKET NUMBER: 11972-58-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-170-290A-1

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCGCGGC 15
|||||
Db 9 GCGCGGC 3

RESULT 66
US-08-171-718-36/c
; Sequence 36, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:

;; NAME: Brown, Anne
;; REGISTRATION NUMBER: 36,463
;; REFERENCE/DOCKET NUMBER: 0609.3850003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-171-718-36

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
|||||
Db 10 CTGTGGC 4

RESULT 67
US-08-477-396A-12
; Sequence 12, Application US/08477396A
; Patent No. 5872235
; GENERAL INFORMATION:
; APPLICANT: Chen, Lan Bo
; APPLICANT: Bao, Shideng
; APPLICANT: Liu, Yuan
; TITLE OF INVENTION: A NOVEL TUMOR MARKER AND NOVEL METHOD OF
; TITLE OF INVENTION: ISOLATING SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,396A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,488
; FILING DATE: 29-OCT-1993
; APPLICATION NUMBER: US 08/448,388
; FILING DATE: 28-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12502
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-333BX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO

ANTI-SENSE: NO
US-08-477-396A-12

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCCCGC 11
Db 2 GCCCGC 8

RESULT 68
US-08-734-973-19/c
; Sequence 19, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 19 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
US-08-734-973-19

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCGGC 15
Db 10 GGCGGC 4

RESULT 69
US-08-734-973-20
; Sequence 20, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating

; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 20 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
US-08-734-973-20

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCGCGCT 16
Db 4 GCGCGCT 10

RESULT 70
US-08-734-973-21
; Sequence 21, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021

TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 21 :
SEQUENCE CHARACTERISTICS:
LENGTH: 10 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No
US-08-734-973-21

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCGCGCT 16
| | | | |
Db 4 GCGGCGU 10

RESULT 71
US-08-265-484B-6
; Sequence 6, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-265-484B-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
| : | : | : |
Db 4 CUGUGGC 10

RESULT 72
US-08-265-484B-30/c
; Sequence 30, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-265-484B-30

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
| | | | |
Db 8 GCTGGCC 2

RESULT 73
US-08-388-353-388/c
; Sequence 388, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States

ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 388:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-388

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCC 8
Db 8 CTGGCCC 2

RESULT 74
US-08-388-353-389/c
Sequence 389, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 389:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-389
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCC 8
Db 7 CTGGCCC 1

RESULT 75
US-08-388-353-579
Sequence 579, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 579:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-579

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGCCCG 9
Db 4 TGGCCCG 10

RESULT 76
US-08-388-353-580


```
; Sequence 580, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-580

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TGGCCCCG 9
Db 3 TGGCCCCG 9

RESULT 77
US-08-388-353-581
; Sequence 581, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 581:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-581

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TGGCCCCG 9
Db 2 TGGCCCCG 8

RESULT 78
US-08-388-353-582
; Sequence 582, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-582

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCCCG 9
| | | | |
Db 1 TGGCCCG 7

RESULT 79

US-08-488-551B-388/c
; Sequence 388, Application US/08488551B
; Patent No. 6015661

; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366

; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-488-551B-388

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTGGCCC 8
| | | | |
Db 8 CTGGCCC 2

RESULT 80

US-08-488-551B-389/c
; Sequence 389, Application US/08488551B
; Patent No. 6015661

; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366

; INFORMATION FOR SEQ ID NO: 389:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

US-08-488-551B-389

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTGGCCC 8
| | | | |
Db 7 CTGGCCC 1

RESULT 81

US-08-488-551B-579
; Sequence 579, Application US/08488551B
; Patent No. 6015661

; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

```

; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 579:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-579

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGCCCG 9
Db 4 TGGCCCG 10

RESULT 82
US-08-488-551B-580
; Sequence 580, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-580

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGGCCCG 9
Db 3 TGGCCCG 9

RESULT 83
US-08-488-551B-581
; Sequence 581, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
```

REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 581:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-581

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCCCG 9
Db 2 TGGCCCG 8

RESULT 84

US-08-488-551B-582
Sequence 582, Application US/08488551B
Patent No. 6015661

GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGILIO
REFERENCE/DOCKET NUMBER: 9606Z

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366

INFORMATION FOR SEQ ID NO: 582:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-488-551B-582

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCCCG 9
Db 1 TGGCCCG 7

RESULT 85

US-08-478-087-36/c
Sequence 36, Application US/08478087
Patent No. 6077685

GENERAL INFORMATION:
APPLICANT: Trofatter, James A.
APPLICANT: MacCollin, Mia M.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,087
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,718
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:

NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 0609.3850003
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-087-36

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
Db 10 CTGTGGC 4

RESULT 86

US-08-765-257A-6


```
; Sequence 6, Application US/08765257A
; Patent No. 6107078
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes
; TITLE OF INVENTION: and Compositions Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH, 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,257A
; FILING DATE: June 24, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 977 9550
; TELEFAX: 212 977 9809
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-765-257A-6

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
Db      4 CUGUGGC 10

RESULT 87
US-08-765-257A-30/c
; Sequence 30, Application US/08765257A
; Patent No. 6107078
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes
; TITLE OF INVENTION: and Compositions Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH, 1.44Mb
; COMPUTER: IBM PC
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,257A
; FILING DATE: June 24, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 977 9550
; TELEFAX: 212 977 9809
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-765-257A-30

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCC 7
Db      8 GCTGGCC 2

RESULT 88
US-08-522-384-26
; Sequence 26, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
; US-08-522-384-26

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCC 7
Db      4 GCTGGCC 10

RESULT 89
US-08-522-384-48
; Sequence 48, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
```

; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-48

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
| | | | |
Db 4 GCTGTGG 10

RESULT 90
US-08-522-384-71
; Sequence 71, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-71

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
| | | | |
Db 1 GCTGGCC 7

RESULT 91
US-09-307-924-10
; Sequence 10, Application US/09307924
; Patent No. 6303308
; GENERAL INFORMATION:
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: CLONING VECTORS AND THEIR PREPARATION
; TITLE OF INVENTION: AND USE FOR mRNA EXPRESSION PATTERN ANALYSIS
; FILE REFERENCE: 50125/002001
; CURRENT APPLICATION NUMBER: US/09/307,924
; CURRENT FILING DATE: 1999-05-10
; EARLIER APPLICATION NUMBER: DE 19822287.4
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: DNA linker
US-09-307-924-10
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GGCGCGC 15
| | | | |
Db 2 GGCGCGC 8

RESULT 92
US-09-307-924-10/c
; Sequence 10, Application US/09307924
; Patent No. 6303308
; GENERAL INFORMATION:
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: CLONING VECTORS AND THEIR PREPARATION
; TITLE OF INVENTION: AND USE FOR mRNA EXPRESSION PATTERN ANALYSIS
; FILE REFERENCE: 50125/002001
; CURRENT APPLICATION NUMBER: US/09/307,924
; CURRENT FILING DATE: 1999-05-10
; EARLIER APPLICATION NUMBER: DE 19822287.4
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA linker
US-09-307-924-10

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
| | | | |
Db 9 GGCGCGC 3

RESULT 93
US-09-535-754-6
; Sequence 6, Application US/09535754
; Patent No. 6361974
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/535,754
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-535-754-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
| | | | |
Db 1 CGCGCTG 7

RESULT 94
US-09-336-946B-13/c
; Sequence 13, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic oligonucleotide
US-09-336-946B-13

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGCTGT 18
| | | | |
Db 7 GCGCTGT 1

RESULT 95
US-09-508-753B-72/c
; Sequence 72, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 72
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-72

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
| | | | |
Db 10 GCTGTGG 4

RESULT 96
US-09-508-753B-404
; Sequence 404, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 404
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-404

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTG 19
| | | | |
Db 4 CGCTGTG 10

RESULT 97
US-10-042-111-23/c
; Sequence 23, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-23

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
| | | | |
Db 7 GCTGTGG 1

RESULT 98
US-09-769-482-54/c
; Sequence 54, Application US/09769482

; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-54

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
| | | | |
Db 7 GCTGGCC 1

RESULT 99

US-10-108-077-6
; Sequence 6, Application US/10108077
; Patent No. 6635449
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/108,077
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-108-077-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
| | | | |
Db 1 CGCGCTG 7

RESULT 100

US-09-867-262-5

; Sequence 5, Application US/09867262
; Patent No. 6696275
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-867-262-5

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
| | | | |
Db 1 CGCGCTG 7

RESULT 101

US-10-087-426-6
; Sequence 6, Application US/10087426
; Patent No. 6709841
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112


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; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-087-426-6

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 102
US-09-498-557-10
; Sequence 10, Application US/09498557
; Patent No. 6713279
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES AND ENZYMES
; FILE REFERENCE: DIVER1460-12
; CURRENT APPLICATION NUMBER: US/09/498,557
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/332,835
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-498-557-10

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 103
US-09-885-551A-6
; Sequence 6, Application US/09885551A
; Patent No. 6740506
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
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; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/885,551A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-885-551A-6

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 104
US-09-875-453B-197
; Sequence 197, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-197

Query Match          33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GCGCGCT 16
Db      1 GCGCGCT 7

RESULT 105
US-09-875-453B-203/c
; Sequence 203, Application US/09875453B
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Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-203

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCGCGCT 16
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Db 10 GCGCGCT 4

RESULT 106
US-09-479-608A-29/c
; Sequence 29, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-29

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
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Db 10 CTGTGGC 4

RESULT 107
US-09-479-608A-30/c
; Sequence 30, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-30

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
|||||||
Db 9 CTGTGGC 3

RESULT 108
US-09-479-608A-31/c
; Sequence 31, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-31

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
|||||||
Db 8 CTGTGGC 2

RESULT 109
US-09-479-608A-32/c

; Sequence 32, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-32

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
|||||||
Db 7 CTGTGGC 1

RESULT 110
US-10-029-221C-5
; Sequence 5, Application US/10029221C
; Patent No. 6939689
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; APPLICANT: DJAVAKHISHVILI, TSOTNE D.
; APPLICANT: FREY, GERHARD J.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-21
; CURRENT APPLICATION NUMBER: US/10/029,221C
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-029-221C-5

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
|||||||
Db 1 CGCGCTG 7

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:44:15 ; Search time 0.001 Seconds
(without alignments)
144.438 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336
Perfect score: 21
Sequence: 1 gctggccgcgcgtgtgac 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 324 seqs, 3439 residues

Total number of hits satisfying chosen parameters: 648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 356 summaries

Database : gedbl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	14.4	68.6	20	1	AR176785
C 3	12.4	59.0	16	1	CQ786323
C 4	11.4	54.3	16	1	CQ756662
C 5	10.8	51.4	15	1	AR075658
C 6	10.4	49.5	14	1	AX133710
C 7	10	47.6	11	1	AL3334
C 8	10	47.6	12	1	CQ766472
C 9	10	47.6	12	1	AX081331
C 10	9.8	46.7	14	1	AR142945
C 11	9.8	46.7	14	1	CS061169
C 12	9.4	44.8	11	1	CQ836510
C 13	9.4	44.8	11	1	AX628774
C 14	9.4	44.8	11	1	AX630120
C 15	9.4	44.8	11	1	AX630373
C 16	9.4	44.8	12	1	CQ766499
C 17	9.4	44.8	12	1	AR576634
C 18	9.4	44.8	13	1	AR285789
C 19	9.4	44.8	13	1	AR397780
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C 21	9	42.9	10	1	BD238832
C 22	9	42.9	10	1	AR630145
C 23	9	42.9	10	1	AX152988
C 24	9	42.9	10	1	AX153495
C 25	9	42.9	10	1	AX153496
C 26	9	42.9	11	1	CQ833102
C 27	9	42.9	11	1	AX630364
C 28	9	42.9	12	1	CS086764
C 29	9	42.9	12	1	AR630091
C 30	8.8	41.9	12	1	CQ766472
C 31	8.8	41.9	12	1	CQ766470
C 32	8.8	41.9	12	1	CQ983522
C 33	8.8	41.9	12	1	CQ983659

C 34	8.8	41.9	12	1	AX298228
C 35	8.8	41.9	12	1	S88396S1
C 36	8.4	40.0	10	1	AR058606
C 37	8.4	40.0	10	1	BD166545
C 38	8.4	40.0	10	1	BD225304
C 39	8.4	40.0	10	1	BD225338
C 40	8.4	40.0	10	1	BD238621
C 41	8.4	40.0	10	1	CQ986655
C 42	8.4	40.0	10	1	CS114173
C 43	8.4	40.0	10	1	E39738
C 44	8.4	40.0	10	1	E54818
C 45	8.4	40.0	10	1	E54824
C 46	8.4	40.0	10	1	AR630141
C 47	8.4	40.0	10	1	AX152803
C 48	8.4	40.0	10	1	AX224404
C 49	8.4	40.0	10	1	AX224407
C 50	8.4	40.0	10	1	AX301612
C 51	8.4	40.0	10	1	AX339231
C 52	8.4	40.0	10	1	AX753475
C 53	8.4	40.0	10	1	AX814774
C 54	8.4	40.0	11	1	CQ833458
C 55	8.4	40.0	11	1	CQ833790
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C 57	8.4	40.0	11	1	CQ835396
C 58	8.4	40.0	11	1	CQ835763
C 59	8.4	40.0	11	1	CQ837774
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C 61	8.4	40.0	11	1	CQ838018
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C 63	8.4	40.0	11	1	CS058293
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C 65	8.4	40.0	11	1	CS058633
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C 76	8.4	40.0	11	1	AX626754
C 77	8.4	40.0	11	1	AX628541
C 78	8.4	40.0	11	1	AX629212
C 79	8.4	40.0	11	1	AX629295
C 80	8.4	40.0	11	1	AX629700
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C 82	8.4	40.0	11	1	AX631029
C 83	8.4	40.0	12	1	CQ766406
C 84	8.4	40.0	12	1	CQ766468
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C 86	8.4	40.0	12	1	AR678905
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C 92	8	38.1	10	1	BD240458
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C 102	8	38.1	11	1	CQ838061
C 103	8	38.1	11	1	CS058186
C 104	8	38.1	11	1	AR301425
C 105	8	38.1	11	1	AR301589
C 106	8	38.1	11	1	AR301724

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108	8	38.1	11	1	AX471838	ACCESSION:AX471838
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C 110	8	38.1	11	1	AX623147	ACCESSION:AX623147
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C 127	7.8	37.1	11	1	BD250406	ACCESSION:BD250406
128	7.8	37.1	11	1	CQ833470	ACCESSION:CQ833470
C 129	7.8	37.1	11	1	CQ835073	ACCESSION:CQ835073
C 130	7.8	37.1	11	1	CQ835177	ACCESSION:CQ835177
131	7.8	37.1	11	1	CQ835213	ACCESSION:CQ835213
C 132	7.8	37.1	11	1	CQ837144	ACCESSION:CQ837144
C 133	7.8	37.1	11	1	CQ837783	ACCESSION:CQ837783
134	7.8	37.1	11	1	CS058279	ACCESSION:CS058279
135	7.8	37.1	11	1	AR238595	ACCESSION:AR238595
C 136	7.8	37.1	11	1	AX470499	ACCESSION:AX470499
C 137	7.8	37.1	11	1	AX470547	ACCESSION:AX470547
C 138	7.8	37.1	11	1	AX471002	ACCESSION:AX471002
139	7.8	37.1	11	1	AX471274	ACCESSION:AX471274
C 140	7.8	37.1	11	1	AX471596	ACCESSION:AX471596
C 141	7.8	37.1	11	1	AX622989	ACCESSION:AX622989
142	7.8	37.1	11	1	AX623485	ACCESSION:AX623485
C 143	7.8	37.1	11	1	AX623553	ACCESSION:AX623553
144	7.8	37.1	11	1	AX623825	ACCESSION:AX623825
145	7.8	37.1	11	1	AX623949	ACCESSION:AX623949
146	7.8	37.1	11	1	AX624226	ACCESSION:AX624226
C 147	7.8	37.1	11	1	AX624477	ACCESSION:AX624477
148	7.8	37.1	11	1	AX624700	ACCESSION:AX624700
C 149	7.8	37.1	11	1	AX625055	ACCESSION:AX625055
150	7.8	37.1	11	1	AX625310	ACCESSION:AX625310
C 151	7.8	37.1	11	1	AX626546	ACCESSION:AX626546
152	7.8	37.1	11	1	AX626575	ACCESSION:AX626575
C 153	7.8	37.1	11	1	AX626823	ACCESSION:AX626823
154	7.8	37.1	11	1	AX627065	ACCESSION:AX627065
C 155	7.8	37.1	11	1	AX627186	ACCESSION:AX627186
C 156	7.8	37.1	11	1	AX627348	ACCESSION:AX627348
157	7.8	37.1	11	1	AX627678	ACCESSION:AX627678
158	7.8	37.1	11	1	AX628416	ACCESSION:AX628416
159	7.8	37.1	11	1	AX628487	ACCESSION:AX628487
C 160	7.8	37.1	11	1	AX629263	ACCESSION:AX629263
161	7.8	37.1	11	1	AX629341	ACCESSION:AX629341
162	7.8	37.1	11	1	AX629452	ACCESSION:AX629452
C 163	7.8	37.1	11	1	AX629509	ACCESSION:AX629509
164	7.8	37.1	11	1	AX630130	ACCESSION:AX630130
C 165	7.8	37.1	11	1	AX630139	ACCESSION:AX630139
166	7.8	37.1	11	1	AX630178	ACCESSION:AX630178
C 167	7.8	37.1	11	1	AX630197	ACCESSION:AX630197
168	7.8	37.1	11	1	AX630410	ACCESSION:AX630410
C 169	7.8	37.1	11	1	AX630906	ACCESSION:AX630906
C 170	7.8	37.1	11	1	AX630974	ACCESSION:AX630974
171	7.8	37.1	11	1	AX631246	ACCESSION:AX631246
172	7.8	37.1	11	1	AX631370	ACCESSION:AX631370
173	7.8	37.1	11	1	AX631647	ACCESSION:AX631647
C 174	7.8	37.1	11	1	AX631898	ACCESSION:AX631898
175	7.8	37.1	11	1	AX632121	ACCESSION:AX632121
C 176	7.8	37.1	11	1	AX632476	ACCESSION:AX632476
177	7.8	37.1	11	1	AX632731	ACCESSION:AX632731
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183	7.4	35.2	10	1	AR071786	ACCESSION:AR071786
184	7.4	35.2	10	1	AR071787	ACCESSION:AR071787
185	7.4	35.2	10	1	AR105774	ACCESSION:AR105774
186	7.4	35.2	10	1	AR107796	ACCESSION:AR107796
187	7.4	35.2	10	1	BD083124	ACCESSION:BD083124
188	7.4	35.2	10	1	BD091134	ACCESSION:BD091134
C 189	7.4	35.2	10	1	BD091134	ACCESSION:BD091134
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C 192	7.4	35.2	10	1	BD166463	ACCESSION:BD166463
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C 194	7.4	35.2	10	1	BD166500	ACCESSION:BD166500
C 195	7.4	35.2	10	1	BD166712	ACCESSION:BD166712
C 196	7.4	35.2	10	1	BD166714	ACCESSION:BD166714
197	7.4	35.2	10	1	BD166826	ACCESSION:BD166826
198	7.4	35.2	10	1	BD166993	ACCESSION:BD166993
199	7.4	35.2	10	1	BD167029	ACCESSION:BD167029
200	7.4	35.2	10	1	BD167035	ACCESSION:BD167035
201	7.4	35.2	10	1	BD167212	ACCESSION:BD167212
C 202	7.4	35.2	10	1	BD238593	ACCESSION:BD238593
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C 206	7.4	35.2	10	1	CQ772477	ACCESSION:CQ772477
207	7.4	35.2	10	1	CQ945058	ACCESSION:CQ945058
C 208	7.4	35.2	10	1	CS128776	ACCESSION:CS128776
209	7.4	35.2	10	1	E39489	ACCESSION:E39489
210	7.4	35.2	10	1	E54829	ACCESSION:E54829
211	7.4	35.2	10	1	AR222959	ACCESSION:AR222959
C 212	7.4	35.2	10	1	AR222959	ACCESSION:AR222959
C 213	7.4	35.2	10	1	AR241748	ACCESSION:AR241748
C 214	7.4	35.2	10	1	AR241871	ACCESSION:AR241871
215	7.4	35.2	10	1	AR261814	ACCESSION:AR261814
C 216	7.4	35.2	10	1	AR261814	ACCESSION:AR261814
C 217	7.4	35.2	10	1	AR310513	ACCESSION:AR310513
C 218	7.4	35.2	10	1	AR336888	ACCESSION:AR336888
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C 221	7.4	35.2	10	1	AR630153	ACCESSION:AR630153
C 222	7.4	35.2	10	1	AX006877	ACCESSION:AX006877
223	7.4	35.2	10	1	AX152364	ACCESSION:AX152364
224	7.4	35.2	10	1	AX152365	ACCESSION:AX152365
C 225	7.4	35.2	10	1	AX152532	ACCESSION:AX152532
C 226	7.4	35.2	10	1	AX152671	ACCESSION:AX152671
C 227	7.4	35.2	10	1	AX153299	ACCESSION:AX153299
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230	7.4	35.2	10	1	AX153314	ACCESSION:AX153314
231	7.4	35.2	10	1	AX153315	ACCESSION:AX153315
232	7.4	35.2	10	1	AX153316	ACCESSION:AX153316
233	7.4	35.2	10	1	AX153317	ACCESSION:AX153317
234	7.4	35.2	10	1	AX153318	ACCESSION:AX153318
235	7.4	35.2	10	1	AX153319	ACCESSION:AX153319
236	7.4	35.2	10	1	AX224406	ACCESSION:AX224406
C 237	7.4	35.2	10	1	AX224406	ACCESSION:AX224406
238	7.4	35.2	10	1	AX224408	ACCESSION:AX224408
239	7.4	35.2	10	1	AX224412	ACCESSION:AX224412
C 240	7.4	35.2	10	1	AX224412	ACCESSION:AX224412
241	7.4	35.2	10	1	AX224413	ACCESSION:AX224413
C 242	7.4	35.2	10	1	AX224413	ACCESSION:AX224413
243	7.4	35.2	10	1	AX224414	ACCESSION:AX224414
C 244	7.4	35.2	10	1	AX224415	ACCESSION:AX224415
C 245	7.4	35.2	10	1	AX224416	ACCESSION:AX224416
246	7.4	35.2	10	1	AX601650	ACCESSION:AX601650
C 247	7.4	35.2	10	1	AX601650	ACCESSION:AX601650
248	7.4	35.2	10	1	AX958217	ACCESSION:AX958217
C 249	7.4	35.2	10	1	AX958217	ACCESSION:AX958217
C 250	7.4	35.2	10	1	BD007953	ACCESSION:BD007953
C 251	7.4	35.2	10	1	BD007960	ACCESSION:BD007960
252	7.4	35.2	11	1	AX623125	ACCESSION:AX623125

253	7.4	35.2	11	1	AX630546	ACCESSION:AX630546
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255	7.4	35.2	12	1	CQ766499	ACCESSION:CQ766499
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257	7.2	34.3	20	1	AR086219	ACCESSION:AR086219
258	7.2	34.3	20	1	AR176785	ACCESSION:AR176785
259	7	33.3	10	1	E54824	ACCESSION:E54824
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262	7	33.3	10	1	AR071790	ACCESSION:AR071790
263	7	33.3	10	1	AR071791	ACCESSION:AR071791
264	7	33.3	10	1	AR071792	ACCESSION:AR071792
265	7	33.3	10	1	AR092694	ACCESSION:AR092694
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267	7	33.3	10	1	AR098900	ACCESSION:AR098900
268	7	33.3	10	1	AR106678	ACCESSION:AR106678
269	7	33.3	10	1	AR106702	ACCESSION:AR106702
270	7	33.3	10	1	AR107780	ACCESSION:AR107780
271	7	33.3	10	1	AR107802	ACCESSION:AR107802
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274	7	33.3	10	1	AR172413	ACCESSION:AR172413
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297	7	33.3	10	1	BD240437	ACCESSION:BD240437
298	7	33.3	10	1	BD240454	ACCESSION:BD240454
299	7	33.3	10	1	BD240490	ACCESSION:BD240490
300	7	33.3	10	1	BD240601	ACCESSION:BD240601
301	7	33.3	10	1	BD249594	ACCESSION:BD249594
302	7	33.3	10	1	BD251793	ACCESSION:BD251793
303	7	33.3	10	1	CS101365	ACCESSION:CS101365
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313	7	33.3	10	1	I86912	ACCESSION:I86912
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318	7	33.3	10	1	AR306871	ACCESSION:AR306871
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322	7	33.3	10	1	AR477264	ACCESSION:AR477264
323	7	33.3	10	1	AR489166	ACCESSION:AR489166
324	7	33.3	10	1	AR490750	ACCESSION:AR490750
325	7	33.3	10	1	AR568611	ACCESSION:AR568611

326	7	33.3	10	1	AR630143	ACCESSION:AR630143
327	7	33.3	10	1	AR630149	ACCESSION:AR630149
328	7	33.3	10	1	AR642556	ACCESSION:AR642556
329	7	33.3	10	1	AR642557	ACCESSION:AR642557
330	7	33.3	10	1	AR642558	ACCESSION:AR642558
331	7	33.3	10	1	AR642559	ACCESSION:AR642559
332	7	33.3	10	1	AR009254	ACCESSION:AX009254
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336	7	33.3	10	1	AX152322	ACCESSION:AX152322
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338	7	33.3	10	1	AX152392	ACCESSION:AX152392
339	7	33.3	10	1	AX152393	ACCESSION:AX152393
340	7	33.3	10	1	AX152609	ACCESSION:AX152609
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347	7	33.3	10	1	AX391509	ACCESSION:AX391509
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349	7	33.3	10	1	AX391511	ACCESSION:AX391511
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352	7	33.3	10	1	AX753482	ACCESSION:AX753482
353	7	33.3	10	1	AX958222	ACCESSION:AX958222
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355	7	33.3	10	1	BD007922	ACCESSION:BD007922
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ALIGNMENTS

RESULT 1	AR086219/c	AR086219	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AR086219/c	AR086219	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
DEFINITION	AR086219	AR086219	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
ACCESSION	AR086219	AR086219	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
VERSION	AR086219.1	AR086219.1	GI:10012985	20 bp	DNA	linear	PAT 07-SEP-2000
KEYWORDS	AR086219.1	AR086219.1	GI:10012985	20 bp	DNA	linear	PAT 07-SEP-2000
SOURCE	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
ORGANISM	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
REFERENCE	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
AUTHORS	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
TITLE	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
JOURNAL	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
FEATURES	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
source	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
Query Match	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
Best Local Similarity	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
Matches	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
Qy	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
Db	AR086219/c	AR086219/c	Sequence 40 from patent US 5985558.	20 bp	DNA	linear	PAT 07-SEP-2000
RESULT 2	AR176785/c	AR176785	Sequence 40 from patent US 6312900.	20 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR176785/c	AR176785	Sequence 40 from patent US 6312900.	20 bp	DNA	linear	PAT 17-DEC-2001
DEFINITION	AR176785/c	AR176785	Sequence 40 from patent US 6312900.	20 bp	DNA	linear	PAT 17-DEC-2001
ACCESSION	AR176785	AR176785	Sequence 40 from patent US 6312900.	20 bp	DNA	linear	PAT 17-DEC-2001
VERSION	AR176785.1	AR176785.1	GI:17919140	20 bp	DNA	linear	PAT 17-DEC-2001
KEYWORDS	AR176785.1	AR176785.1	GI:17919140	20 bp	DNA	linear	PAT 17-DEC-2001
SOURCE	AR176785/c	AR176785/c	Sequence 40 from patent US 6312900.	20 bp	DNA	linear	PAT 17-DEC-2001

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE Antisense oligonucleotide compositions and methods for the modulation of activating protein 1
JOURNAL Patent: US 6312900-A 40 06-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 68.6%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 6.7;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCGGGCGGCTGTGGC 21
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Db 16 CCGGGCGGCTGTGC 1

RESULT 3
CQ786323
LOCUS CQ786323 16 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 131 from Patent WO2004020668.
ACCESSION CQ786323
VERSION CQ786323.1 GI:45721425
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Nakamura,Y. and Katagiri,T.
TITLE Method for treating synovial sarcoma
JOURNAL Patent: WO 2004020668-A 131 11-MAR-2004;
Oncotherapy Science, Inc. (JP); The University of Tokyo (JP)
FEATURES Location/Qualifiers
source 1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: synthetic oligonucleotide"

Query Match 59.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGCGCGC 15
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Db 3 CCGGCCCGCGCGC 16

RESULT 4
CQ756662
LOCUS CQ756662 16 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 91 from Patent WO2003104276.
ACCESSION CQ756662
VERSION CQ756662.1 GI:44847467
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Nakamura,Y. and Furukawa,Y.
TITLE Genes and polypeptides relating to hepatocellular or colorectal carcinoma
JOURNAL Patent: WO 2003104276-A 91 18-DEC-2003;
Oncotherapy Science, Inc. (JP) ; Japan as Represented by the President of the University of Tokyo (JP)
FEATURES Location/Qualifiers
source 1..16
/organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="an artificially synthesized S-oligonucleotide"

Query Match 54.3%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 30;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGCGCGC 14
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Db 3 CTGGTCCGGCGCG 15

RESULT 5
AR075658/c
LOCUS AR075658 15 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 42 from patent US 5958689.
ACCESSION AR075658
VERSION AR075658.1 GI:10002404
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)
AUTHORS Scholin,C.A., Cangelosi,G.A. and Haydock,P.V.
TITLE Detection of toxicogenic marine diatoms of the genus Pseudo-nitzschia
JOURNAL Patent: US 5958689-A 42 28-SEP-1999;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CCGGCGCGCTGTGG 20
| | | | | | | | | | | | | | | | | | | |
Db 15 CCTGGGCGCTGTGG 2

RESULT 6
AX133710
LOCUS AX133710 14 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 8 from Patent WO0130381.
ACCESSION AX133710
VERSION AX133710.1 GI:14139720
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Aharnejad,S.
TITLE Use of csf-1 inhibitors
JOURNAL Patent: WO 0130381-A 8 03-MAY-2001;
Hofbauer, Reinhold (AT)
FEATURES Location/Qualifiers
source 1..14
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"

Query Match 49.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 39;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGGCGCGCT 16
| | | | | | | | | | | | | | | | | | | |
Db 1 GCCCGGCGCGGT 12

RESULT 7

A13334
LOCUS
DEFINITION B.pertussis DNA for pertussis toxin (S1, AA 956-966).
ACCESSION A13334
VERSION A13334.1 GI:489617
KEYWORDS
SOURCE Bordetella pertussis
ORGANISM Bordetella pertussis
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
REFERENCE
1 (bases 1 to 11)
AUTHORS Pizza,M., Rappuoli,R. and Bartoloni,A.
TITLE Bordetella pertussis toxin with altered toxicity
JOURNAL Patent: EP 0322533-A 14 05-JUL-1989;
SCLAVO S.p.A
FEATURES
source
Location/Qualifiers
1..11
/organism="Bordetella pertussis"
/mol_type="unassigned DNA"
/db_xref="taxon:520"
Query Match 47.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCGGCGCGCT 16
Db 2 CCGGCGCGCT 11
RESULT 8
CQ766472/c
LOCUS
DEFINITION Sequence 433 from Patent WO2004005547.
ACCESSION CQ766472
VERSION CQ766472.1 GI:44908732
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Weinzierl,R.
TITLE Method
JOURNAL Patent: WO 2004005547-A 433 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HS motif"
Query Match 47.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CCCGGCGCGC 15
Db 11 CCCGGCGCGC 2
RESULT 9
AX081331/c
LOCUS
DEFINITION Sequence 10 from Patent WO0108707.
ACCESSION AX081331
VERSION AX081331.1 GI:13170173
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.
A13334
LOCUS
DEFINITION B.pertussis DNA for pertussis toxin (S1, AA 956-966).
ACCESSION A13334
VERSION A13334.1 GI:489617
KEYWORDS
SOURCE Bordetella pertussis
ORGANISM Bordetella pertussis
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
REFERENCE
1 (bases 1 to 11)
AUTHORS Pizza,M., Rappuoli,R. and Bartoloni,A.
TITLE Bordetella pertussis toxin with altered toxicity
JOURNAL Patent: EP 0322533-A 14 05-JUL-1989;
SCLAVO S.p.A
FEATURES
source
Location/Qualifiers
1..11
/organism="Bordetella pertussis"
/mol_type="unassigned DNA"
/db_xref="taxon:520"
Query Match 47.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CCGGCGCGCT 16
Db 2 CCGGCGCGCT 11
RESULT 8
CQ766472/c
LOCUS
DEFINITION Sequence 433 from Patent WO2004005547.
ACCESSION CQ766472
VERSION CQ766472.1 GI:44908732
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Weinzierl,R.
TITLE Method
JOURNAL Patent: WO 2004005547-A 433 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..12
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HS motif"
Query Match 47.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CCCGGCGCGC 15
Db 11 CCCGGCGCGC 2
RESULT 9
AX081331/c
LOCUS
DEFINITION Sequence 10 from Patent WO0108707.
ACCESSION AX081331
VERSION AX081331.1 GI:13170173
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.

TITLE
Conjugates and methods for the production thereof, and their use
for transporting molecules via biological membranes
JOURNAL Patent: WO 0108707-A 10 08-FEB-2001;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
Location/Qualifiers
1..12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="modified Oligonucleotide"
Query Match 47.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GGCCCGCGCG 13
Db 12 GGCCCGCGCG 3
RESULT 10
AR142945/c
LOCUS
DEFINITION Sequence 7 from patent US 6204026.
ACCESSION AR142945
VERSION AR142945.1 GI:15104231
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS Desjardin,L.Ellen., Cave,M.Donald. and Eisenach,K.Davis.
TITLE Detection of M. tuberculosis complex via reverse transcriptase SDA
JOURNAL Patent: US 6204026-A 7 20-MAR-2001;
FEATURES
source
Location/Qualifiers
1..14
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 46.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 CGGCGCGCTGTGG 20
Db 14 CGGCTCGCTGTGC 2
RESULT 11
CS061169
LOCUS
DEFINITION Sequence 43 from Patent WO2005026338.
ACCESSION CS061169
VERSION CS061169.1 GI:62553190
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Stampfer,W., Kosjek,B., Kroutil,W., Faber,K., Niehaus,F. and Eck,J.
TITLE Alcohol dehydrogenases with increased solvent and temperature
stability
JOURNAL Patent: WO 2005026338-A 43 24-MAR-2005;
Ciba Specialty Chemicals Holding Inc. (CH)
FEATURES
source
Location/Qualifiers
1..14
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Sequence used as potential probe for identifying
Rhodococcus ruber DSM 14855 alcohol dehydrogenase A gene"
Query Match 46.7%; Score 9.8; DB 1; Length 14;

Best Local Similarity 84.6%; Pred. No. 61;										
Matches		11;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	GCTGGCCCCGGCGC	13							
Db	1	GCCGCCCGCGCGC	13							
RESULT 12										
CQ836510										
LOCUS		CQ836510	Sequence 1568 from Patent WO2004059001.	11 bp	DNA	linear	PAT 29-JUL-2004			
DEFINITION		ACCESSION	CQ836510							
VERSION		CQ836510.1	GI:50836044							
KEYWORDS		.	Homo sapiens (human)							
SOURCE			Homo sapiens							
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE										
AUTHORS		Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K.								
TITLE		Method for determining markers of human facial skin								
JOURNAL		Patent: WO 2004059001-A 1568 15-JUL-2004;								
FEATURES		Henkel Kommanditgesellschaft auf Aktien (DE)								
source		Location/Qualifiers								
		1. .11								
		/organism="Homo sapiens"								
		/mol_type="unassigned DNA"								
		/db_xref="taxon:9606"								
Query Match										
Best Local Similarity		44.8%;	Score 9.4;	DB 1;	Length 11;					
Matches		10;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	GCTGGCCCCGGC	11							
Db	1	GCCGCCCGCGC	11							
RESULT 13										
AX628774										
LOCUS		AX628774	Sequence 5815 from Patent WO02053774.	11 bp	DNA	linear	PAT 21-FEB-2003			
DEFINITION		ACCESSION	AX628774							
VERSION		AX628774.1	GI:28456812							
KEYWORDS		.	Homo sapiens (human)							
SOURCE			Homo sapiens							
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE										
AUTHORS		Petersohn,D., Conradt,M. and Hofmann,K.								
TITLE		Method for determining homeostasis of the skin								
JOURNAL		Patent: WO 02053774-A 5815 11-JUL-2002;								
FEATURES		Henkel Kommanditgesellschaft auf Aktien (DE)								
source		Location/Qualifiers								
		1. .11								
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		/mol_type="unassigned DNA"								
		/db_xref="taxon:9606"								
Query Match										
Best Local Similarity		44.8%;	Score 9.4;	DB 1;	Length 11;					
Matches		10;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	GCTGGCCCCGGC	11							
Db	1	GCCGCCCGCGC	11							

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other sequences; artificial sequences.
REFERENCE
1
AUTHORS Weinzierl,R.
TITLE Method
JOURNAL Patent: WO 2004005547-A 460 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source
1. .12
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="HS motif"

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGC 12
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Db 2 CGGCCCGCGC 12

RESULT 17
AR576634/c
LOCUS AR576634 12 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 20 from patent US 6777180.
ACCESSION AR576634
VERSION AR576634.1 GI:56578919
KEYWORDS
SOURCE
ORGANISM
Unassigned.
Unassigned.
REFERENCE
1 (bases 1 to 12)
AUTHORS Fisher,P.B. and Kang,D.-C.
TITLE Method for full-length cDNA cloning using degenerate stem-loop
annealing primers
JOURNAL Patent: US 6777180-A 20 17-AUG-2004;
Trustees of Columbia University in the City of New York; New York,
NY;
WOX;

FEATURES
source
1. .12
/organism="unknown"
/mol_type="genomic DNA"

Query Match 44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
| | | | | | | | | |
Db 11 GCCCGCGCGC 1

RESULT 18
AR285789
LOCUS AR285789 13 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 161 from patent US 6528640.
ACCESSION AR285789
VERSION AR285789.1 GI:29723383
KEYWORDS
SOURCE
ORGANISM
Unassigned.
Unassigned.
REFERENCE
1 (bases 1 to 13)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 161 04-MAR-2003;
Ribozyme Pharmaceuticals, incorporated; Boulder, CO

FEATURES
source
1. .13
/organism="unknown"
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/mol_type="unassigned RNA"

Query Match 44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGGC 11
| | | | | | | | | |
Db 3 GCTGGCTCGGC 13

RESULT 19
AR397780
LOCUS AR397780 13 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 161 from patent US 6617438.
ACCESSION AR397780
VERSION AR397780.1 GI:40135041
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unknown.
REFERENCE
1 (bases 1 to 13)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 161 09-SEP-2003;
Sirna Therapeutics, Inc.; Boulder, CO

FEATURES
source
1. .13
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGGC 11
| | | | | | | | | |
Db 3 GCTGGCTCGGC 13

RESULT 20
BD161333/c
LOCUS BD161333 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161333
VERSION BD161333.1 GI:27867091
KEYWORDS JP 2002186482-A/155.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 155 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/155
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers
FT source 1. .10
/organism='Homo sapiens (human)'.
FT Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCGCGCTG 17
Db 9 GGCGCGCTG 1

RESULT 21
BD238832/c

LOCUS BD238832 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD238832

VERSION BD238832.1 GI:33048602

KEYWORDS JP 2002534056-A/250.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)

AUTHORS Roberts,B.L. and Shankara,S.

TITLE Preparation and use of superior vaccines

JOURNAL Patent: JP 2002534056-A 250 15-OCT-2002;

GENZYME CORP

COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/250
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,

PC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

FH Key Location/Qualifiers

FT source 1. .10

FT /organism='Homo sapiens (human)'.
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source

Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCGCGCTG 17
Db 9 GGCGCGCTG 1

RESULT 22
AR630145

LOCUS AR630145 10 bp DNA linear PAT 14-FEB-2005

DEFINITION Sequence 199 from patent US 6838556.

ACCESSION AR630145

VERSION AR630145.1 GI:59762469

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 10)

AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.

TITLE Promoters for regulated gene expression

JOURNAL Patent: US 6838556-A 199 04-JAN-2005;

FEATURES Genelabs Technologies, Inc.; Redwood City, CA
source Location/Qualifiers
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCGCGCTG 17
Db 1 GGCGCGCTG 9

RESULT 23
AX152988/c

LOCUS AX152988 10 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 903 from Patent WO0138577.

ACCESSION AX152988

VERSION AX152988.1 GI:14534639

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.

TITLE Human transcriptomes

JOURNAL Patent: WO 0138577-A 903 31-MAY-2001;

FEATURES The Johns Hopkins University (US)
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCGCGCTG 17
Db 9 GGCGCGCTG 1

RESULT 24
AX153495

LOCUS AX153495 10 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 1410 from Patent WO0138577.

ACCESSION AX153495

VERSION AX153495.1 GI:14535146

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1410 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
    source
        Location/Qualifiers
            1..10
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match
Best Local Similarity 42.9%; Score 9; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
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Db 1 CTGGCCCGG 9

RESULT 25
AX153496
LOCUS AX153496 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1411 from Patent WO0138577.
ACCESSION AX153496
VERSION AX153496.1 GI:14535147
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1411 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
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            1..10
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match
Best Local Similarity 42.9%; Score 9; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
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Db 1 CTGGCCCGG 9

RESULT 26
CQ833102/c
LOCUS CQ833102 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 473 from Patent WO2004059002.
ACCESSION CQ833102
VERSION CQ833102.1 GI:50832709
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 473 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
    source
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            1..11
                /organism="Homo sapiens"
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REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1410 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
    source
        Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match
Best Local Similarity 42.9%; Score 9; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
    |||||
Db 9 GGCGCGCTG 1

RESULT 27
AX630364/c
LOCUS AX630364 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7405 from Patent WO02053774.
ACCESSION AX630364
VERSION AX630364.1 GI:28458402
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7405 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match
Best Local Similarity 42.9%; Score 9; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
    |||||
Db 9 GGCGCGCTG 1

RESULT 28
CS086764
LOCUS CS086764 12 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 13 from Patent WO2005042018.
ACCESSION CS086764
VERSION CS086764.1 GI:66712215
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Vollmer,J., Krieg,A.M. and Noll,B.O.
TITLE C-class oligonucleotide analogs with enhanced immunostimulatory
JOURNAL potency
Patent: WO 2005042018-A 13 12-MAY-2005;
Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc.
(US)
FEATURES
    source
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic oligonucleotide"

Query Match
Best Local Similarity 42.9%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
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Db          1  GCGCGCTG 9
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RESULT 29
AR630091/c
LOCUS      AR630091          12 bp    DNA          linear    PAT 14-FEB-2005
DEFINITION Sequence 145 from patent US 6838556.
ACCESSION  AR630091
VERSION     AR630091.1  GI:59762360
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1  (bases 1 to 12)
AUTHORS     Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE       Promoters for regulated gene expression
JOURNAL     Patent: US 6838556-A 145 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES    source
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      42.9%;  Score 9;  DB 1;  Length 12;
Best Local Similarity 100.0%;  Pred. No. 66;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy 10 GCGCGCTGT 18
|||||
Db 9 GCGCGCTGT 1

RESULT 30
CQ766472
LOCUS      CQ766472          12 bp    DNA          linear    PAT 03-MAR-2004
DEFINITION Sequence 433 from Patent WO2004005547.
ACCESSION  CQ766472
VERSION     CQ766472.1  GI:44908732
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Weinzierl,R.
TITLE       Method
JOURNAL     Patent: WO 2004005547-A 433 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES    source
            1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="HS motif"

Query Match      41.9%;  Score 8.8;  DB 1;  Length 12;
Best Local Similarity 83.3%;  Pred. No. 76;
Matches 10;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy 9 GCGCGCTGTGG 20
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Db 1 GCGCGCGCGGG 12

RESULT 31
CQ766470/c
LOCUS      CQ766470          12 bp    DNA          linear    PAT 03-MAR-2004
DEFINITION Sequence 431 from Patent WO2004005547.
ACCESSION  CQ766470
VERSION     CQ766470.1  GI:44908730
KEYWORDS    .
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SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Weinzierl,R.
TITLE       Method
JOURNAL     Patent: WO 2004005547-A 431 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES    Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="HS motif"

Query Match      41.9%;  Score 8.8;  DB 1;  Length 12;
Best Local Similarity 83.3%;  Pred. No. 76;
Matches 10;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy 2 CTGGCCCGCGC 13
|||||
Db 12 CTGCCCCGCCG 1

RESULT 32
CQ983522
LOCUS      CQ983522          12 bp    DNA          linear    PAT 25-JAN-2005
DEFINITION Sequence 17 from Patent WO2005003384.
ACCESSION  CQ983522
VERSION     CQ983522.1  GI:58191883
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Bender,M. and Jacobsen,C.S.
TITLE       Method for selective detection of a target nucleic acid
JOURNAL     Patent: WO 2005003384-A 17 13-JAN-2005;
Danmarks og Gronlands Geologiske Undersogelse (DK)
FEATURES    Location/Qualifiers
            source
            1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Universal Bacterial 16S primer"

Query Match      41.9%;  Score 8.8;  DB 1;  Length 12;
Best Local Similarity 83.3%;  Pred. No. 76;
Matches 10;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

Qy 1 GCTGGCCCGCGC 12
|||||
Db 1 GCTGGCACGGAG 12

RESULT 33
CQ983659
LOCUS      CQ983659          12 bp    DNA          linear    PAT 25-JAN-2005
DEFINITION Sequence 154 from Patent WO2005003384.
ACCESSION  CQ983659
VERSION     CQ983659.1  GI:58192020
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Bender,M. and Jacobsen,C.S.
TITLE       Method for selective detection of a target nucleic acid
JOURNAL     Patent: WO 2005003384-A 154 13-JAN-2005;
Danmarks og Gronlands Geologiske Undersogelse (DK)
FEATURES    Location/Qualifiers
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            /organism="synthetic construct"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="511R2"

Query Match      41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGC 12
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Db 1 GCTGGCACGGAG 12

RESULT 34
AX298228/c
LOCUS AX298228 12 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 9 from Patent WO0183735.
ACCESSION AX298228
VERSION AX298228.1 GI:17128282
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Dutreix,M., Sun,J.S., Biet,E., Maurisse,R. and Feugeas,J.P.
TITLE Methods and compositions for effecting homologous recombination
JOURNAL Patent: WO 0183735-A 9 08-NOV-2001;
INSTITUT Institut Curie (FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
(CNRS) (FR) ; MUSEUM NATIONAL D'HISTOIRE NATURELLE (FR) ; INSTITUT
NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR)
FEATURES
    source
        1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="oligonucleotide"

Query Match      41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGC 12
   ||||| |||
Db 12 GCTGGCCACGCG 1

RESULT 35
S88396S1/c
LOCUS S88396S1 12 bp DNA linear PRI 19-JUL-1993
DEFINITION dystrophin, dystrophin [human, Genomic Mutant; 12 nt, segment 1 of
2].
ACCESSION S88396
VERSION S88396.1 GI:247278
KEYWORDS 1 of 2
SEGMENT Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12)
AUTHORS Roberts,R.G., Bobrow,M. and Bentley,D.R.
TITLE Point mutations in the dystrophin gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (6), 2331-2335 (1992)
PUBMED 1549596
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 88396] from the original journal article.
FEATURES
    source
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            1..12

CDS
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/gene="dystrophin"
/codon_start=1
/product="dystrophin"
/protein_id="AAB21812.1"
/db_xref="GI:247281"
/translation="PRAS"

Query Match      41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGC 12
   ||||| |||
Db 12 GCTGGCTCGGG 1

RESULT 36
AR058606
LOCUS AR058606 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 183 from patent US 5837832.
ACCESSION AR058606
VERSION AR058606.1 GI:5984183
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 183 17-NOV-1998;
FEATURES
    source
        1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCCGCGCGC 13
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Db 1 GGCCCGGAGC 10

RESULT 37
BD166545/c
LOCUS BD166545 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166545
VERSION BD166545.1 GI:27872357
KEYWORDS JP 2002209591-A/90.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 90 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/90
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.


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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCGG 10
||||||| |

Db 10 GCTGGCCCGAG 1

RESULT 38
BD225304

LOCUS BD225304 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for the diagnosis and treatment of lung cancer.
ACCESSION BD225304
VERSION BD225304.1 GI:33035074
KEYWORDS JP 2002509706-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 10)
AUTHORS Jen,J., Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Methods for the diagnosis and treatment of lung cancer
JOURNAL Patent: JP 2002509706-A 3 02-APR-2002;
GENZYME CORP,JOHN HOPKINS UNIVERSITY

COMMENT OS Artificial Sequence
PN JP 2002509706-A/3
PD 02-APR-2002
PF 30-MAR-1999 JP 2000540746
PR 31-MAR-1998 US 60/080044
PI JIN JEN,GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
C12N15/09,A61K45/00,A61K48/00,A61P35/00,C12Q1/68,G01N33/50, PC
G01N33/574,
PC C12N15/00
CC Description of Artificial Sequence: Probe
FH Key Location/Qualifiers
FT source 1. .10
FT /organism='Artificial Sequence'.

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGCGG 12
||||||| |

Db 1 TGGCCCGGACG 10

RESULT 39
BD225338

LOCUS BD225338 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for the identification of lung tumor cells.
ACCESSION BD225338
VERSION BD225338.1 GI:33035108
KEYWORDS JP 2002509707-A/20.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 10)
AUTHORS Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Compositions and methods for the identification of lung tumor cells
JOURNAL Patent: JP 2002509707-A 20 02-APR-2002;

GENZYME CORP

OS Artificial Sequence
PN JP 2002509707-A/20
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180
PR 31-MAR-1998 US 60/080037
PI GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
G01N33/566//
PC A61K45/00,A61P9/00,A61P35/00,C12N15/00,C12N5/00 CC
Compositions and methods for the identification of lung tumor cells

FH Key Location/Qualifiers
FT source 1. .10
FT /organism='Artificial Sequence'.

FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGCGG 12
||||||| |

Db 1 TGGCCCGGACG 10

RESULT 40
BD238621/c

LOCUS BD238621 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238621
VERSION BD238621.1 GI:33048391
KEYWORDS JP 2002534056-A/39.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 39 15-OCT-2002;
GENZYME CORP

COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/39
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,

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PC      C12N15/00,C12N5/00,C12N15/00
CC      Preparation and use of superior vaccines
FH      Key
FT      Location/Qualifiers
FT      source
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FEATURES
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          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCCG 10
          |||||
Db      10 GCTGGCCCAG 1

RESULT 41
CQ986655/c
LOCUS      CQ986655
DEFINITION      Sequence 199 from Patent WO2005001142.
ACCESSION      CQ986655
VERSION      CQ986655.1 GI:58194572
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
REFERENCE      1
AUTHORS      Lofton-Day,C., Sledziewski,A., Thomas,J., Day,R.W.,
              Tonnes-Priddy,L. and Cardon,K.
TITLE      Methods and nucleic acids for the analysis of colorectal cell
              proliferative disorders
JOURNAL      Patent: WO 2005001142-A 199 06-JAN-2005;
              Epigenomics AG (DE)
FEATURES
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          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCCGGCGCGC 15
          |||||
Db      10 CGCGCGCGC 1

RESULT 42
CS114173/c
LOCUS      CS114173
DEFINITION      Sequence 931 from Patent WO2005054517.
ACCESSION      CS114173
VERSION      CS114173.1 GI:68225718
KEYWORDS
SOURCE      synthetic construct
              synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Day,K.J., Cottrell,S., Distler,J., Morotti,A., Yamamura,S.,
              Dekker,S., Ocamp,Y. and Devos,T.
TITLE      Methods and nucleic acids for the analysis of gene expression
              associated with the development of prostate cell proliferative
              disorders
JOURNAL      Patent: WO 2005054517-A 931 16-JUN-2005;
              Epigenomics AG (DE)
FEATURES
    Location/Qualifiers
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          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="chemically treated genomic DNA (Homo sapiens)"

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCCGGCGCGC 15
          | |||||
Db      10 CGCGCGCGC 1

RESULT 43
E39738/c
LOCUS      E39738
DEFINITION      Genes with human dendritic cell expression.
ACCESSION      E39738
VERSION      E39738.1 GI:18621829
KEYWORDS      JP 2000279181-A/271.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE      Genes with human dendritic cell expression
JOURNAL      Patent: JP 2000279181-A 271 10-OCT-2000;
              SCIENCE & TECH AGENCY
COMMENT      OS Homo sapiens (human)
              PN JP 2000279181-A/271
              PD 10-OCT-2000
              PF 01-APR-1999 JP 1999095481
              PR
              PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
              C12N15/09,C07K14/475,C07K16/18,C12N15/00
              CC
              FH Key
              FT source
              FT Location/Qualifiers
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                  /organism='Homo sapiens (human)'.

FEATURES
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          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCCG 10
          |||||
Db      10 GCTGGCCCAG 1

RESULT 44
E54818
LOCUS      E54818
DEFINITION      Human normal liver cell expression genes.
ACCESSION      E54818
VERSION      E54818.1 GI:22556301
KEYWORDS      JP 2001211883-A/170.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human normal liver cell expression genes
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JOURNAL Patent: JP 2001211883-A 170 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/170
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES source
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GCGCGCTGTG 19
| |||||
Db 1 GGGCGCTGTG 10

RESULT 45
E54824/c
LOCUS E54824 Human normal liver cell expression genes. 10 bp DNA linear PAT 27-AUG-2002
DEFINITION E54824
ACCESSION E54824
VERSION E54824.1 GI:22556307
KEYWORDS JP 2001211883-A/176.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 176 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/176
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES source
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGGCGCG 14
| |||||
Db 10 GCCGGGCGCG 1

RESULT 46
AR630141/c
LOCUS AR630141 Sequence 195 from patent US 6838556. 10 bp DNA linear PAT 14-FEB-2005
DEFINITION AR630141
ACCESSION AR630141
VERSION AR630141.1 GI:59762461

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 195 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES Location/Qualifiers
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCGGCGCGC 15
| |||||
Db 10 CCGGCGCGC 1

RESULT 47
AX152803
LOCUS AX152803 Sequence 718 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION AX152803
ACCESSION AX152803
VERSION AX152803.1 GI:14534454
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 718 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GCGCGCTGTG 19
| |||||
Db 1 GGGCGCTGTG 10

RESULT 48
AX224404/c
LOCUS AX224404 Sequence 11 from Patent WO0160997. 10 bp DNA linear PAT 10-SEP-2001
DEFINITION AX224404
ACCESSION AX224404
VERSION AX224404.1 GI:15554646
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 11 23-AUG-2001;

FEATURES
source
PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
| | | | | | | |
Db 10 CGGGCCCGGC 1

RESULT 49
AX224407
LOCUS AX224407 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 14 from Patent WO0160997.
ACCESSION AX224407
VERSION AX224407.1 GI:15554649
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 14 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
| | | | | | | |
Db 1 CGGGCCCGGC 10

RESULT 50
AX301612
LOCUS AX301612 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 326 from Patent WO0185941.
ACCESSION AX301612
VERSION AX301612.1 GI:17382695
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Versteeg,R. and Caron,H.N.
TITLE Myc targets
JOURNAL Patent: WO 0185941-A 326 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;

FEATURES
source
PIONEER HI-BRED INTERNATIONAL, INC. (US)
Location/Qualifiers
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGTG 19
| | | | | | | |
Db 1 GGGCGCTGTG 10

RESULT 51
AX339231
LOCUS AX339231 10 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 25 from Patent WO0196602.
ACCESSION AX339231
VERSION AX339231.1 GI:18135492
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Yang,A.L. and Festing,M.
TITLE Methods and materials to determine the p53 status of a sample by
determining the binding of p53 to a vector
JOURNAL Patent: WO 0196602-A 25 20-DEC-2001;
MEDICAL RESEARCH COUNCIL (GB)
FEATURES
source
1. .10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGGCGCGCTG 17
| | | | | | | |
Db 1 CGGCGCGGTG 10

RESULT 52
AX753475
LOCUS AX753475 10 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 20 from Patent EP1310556.
ACCESSION AX753475
VERSION AX753475.1 GI:32166235
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE
AUTHORS Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Composition and methods for the identification of lung tumor cells
JOURNAL Patent: EP 1310556-A 20 14-MAY-2003;
GENZYME CORPORATION (US)
FEATURES
source
1. .10
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGCGC 12
| | | | | | | |
Db 1 TGGCCCGGACG 10

RESULT 53
AX814774/c
LOCUS AX814774 10 bp DNA linear PAT 05-DEC-2003

DEFINITION Sequence 20 from Patent WO03064701.
ACCESSION AX814774
VERSION AX814774.1 GI:39103968
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Sledziewski,A. and Schweikhardt,R.G.
TITLE Method for the analysis of cytosine methylation patterns
JOURNAL Patent: WO 03064701-A 20 07-AUG-2003;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AP-PCR Primer CG4"
Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 CCCGGCGCGC 15
Db 10 CGCGGCGCGC 1
RESULT 54
CQ833458
LOCUS CQ833458 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 829 from Patent WO2004059002.
ACCESSION CQ833458
VERSION CQ833458.1 GI:50833065
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 829 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 GCGCTGTGGC 21
Db 2 GGGCTGTGGC 11
RESULT 55
CQ833790
LOCUS CQ833790 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1161 from Patent WO2004059002.
ACCESSION CQ833790
VERSION CQ833790.1 GI:50833397
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 1161 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCTGGCCCCG 10
Db 1 GGTGGCCCCG 10
RESULT 56
CQ835173/c
LOCUS CQ835173 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 231 from Patent WO2004059001.
ACCESSION CQ835173
VERSION CQ835173.1 GI:50834707
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 231 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 GCGCTGTGGC 21
Db 11 GCGCAGTGGC 2
RESULT 57
CQ835396/c
LOCUS CQ835396 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 454 from Patent WO2004059001.
ACCESSION CQ835396
VERSION CQ835396.1 GI:50834930
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 454 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers

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source      1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCCCGGCGCG 14
      ||| |||||
Db      11 GCCTGGCGCG 2

RESULT 58
CQ835763
LOCUS      CQ835763      11 bp      DNA      PAT 29-JUL-2004
DEFINITION      Sequence 821 from Patent WO2004059001.
ACCESSION      CQ835763
VERSION      CQ835763.1 GI:50835297
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 821 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGCG 11
      ||| |||||
Db      2 CTGGCCCGCG 11

RESULT 59
CQ837774
LOCUS      CQ837774      11 bp      DNA      PAT 29-JUL-2004
DEFINITION      Sequence 2832 from Patent WO2004059001.
ACCESSION      CQ837774
VERSION      CQ837774.1 GI:50837308
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2832 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGCG 11
      ||| |||||
Db      2 CTGGACCGCG 11

RESULT 60
CQ837882
LOCUS      CQ837882      11 bp      DNA      PAT 29-JUL-2004
DEFINITION      Sequence 2940 from Patent WO2004059001.
ACCESSION      CQ837882
VERSION      CQ837882.1 GI:50837416
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2940 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCCCGGCGCG 14
      ||| |||||
Db      2 GCCCGGCGCG 11

RESULT 61
CQ838018
LOCUS      CQ838018      11 bp      DNA      PAT 29-JUL-2004
DEFINITION      Sequence 3076 from Patent WO2004059001.
ACCESSION      CQ838018
VERSION      CQ838018.1 GI:50837552
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 3076 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 GCGCTGTGGC 21
      | |||||
Db      2 GCGCTGTGGC 11

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RESULT 62
CS058243/c
LOCUS          CS058243          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 140 from Patent WO2005028671.
ACCESSION      CS058243
VERSION        CS058243.1  GI:62551426
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
               Kessler-Becker,D.
TITLE          Method for determining hair cycle markers
JOURNAL        Patent: WO 2005028671-A 140 31-MAR-2005;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

               Query Match          40.0%;   Score 8.4;   DB 1;   Length 11;
               Best Local Similarity 90.0%;   Pred. No. 76;
               Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy             5  GCCCGCGGCG 14
               |||||||
Db             11 GCCCGCGGCG 2

RESULT 63
CS058293
LOCUS          CS058293          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 190 from Patent WO2005028671.
ACCESSION      CS058293
VERSION        CS058293.1  GI:62551476
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
               Kessler-Becker,D.
TITLE          Method for determining hair cycle markers
JOURNAL        Patent: WO 2005028671-A 190 31-MAR-2005;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

               Query Match          40.0%;   Score 8.4;   DB 1;   Length 11;
               Best Local Similarity 90.0%;   Pred. No. 76;
               Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy             3  TGGCCCGGCG 12
               |||||||
Db             1  TGGCCCGGCG 10

RESULT 64
CS058370
LOCUS          CS058370          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 267 from Patent WO2005028671.
ACCESSION      CS058370
VERSION        CS058370.1  GI:62551553
KEYWORDS       .
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SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
               Kessler-Becker,D.
TITLE          Method for determining hair cycle markers
JOURNAL        Patent: WO 2005028671-A 267 31-MAR-2005;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

               Query Match          40.0%;   Score 8.4;   DB 1;   Length 11;
               Best Local Similarity 90.0%;   Pred. No. 76;
               Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy             3  TGGCCCGGCG 12
               |||||||
Db             1  TGGCCCGGCG 10

RESULT 65
CS058633/c
LOCUS          CS058633          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 530 from Patent WO2005028671.
ACCESSION      CS058633
VERSION        CS058633.1  GI:62551816
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
               Kessler-Becker,D.
TITLE          Method for determining hair cycle markers
JOURNAL        Patent: WO 2005028671-A 530 31-MAR-2005;
               Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       Location/Qualifiers
               source
               1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

               Query Match          40.0%;   Score 8.4;   DB 1;   Length 11;
               Best Local Similarity 90.0%;   Pred. No. 76;
               Matches      9;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

Qy             5  GCCCGCGGCG 14
               |||||||
Db             11 GCCCGCGGCG 2

RESULT 66
CS058641/c
LOCUS          CS058641          11 bp      DNA          linear          PAT 13-APR-2005
DEFINITION     Sequence 538 from Patent WO2005028671.
ACCESSION      CS058641
VERSION        CS058641.1  GI:62551824
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
AUTHORS        Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
```

Kessler-Becker,D.
Method for determining hair cycle markers
Patent: WO 2005028671-A 538 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCGCTGTGGC 21
| | | | |
Db 11 GCGCGGTGGC 2

RESULT 67
AX470640/c
LOCUS AX470640 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 217 from Patent WO02053773.
ACCESSION AX470640
VERSION AX470640.1 GI:22205765
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 217 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGG 10
| | | | |
Db 10 GCTGGCCCGG 1

RESULT 68
AX470863
LOCUS AX470863 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 440 from Patent WO02053773.
ACCESSION AX470863
VERSION AX470863.1 GI:22205988
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 440 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
| | | | |
Db 2 CTGGCCCGGC 11

RESULT 69
AX471737/c
LOCUS AX471737 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1314 from Patent WO02053773.
ACCESSION AX471737
VERSION AX471737.1 GI:22206862
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1314 11-JUL-2002;
HENKEL KGAA (DE)

FEATURES
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGGCGCG 14
| | | | |
Db 11 GCCCGGCGCG 2

RESULT 70
AX482034
LOCUS AX482034 11 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 11 from Patent EPI225233.
ACCESSION AX482034
VERSION AX482034.1 GI:22316756
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS van der Kuyt,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1225233-A 11 24-JUL-2002;
Amsterdam Support Diagnostics B.V. (NL)

FEATURES
source 1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="TAG sequence Hs183"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
| | | | |
Db 2 CTGGCCCGGC 11

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RESULT 71
AX511273
LOCUS AX511273 11 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 11 from Patent WO02059558.
ACCESSION AX511273
VERSION AX511273.1 GI:23392150
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: WO 02059558-A 11 01-AUG-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source Location/Qualifiers
1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="TAG sequence Hs183"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCCGC 11
|||||
Db 2 CTGGCCCAGC 11

RESULT 72
AX623125/c
LOCUS AX623125 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 166 from Patent WO02053774.
ACCESSION AX623125
VERSION AX623125.1 GI:28451066
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 166 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCCGC 11
|||||
Db 10 CTGGCCCAG 1

RESULT 73
AX623608
LOCUS AX623608 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 649 from Patent WO02053774.
ACCESSION AX623608
VERSION AX623608.1 GI:28451549
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 649 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCCGC 11
|||||
Db 2 CTGGCCCAGC 11

RESULT 74
AX625821/c
LOCUS AX625821 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2862 from Patent WO02053774.
ACCESSION AX625821
VERSION AX625821.1 GI:28453762
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2862 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 10
|||||
Db 10 GCTGGCCCAG 1

RESULT 75
AX625842
LOCUS AX625842 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2883 from Patent WO02053774.
ACCESSION AX625842
VERSION AX625842.1 GI:28453878
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2883 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGGC 11
| | | | | | | |
Db 1 CTGGCCAGGC 10

RESULT 76
AX626754/c
LOCUS AX626754 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3795 from Patent WO02053774.
ACCESSION AX626754
VERSION AX626754.1 GI:28454792
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3795 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCGCTGTGGC 21
| | | | | | | |
Db 11 GCGCAGTGGC 2

RESULT 77
AX628541
LOCUS AX628541 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5582 from Patent WO02053774.
ACCESSION AX628541
VERSION AX628541.1 GI:28456579
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5582 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GCGCTGTGGC 21

Db 2 GGGCTGTGGC 11
| | | | | | | |

RESULT 78
AX629212
LOCUS AX629212 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6253 from Patent WO02053774.
ACCESSION AX629212
VERSION AX629212.1 GI:28457250
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6253 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTGGCCCGGC 11
| | | | | | | |
Db 2 CTGGACCGGC 11

RESULT 79
AX629295
LOCUS AX629295 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6336 from Patent WO02053774.
ACCESSION AX629295
VERSION AX629295.1 GI:28457333
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6336 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCCCGGCGCG 14
| | | | | | | |
Db 1 GCCCGGCGCG 10

RESULT 80
AX629700
LOCUS AX629700 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6741 from Patent WO02053774.
ACCESSION AX629700


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VERSION      AX629700.1  GI:28457738
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominiidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6741 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCCCGCGCGC 14
        ||||| ||||
Db      2 GCCCGCGCGC 11

RESULT 81
AX630546/c
LOCUS      AX630546      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7587 from Patent WO02053774.
ACCESSION  AX630546
VERSION     AX630546.1  GI:28458584
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominiidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7587 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGGC 11
        ||||| ||||
Db      10 CTGGCCCGGC 1

RESULT 82
AX631029
LOCUS      AX631029      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8070 from Patent WO02053774.
ACCESSION  AX631029
VERSION     AX631029.1  GI:28459071
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominiidae; Homo.
REFERENCE    1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.

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TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 8070 11-JUL-2002;
             Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGGC 11
        ||||| ||||
Db      2 CTGGCCCGGC 11

RESULT 83
CQ766406
LOCUS      CQ766406      12 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 367 from Patent WO2004005547.
ACCESSION  CQ766406
VERSION     CQ766406.1  GI:44908666
KEYWORDS    .
SOURCE      synthetic construct
             synthetic construct
             other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Weinzierl,R.
TITLE        Method
JOURNAL      Patent: WO 2004005547-A 367 15-JAN-2004;
             IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source       1. .12
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="HS motif"

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGGC 11
        ||||| ||||
Db      3 CTGGCCCGGC 12

RESULT 84
CQ766468
LOCUS      CQ766468      12 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 429 from Patent WO2004005547.
ACCESSION  CQ766468
VERSION     CQ766468.1  GI:44908728
KEYWORDS    .
SOURCE      synthetic construct
             synthetic construct
             other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Weinzierl,R.
TITLE        Method
JOURNAL      Patent: WO 2004005547-A 429 15-JAN-2004;
             IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source       1. .12
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="HS motif"

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGGC 11
        ||||| ||||
Db      3 CTGGCCCGGC 12

RESULT 85
CQ766468
LOCUS      CQ766468      12 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 429 from Patent WO2004005547.
ACCESSION  CQ766468
VERSION     CQ766468.1  GI:44908728
KEYWORDS    .
SOURCE      synthetic construct
             synthetic construct
             other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Weinzierl,R.
TITLE        Method
JOURNAL      Patent: WO 2004005547-A 429 15-JAN-2004;
             IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source       1. .12
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="HS motif"

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGGC 11
        ||||| ||||
Db      3 CTGGCCCGGC 12

```

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCCGGCGC 13

Db 1 GTCCCGGCGC 10

RESULT 85
CQ766480/c

LOCUS CQ766480

DEFINITION Sequence 441 from Patent WO2004005547.

ACCESSION CQ766480

VERSION CQ766480.1 GI:44908740

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE other sequences; artificial sequences.

AUTHORS 1

TITLE Weinzierl,R.

JOURNAL Method

FEATURES

source

1. .12

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="HS motif"

Query Match 40.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGCT 16

Db 10 CCGGCGCGCT 1

RESULT 86
AR678905/c

LOCUS AR678905

DEFINITION Sequence 50 from patent US 6902894.

ACCESSION AR678905

VERSION AR678905.1 GI:67620099

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 12)

TITLE Yang,M. and Woo,H.S.

JOURNAL Mutation detection on RNA polymerase beta subunit gene having rifampin resistance

FEATURES

source

1. .12

/organism="unknown"

/mol_type="genomic DNA"

Query Match 40.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCGCTGTGGC 21

Db 11 GCGCTGTGGC 2

RESULT 87
AR103254/c

LOCUS AR103254

DEFINITION Sequence 4 from patent US 6087170.

ACCESSION AR103254

VERSION AR103254.1 GI:12814842

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 10)

TITLE Kemble,G.William.

JOURNAL VZV gene, mutant VZV and immunogenic compositions

FEATURES

source

1. .10

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 38.1%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 75;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCGCGC 15

Db 10 CGGCGCGC 3

RESULT 88
BD083308

LOCUS BD083308

DEFINITION Human matured/activated dendritic cell expression genes.

ACCESSION BD083308

VERSION BD083308.1 GI:22628918

KEYWORDS JP 2001327293-A/229.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 10)

TITLE Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.

JOURNAL Human matured/activated dendritic cell expression genes

COMMENT Patent: JP 2001327293-A 229 27-NOV-2001; JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2001327293-A/229

PD 27-NOV-2001

PF 22-MAY-2000 JP 2000150562

PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI NAGAI

PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00

CC

FH Key Location/Qualifiers.

FEATURES

source

1. .10

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 75;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCCG 9

Db 1 CTGGCCCG 8

RESULT 89
BD167068/c

LOCUS BD167068

DEFINITION Human liver disease-expressing genes.

ACCESSION BD167068

VERSION BD167068.1 GI:27872880

KEYWORDS JP 2002209591-A/613.

SOURCE unidentified

ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 613 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/613
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
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source Location/Qualifiers
1..10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GGCCCGGC 11
|||||
Db 8 GGCCCGGC 1
RESULT 90
BD167170/c
LOCUS BD167170 Human liver disease-expressing genes. linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167170
VERSION BD167170.1 GI:27872982
KEYWORDS JP 2002209591-A/715.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 715 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/715
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GGCCCGGC 11
|||||
Db 8 GGCCCGGC 1
RESULT 90
BD167170/c
LOCUS BD167170 Human liver disease-expressing genes. linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167170
VERSION BD167170.1 GI:27872982
KEYWORDS JP 2002209591-A/715.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 715 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/715
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Qy 4 GGCCCGGC 11
|||||
Db 8 GGCCCGGC 1
RESULT 91
BD238855
LOCUS BD238855 Preparation and use of superior vaccines. linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238855
VERSION BD238855.1 GI:33048625
KEYWORDS JP 2002534056-A/273.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 273 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/273
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 CGCTGTGG 20
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Db 1 CGCTGTGG 8
RESULT 92
BD240458/c
LOCUS BD240458 Preparation and use of superior vaccines. linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240458
VERSION BD240458.1 GI:33050228
KEYWORDS JP 2002534056-A/1876.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1876 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1876
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/08997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
G01N37/00,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
CC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTGGCCC 8
Db 9 GCTGGCCC 2
RESULT 93
E54660/c
LOCUS Human normal liver cell expression genes.
DEFINITION E54660
ACCESSION E54660.1 GI:22556143
VERSION JP 2001211883-A/12.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 12 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/12

PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers.
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source Location/Qualifiers
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/db_xref="taxon:9606"
Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GGCCCGGC 11
Db 8 GGCCCGGC 1
RESULT 94
AR490899/c
LOCUS AR490899 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 4 from patent US 6713296.
ACCESSION AR490899
VERSION AR490899.1 GI:47258429
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kemble,G.W.
TITLE VZV gene, mutant VZV and immunogenic compositions
JOURNAL Patent: US 6713296-A 4 30-MAR-2004;
MedImmune Vaccines, Inc.; Mountain View, CA
FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 CGGCGCGC 15
Db 10 CGGCGCGC 3
RESULT 95
AR630146/c
LOCUS AR630146 10 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 200 from patent US 6838556.
ACCESSION AR630146
VERSION AR630146.1 GI:59762471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 200 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCGCGCTG 17
| | | | | | | |
Db 9 GCGCGCTG 2

RESULT 96
AX224410/c
LOCUS AX224410 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 17 from Patent WO0160997.
ACCESSION AX224410
VERSION AX224410.1 GI:15554652
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 17 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source 1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGCCCGGC 11
| | | | | | | |
Db 9 GGCCCGGC 2

RESULT 97
BD124175
LOCUS BD124175 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124175
VERSION BD124175.1 GI:23219120
KEYWORDS JP 2002503460-A/6.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 6 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/6
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1. .11
/organism='Mus musculus (mouse)'.
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source 1. .11
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Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGCCCGGC 11
| | | | | | | |
Db 9 GGCCCGGC 2

RESULT 99
BD124474
LOCUS BD124474 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124474
VERSION BD124474.1 GI:23219419
KEYWORDS JP 2002503460-A/305.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 6 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/6
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1. .11
/organism='Mus musculus (mouse)'.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:10090"

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCCC 8
| | | | | | | |
Db 1 GCTGGCCC 8

RESULT 98
BD124339
LOCUS BD124339 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124339
VERSION BD124339.1 GI:23219284
KEYWORDS JP 2002503460-A/170.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 170 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/170
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1. .11
/organism='Mus musculus (mouse)'.
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source 1. .11
/organism="Mus musculus"
/mol_type="genomic DNA"
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCCC 8
| | | | | | | |
Db 1 GCTGGCCC 8

RESULT 99
BD124474
LOCUS BD124474 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124474
VERSION BD124474.1 GI:23219419
KEYWORDS JP 2002503460-A/305.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 6 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/6
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1. .11
/organism='Mus musculus (mouse)'.
FEATURES
source 1. .11
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

JOURNAL Patent: JP 2002503460-A 305 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/305
PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1..11
FT Location/Qualifiers
/organism='Mus musculus (mouse)'.
1..11
/organism='Mus musculus'
/mol_type='genomic DNA'
/db_xref='taxon:10090'

FEATURES source
Location/Qualifiers
1..11
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
Db 1 GCTGTGGC 8

RESULT 100
CQ834999
LOCUS CQ834999 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 57 from Patent WO2004059001.
ACCESSION CQ834999
VERSION CQ834999.1 GI:50834533
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 57 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES source
Location/Qualifiers
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 4 GCTGGCCC 11

RESULT 102
CQ838061
LOCUS CQ838061 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 3119 from Patent WO2004059001.
ACCESSION CQ838061
VERSION CQ838061.1 GI:50837595
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 3119 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES source
Location/Qualifiers
1..11
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGG 20
Db 1 CGCTGTGG 8

RESULT 103
CS058186/c
LOCUS CS058186 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 83 from Patent WO2005028671.
ACCESSION CS058186
VERSION CS058186.1 GI:62551138
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 83 31-MAR-2005;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2002 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES source
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 4 GCTGGCCC 11

RESULT 102
CQ838061
LOCUS CQ838061 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 3119 from Patent WO2004059001.
ACCESSION CQ838061
VERSION CQ838061.1 GI:50837595
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 3119 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES source
Location/Qualifiers
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/mol_type='unassigned DNA'
/db_xref='taxon:9606'

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGG 20
Db 1 CGCTGTGG 8

RESULT 103
CS058186/c
LOCUS CS058186 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 83 from Patent WO2005028671.
ACCESSION CS058186
VERSION CS058186.1 GI:62551138
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 83 31-MAR-2005;

FEATURES		Henkel Kommanditgesellschaft auf Aktien (DE)	
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		/db_xref="taxon:9606"	
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Best Local Similarity		100.0%; Pred. No. 1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 GCTGTGGC 21		
Db	8 GCTGTGGC 1		
RESULT 104			
AR301425			
LOCUS	AR301425	11 bp DNA	PAT 12-JUN-2003
DEFINITION	Sequence 6 from patent US 6538173.		
ACCESSION	AR301425		
VERSION	AR301425.1	GI:31689227	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 11)		
AUTHORS	Heber-Katz,E.		
TITLE	Compositions and methods for wound healing		
JOURNAL	Patent: US 6538173-A 6 25-MAR-2003;		
	The Wistar Institute; Philadelphia, PA;		
WOX;			
FEATURES		Location/Qualifiers	
source		1. .11	
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Query Match		38.1%; Score 8; DB 1; Length 11;	
Best Local Similarity		100.0%; Pred. No. 1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCTGGCCC 8		
Db	1 GCTGGCCC 8		
RESULT 105			
AR301589			
LOCUS	AR301589	11 bp DNA	PAT 12-JUN-2003
DEFINITION	Sequence 170 from patent US 6538173.		
ACCESSION	AR301589		
VERSION	AR301589.1	GI:31689391	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 11)		
AUTHORS	Heber-Katz,E.		
TITLE	Compositions and methods for wound healing		
JOURNAL	Patent: US 6538173-A 170 25-MAR-2003;		
	The Wistar Institute; Philadelphia, PA;		
WOX;			
FEATURES		Location/Qualifiers	
source		1. .11	
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		/mol_type="genomic DNA"	
Query Match		38.1%; Score 8; DB 1; Length 11;	
Best Local Similarity		100.0%; Pred. No. 1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCTGGCCC 8		
Db	1 GCTGGCCC 8		
RESULT 106			
AR301724			
LOCUS	AR301724	11 bp DNA	PAT 12-JUN-2003
DEFINITION	Sequence 305 from patent US 6538173.		
ACCESSION	AR301724		
VERSION	AR301724.1	GI:31689526	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 11)		
AUTHORS	Heber-Katz,E.		
TITLE	Compositions and methods for wound healing		
JOURNAL	Patent: US 6538173-A 305 25-MAR-2003;		
	The Wistar Institute; Philadelphia, PA;		
WOX;			
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Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 GCTGTGGC 21		
Db	1 GCTGTGGC 8		
RESULT 107			
AR605251/c			
LOCUS	AR605251	11 bp DNA	PAT 15-DEC-2004
DEFINITION	Sequence 42 from patent US 6818747.		
ACCESSION	AR605251		
VERSION	AR605251.1	GI:56656825	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 11)		
AUTHORS	Yao,Y. and Xu,H.		
TITLE	G.alpha.q protein variants and their use in the analysis and		
	discovery of agonists and antagonists of chemosensory receptors		
JOURNAL	Patent: US 6818747-A 42 16-NOV-2004;		
	Senomyx, Inc.; La Jolla, CA		
FEATURES		Location/Qualifiers	
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Query Match		38.1%; Score 8; DB 1; Length 11;	
Best Local Similarity		100.0%; Pred. No. 1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	8 CGGCGCGC 15		
Db	9 CGGCGCGC 2		
RESULT 108			
AX471838			
LOCUS	AX471838	11 bp DNA	PAT 09-AUG-2002
DEFINITION	Sequence 1415 from Patent WO02053773.		
ACCESSION	AX471838		
VERSION	AX471838.1	GI:22206963	
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

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REFERENCE
1
AUTHORS
TITLE
JOURNAL
METHOD for determining skin stress or skin ageing in vitro
PATENT: WO 02053773-A 1415 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 4 GCTGGCCC 11

RESULT 109
AX623061
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX623061
Sequence 102 from Patent WO02053774.
AX623061
AX623061.1 GI:28451002
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 102 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 3 GCTGGCCC 10

RESULT 110
AX623147/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX623147
Sequence 188 from Patent WO02053774.
AX623147
AX623147.1 GI:28451088
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 188 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
Db 3 GCTGGCCC 10

RESULT 111
AX6233827
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX6233827
Sequence 868 from Patent WO02053774.
AX6233827
AX6233827.1 GI:28451768
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 868 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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/organism="Homo sapiens"
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Query Match
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGGC 21
Db 8 GCTGTGGC 1

RESULT 112
AX626346
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX626346
Sequence 3387 from Patent WO02053774.
AX626346
AX626346.1 GI:28454384
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 3387 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Query Match
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
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REFERENCE
1
AUTHORS
TITLE
JOURNAL
METHOD for determining skin stress or skin ageing in vitro
PATENT: WO 02053773-A 1415 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
Db 8 GCTGTGGC 1

RESULT 111
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LOCUS
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Sequence 868 from Patent WO02053774.
AX6233827
AX6233827.1 GI:28451768
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 868 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/mol_type="unassigned DNA"
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Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCCGC 11
Db 1 GGCCCCGC 8

RESULT 112
AX626346
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX626346
Sequence 3387 from Patent WO02053774.
AX626346
AX626346.1 GI:28454384
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
TITLE
JOURNAL
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 3387 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 38.1%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
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Db 3 GCTGGCCC 10
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RESULT 113
AX627953
LOCUS AX627953 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4994 from Patent WO02053774.
ACCESSION AX627953
VERSION AX627953.1 GI:28455991
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4994 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Best Local Similarity 100.0%; Pred. No.1e+02;
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QY 1 GCTGGCCC 8
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Db 4 GCTGGCCC 11
RESULT 114
AX628349/c
LOCUS AX628349 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5390 from Patent WO02053774.
ACCESSION AX628349
VERSION AX628349.1 GI:28456387
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5390 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 100.0%; Pred. No.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GCTGTGGC 21
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Db 8 GCTGTGGC 1
RESULT 115
AX628842
LOCUS AX628842 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5883 from Patent WO02053774.
ACCESSION AX628842

VERSION AX628842.1 GI:28456880
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5883 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 100.0%; Pred. No.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGCCCGGC 8
RESULT 116
AX629565
LOCUS AX629565 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6606 from Patent WO02053774.
ACCESSION AX629565
VERSION AX629565.1 GI:28457603
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6606 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 CGCTGTGG 20
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Db 1 CGCTGTGG 8
RESULT 117
AX629711
LOCUS AX629711 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6752 from Patent WO02053774.
ACCESSION AX629711
VERSION AX629711.1 GI:28457749
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6752 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGCGCG 14
|||||
Db 1 CCGGCGCG 8

RESULT 118
AX630482
LOCUS AX630482 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7523 from Patent WO02053774.
ACCESSION AX630482
VERSION AX630482.1 GI:28458520
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7523 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
|||||
Db 3 GCTGGCCC 10

RESULT 119
AX630568/c
LOCUS AX630568 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7609 from Patent WO02053774.
ACCESSION AX630568
VERSION AX630568.1 GI:28458606
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7609 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
|||||
Db 8 GCTGTGGC 1

RESULT 120
AX631248
LOCUS AX631248 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8290 from Patent WO02053774.
ACCESSION AX631248
VERSION AX631248.1 GI:28459294
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8290 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCGGC 11
|||||
Db 1 GGCCCGGC 8

RESULT 121
CQ836510/c
LOCUS CQ836510 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1568 from Patent WO2004059001.
ACCESSION CQ836510
VERSION CQ836510.1 GI:50836044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1568 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGC 11
|||||
Db 11 GCCGGCCCGC 1

```
RESULT 122
AX628774/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 5815 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGGC 11
||| || |||||
Db 11 GCCGGGCCGGC 1

RESULT 123
CQ837882/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
Method for determining markers of human facial skin
JOURNAL
Patent: WO 2004059001-A 2940 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
| ||||| |||
Db 11 CGCGGCGGGCT 1

RESULT 124
AX629700/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
```

```

SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Petersohn,D., Conradt,M. and Hofmann,K.
TITLE
Method for determining homeostasis of the skin
JOURNAL
Patent: WO 02053774-A 6741 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
| ||||| |||
Db 11 CGCGGCGGGCT 1

RESULT 125
AR169386
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unassigned.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Borchert,T.Vedel., Kretzschmar,T. and Cherry,J.R.
TITLE
Shuffling of heterologous DNA sequences
JOURNAL
Patent: US 6291165-A 51 18-SEP-2001;
FEATURES
Location/Qualifiers
source
1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
| ||||| |||
Db 1 CCCGACGCGTT 11

RESULT 126
BD226182/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 11)
AUTHORS
Sheffield,V.C., Alward,W.L.M., Stone,E.M., Nishimura,D. and
Patil,S.
TITLE
Glaucoma therapeutics and diagnostics based on a novel human
transcription factor
JOURNAL
Patent: JP 2002511265-A 33 16-APR-2002;
THE UNIVERSITY OF IOWA RESEARCH FOUNDATION
```

```
COMMENT      OS      Homo sapiens (human)
PN      JP 2002511265-A/33
PD      16-APR-2002
PF      14-APR-1999 JP 2000543608
PR      15-APR-1998 US 60/081870,22-MAY-1998 US 09/083352 PI
VAL C SHEFFIELD,WALLACE L M ALWARD,EDWIN M STONE,DARRYL PI
NISHIMURA,
PI      SHIVA PATIL
PC      C12N15/00,A61K45/00,A61P27/06,C07K14/47,C12N1/15,C12N1/19, PC
      C12N1/21,
PC      C12N5/10,C12P21/02,C12Q1/68,G01N33/15,G01N33/50,C12N15/00, PC
      C12N5/00
CC      11 base pair deletion
FH      Key      Location/Qualifiers
FT      source      1. .11
FT      Location/Qualifiers
      1. .11
      /organism="Homo sapiens (human)".
FEATURES
source
      1. .11
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity      81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      5 GCCCGGCGCGC 15
Db      11 GCTCGGCGTGC 1

RESULT 127
BD250406/c
LOCUS
DEFINITION
      Methods for determination of single nucleic acid polymorphisms
      using a bioelectric microchip.
BD250406
VERSION      BD250406.1 GI:33060176
KEYWORDS      JP 2002541823-A/16.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Hominidae; Homo.
REFERENCE
AUTHORS      Nerenberg,M.I., Canter,D.M., Radtkey,R.R., OGconnell,J.P., Wang,L.
      and Sosnowski,R.G.
TITLE      Methods for determination of single nucleic acid polymorphisms
      using a bioelectric microchip
JOURNAL      Patent: JP 2002541823-A 16 10-DEC-2002;
      NANOGEN INC
COMMENT      OS      Homo sapiens (human)
PN      JP 2002541823-A/16
PD      10-DEC-2002
PF      28-MAR-2000 JP 2000611727
PR      12-APR-1999 US 09/290129
PI      MICHAEL I NERENBERG,DAVID M CANTER,RAY R RADTKEY,JAMES P PI
      O'CONNELL,
PI      LING WANG,RONALD G SOSNOWSKI
PC      C12N15/09,C12Q1/68,G01N33/53,G01N37/00,C12N15/00 CC      Methods
      for determination of single nucleic
      acid polymorphisms
CC      using a
CC      bioelectric microchip
FH      Key      Location/Qualifiers
FT      source      1. .11
FT      Location/Qualifiers
      1. .11
      /organism="Homo sapiens (human)".
FEATURES
source
      1. .11
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
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Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity      81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      2 CTGGCCCGCGC 12
Db      11 CTGCACAGCG 1

RESULT 128
CQ833470
LOCUS
DEFINITION
      Sequence 841 from Patent WO2004059002.
ACCESSION      CQ833470
VERSION      CQ833470.1 GI:50833077
KEYWORDS
      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
      Conradt,M. and Hofmann,K.
TITLE      Method for determining the homeostasis of hairy skin
JOURNAL      Patent: WO 2004059002-A 841 15-JUL-2004;
      Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
      Location/Qualifiers
      source      1. .11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity      81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      6 CCCGGCGCGCT 16
Db      1 CCCAACGCGCT 11

RESULT 129
CQ835047/c
LOCUS
DEFINITION
      Sequence 105 from Patent WO2004059001.
ACCESSION      CQ835047
VERSION      CQ835047.1 GI:50834581
KEYWORDS
      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
      Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
      Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 105 15-JUL-2004;
      Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
      Location/Qualifiers
      source      1. .11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity      81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      10 GCGCGCTGTGG 20
Db      11 GAGCGCAGTGG 1
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```
RESULT 130
CQ835073/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CQ835073
Sequence 131 from Patent WO2004059001.
CQ835073
CQ835073.1 GI:50834607
.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
JOURNAL
Patent: WO 2004059001-A 131 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGC 12
||||| ||
Db 11 CTGGCCCTCG 1

RESULT 131
CQ835177
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CQ835177
Sequence 235 from Patent WO2004059001.
CQ835177
CQ835177.1 GI:50834711
.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
JOURNAL
Patent: WO 2004059001-A 235 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
|| ||| |||
Db 1 CCAGGCACGCT 11

RESULT 132
CQ835213/c
LOCUS
DEFINITION
ACCESSION
CQ835213
Sequence 271 from Patent WO2004059001.
CQ835213
```

```
VERSION
KEYWORDS
SOURCE
ORGANISM
CQ835213.1 GI:50834747
.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
JOURNAL
Patent: WO 2004059001-A 271 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGGC 11
||||| |||
Db 11 GCTGGCTGGC 1

RESULT 133
CQ837144/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CQ837144
Sequence 2202 from Patent WO2004059001.
CQ837144
CQ837144.1 GI:50836678
.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE
JOURNAL
Patent: WO 2004059001-A 2202 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 37.1%; Score 7.8; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCCGGC 11
||||| |||
Db 11 GATGCCAGGC 1

RESULT 134
CQ837783
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CQ837783
Sequence 2841 from Patent WO2004059001.
CQ837783
CQ837783.1 GI:50837317
.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
```

```
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
        Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2841 15-JUL-2004;
        Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1. .11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGGCCCGGCG 12
    |||||
Db 1 CTGGCCCGGAG 11

RESULT 135
CS058279
LOCUS CS058279 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 176 from Patent WO2005028671.
ACCESSION CS058279
VERSION CS058279.1 GI:62551462
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
REFERENCE 1
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
        Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 176 31-MAR-2005;
        Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1. .11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCGCGCTGTG 19
    |||||
Db 1 GGGGTGCTGTG 11

RESULT 136
AR238595/c
LOCUS AR238595 11 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 16 from patent US 6468742.
ACCESSION AR238595
VERSION AR238595.1 GI:27283665
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
        Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Nerenberg,M.I., Canter,D.M., Radtkey,R.R., Wang,L., O'connell,J.P.
        and Sosnowski,R.G.
TITLE Methods for determination of single nucleic acid polymorphisms
        using bioelectronic microchip
JOURNAL Patent: US 6468742-A 16 22-OCT-2002;
        Nanogen, Inc.; San Diego, CA
FEATURES
source 1. .11
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        /organism="unknown"
        /mol_type="genomic DNA"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGGCCCGGCG 12
    |||||
Db 11 CTGGACAGGCG 1

RESULT 137
AX470499
LOCUS AX470499 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 76 from Patent WO02053773.
ACCESSION AX470499
VERSION AX470499.1 GI:22205624
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 76 11-JUL-2002;
        HENKEL KGAA (DE)
FEATURES
source 1. .11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
    |||||
Db 1 CCAGGCACGCT 11

RESULT 138
AX470547/c
LOCUS AX470547 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 124 from Patent WO02053773.
ACCESSION AX470547
VERSION AX470547.1 GI:22205672
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 124 11-JUL-2002;
        HENKEL KGAA (DE)
FEATURES
source 1. .11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
    |||||
```


JOURNAL Patent: WO 02053774-A 526 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGCG 15
| | | | |
Db 11 GCCAGGCGCCC 1

RESULT 144
AX623553
LOCUS AX623553 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 594 from Patent WO02053774.
ACCESSION AX623553
VERSION AX623553.1 GI:28451494
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 594 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCCGCGCGCT 16
| | | | |
Db 1 CCCAACGCGCT 11

RESULT 145
AX623825
LOCUS AX623825 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 866 from Patent WO02053774.
ACCESSION AX623825
VERSION AX623825.1 GI:28451766
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 866 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;

Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 GGCCCGGCGCG 14
| | | | |
Db 1 GGCTGGGCGCG 11

RESULT 146
AX623949
LOCUS AX623949 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 990 from Patent WO02053774.
ACCESSION AX623949
VERSION AX623949.1 GI:28451890
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 990 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCCGGCGCG 14
| | | | |
Db 1 GGCCAGGCGTG 11

RESULT 147
AX624226/c
LOCUS AX624226 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1267 from Patent WO02053774.
ACCESSION AX624226
VERSION AX624226.1 GI:28452167
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1267 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
| | | | |
Db 11 GAGTGTGTGG 1

RESULT 148

AX624477
LOCUS AX624477 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1518 from Patent WO02053774.
ACCESSION AX624477
VERSION AX624477.1 GI:28452418
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1518 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGGCCCCGGCGC 13
|| || |||||
Db 1 TGACCAAGGCGC 11

RESULT 149
AX624700/c
LOCUS AX624700 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1741 from Patent WO02053774.
ACCESSION AX624700
VERSION AX624700.1 GI:28452641
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1741 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GCGCGCTGTGG 20
| ||||| |||||
Db 11 GAGCGCAGTGG 1

RESULT 150
AX625055
LOCUS AX625055 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2096 from Patent WO02053774.
ACCESSION AX625055
VERSION AX625055.1 GI:28452996
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2096 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCCCGCGCGCGC 15
||||| |||
Db 1 GCCCGGTGCC 11

RESULT 151
AX625310/c
LOCUS AX625310 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2351 from Patent WO02053774.
ACCESSION AX625310
VERSION AX625310.1 GI:28453251
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2351 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GCGCGCTGTGG 20
||| || |||||
Db 11 GCGTGCAGTGG 1

RESULT 152
AX626546
LOCUS AX626546 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3587 from Patent WO02053774.
ACCESSION AX626546
VERSION AX626546.1 GI:28454584
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3587 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCGGCGCGCT 16
| | | | |
Db 1 CCAGGCACGCT 11

RESULT 153
AX626575/c
LOCUS AX626575 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3616 from Patent WO02053774.
ACCESSION AX626575
VERSION AX626575.1 GI:28454613
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3616 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGGCCCGCG 12
| | | | |
Db 11 CTGGCCCGCTCG 1

RESULT 154
AX626823
LOCUS AX626823 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3864 from Patent WO02053774.
ACCESSION AX626823
VERSION AX626823.1 GI:28454861
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3864 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCCCGCGC 13

Db 1 TGGTCCAGCG 11
| | | | |

RESULT 155
AX627065/c
LOCUS AX627065 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4106 from Patent WO02053774.
ACCESSION AX627065
VERSION AX627065.1 GI:28455103
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4106 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
| | | | |
Db 11 GAGAGCTGTGG 1

RESULT 156
AX627186/c
LOCUS AX627186 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4227 from Patent WO02053774.
ACCESSION AX627186
VERSION AX627186.1 GI:28455224
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4227 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCGCGCTGTG 19
| | | | |
Db 11 GGCAGGCTGTG 1

RESULT 157
AX627348
LOCUS AX627348 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4389 from Patent WO02053774.
ACCESSION AX627348

VERSION AX627348.1 GI:28455386
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4389 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 9 GGCGCGCTGTG 19
| | | | | | | |
Db 1 GGAGGGCTGTG 11
RESULT 158
AX627678
LOCUS AX627678 4719 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4719 from Patent WO02053774.
ACCESSION AX627678
VERSION AX627678.1 GI:28455716
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4719 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 9 GGCGCGCTGTG 19
| | | | | | | |
Db 1 GGCGCACTCTG 11
RESULT 159
AX628416
LOCUS AX628416 5457 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5457 from Patent WO02053774.
ACCESSION AX628416
VERSION AX628416.1 GI:28456454
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5457 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 9 GGCGCGCTGTG 19
| | | | | | | |
Db 1 GGCGTGCTGTG 11
RESULT 160
AX628487/c
LOCUS AX628487 5528 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5528 from Patent WO02053774.
ACCESSION AX628487
VERSION AX628487.1 GI:28456525
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5528 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 11 CGCGCTGTGGC 21
| | | | | | | |
Db 11 CTCGCTGGGGC 1
RESULT 161
AX629263
LOCUS AX629263 6304 from Patent WO02053774. 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6304 from Patent WO02053774.
ACCESSION AX629263
VERSION AX629263.1 GI:28457301
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6304 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;									
Best Local Similarity 81.8%; Pred. No. 1.2e+02;									
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	2	CTGGCCCGCGC	12						
Db	1	CTGGCCCCGAG	11						
RESULT 162									
AX629341									
LOCUS									
DEFINITION Sequence 6382 from Patent WO02053774.									
ACCESSION AX629341									
VERSION AX629341.1 GI:28457379									
KEYWORDS									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;									
Hominidae; Homo.									
REFERENCE									
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.									
TITLE Method for determining homeostasis of the skin									
JOURNAL Patent: WO 02053774-A 6382 11-JUL-2002;									
Henkel Kommanditgesellschaft auf Aktien (DE)									
FEATURES									
source									
1. .11									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match 37.1%; Score 7.8; DB 1; Length 11;									
Best Local Similarity 81.8%; Pred. No. 1.2e+02;									
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	9	GGCGCGCTGTG	19						
Db	1	GGCAGGCTGTG	11						
RESULT 163									
AX629452									
LOCUS									
DEFINITION Sequence 6493 from Patent WO02053774.									
ACCESSION AX629452									
VERSION AX629452.1 GI:28457490									
KEYWORDS									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;									
Hominidae; Homo.									
REFERENCE									
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.									
TITLE Method for determining homeostasis of the skin									
JOURNAL Patent: WO 02053774-A 6493 11-JUL-2002;									
Henkel Kommanditgesellschaft auf Aktien (DE)									
FEATURES									
source									
1. .11									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match 37.1%; Score 7.8; DB 1; Length 11;									
Best Local Similarity 81.8%; Pred. No. 1.2e+02;									
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	9	GGCGCGCTGTG	19						
Db	1	GGAGCACTGTG	11						
RESULT 164									
AX629452									
LOCUS									
DEFINITION Sequence 6493 from Patent WO02053774.									
ACCESSION AX629452									
VERSION AX629452.1 GI:28457490									
KEYWORDS									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;									
Hominidae; Homo.									
REFERENCE									
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.									
TITLE Method for determining homeostasis of the skin									
JOURNAL Patent: WO 02053774-A 6493 11-JUL-2002;									
Henkel Kommanditgesellschaft auf Aktien (DE)									
FEATURES									
source									
1. .11									
/organism="Homo sapiens"									
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/db_xref="taxon:9606"									
Query Match 37.1%; Score 7.8; DB 1; Length 11;									
Best Local Similarity 81.8%; Pred. No. 1.2e+02;									
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	9	GGCGCGCTGTG	19						
Db	1	GGAGCACTGTG	11						
RESULT 165									
AX629452									
LOCUS									
DEFINITION Sequence 6493 from Patent WO02053774.									
ACCESSION AX629452									
VERSION AX629452.1 GI:28457490									
KEYWORDS									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;									
Hominidae; Homo.									
REFERENCE									
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.									
TITLE Method for determining homeostasis of the skin									
JOURNAL Patent: WO 02053774-A 6493 11-JUL-2002;									
Henkel Kommanditgesellschaft auf Aktien (DE)									
FEATURES									
source									
1. .11									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match 37.1%; Score 7.8; DB 1; Length 11;									
Best Local Similarity 81.8%; Pred. No. 1.2e+02;									
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	9	GGCGCGCTGTG	19						
Db	1	GGAGCACTGTG	11						
RESULT 166									
AX629452									
LOCUS									
DEFINITION Sequence 6493 from Patent WO02053774.									
ACCESSION AX629452									
VERSION AX629452.1 GI:28457490									
KEYWORDS									
SOURCE Homo sapiens (human)									
ORGANISM Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;									
Hominidae; Homo.									
REFERENCE									
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.									
TITLE Method for determining homeostasis of the skin									
JOURNAL Patent: WO 02053774-A 6493 11-JUL-2002;									
Henkel Kommanditgesellschaft auf Aktien (DE)									
FEATURES									
source									
1. .11									
/organism="Homo sapiens"									
/mol_type="unassigned DNA"									
/db_xref="taxon:9606"									
Query Match 37.1%; Score 7.8; DB 1; Length 11;									
Best Local Similarity 81.8%; Pred. No. 1.2e+02;									
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	9	GGCGCGCTGTG	19						
Db	1	GGAGCACTGTG	11						

RESULT 164	AX629509/c	AX629509	Sequence 6550 from Patent WO02053774.	11 bp	DNA	linear	PAT 21-FEB-2003
LOCUS	AX629509	AX629509					
DEFINITION	AX629509	AX629509					
ACCESSION	AX629509.1	GI:28457547					
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							


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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7180 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTGGCCGCGC 11
    | ||||| |||
Db 11 GATGGCCAGGC 1

RESULT 167
AX630178
LOCUS      AX630178      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7219 from Patent WO02053774.
ACCESSION  AX630178
VERSION     AX630178.1 GI:28458216
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7219 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCCGGCGCGC 14
    | |||| | |||
Db 1 GGCCCTGAGCG 11

RESULT 168
AX630197/c
LOCUS      AX630197      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7238 from Patent WO02053774.
ACCESSION  AX630197
VERSION     AX630197.1 GI:28458235
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7238 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCCCGGCGC 13
    ||| |||||
Db 11 TGGGCGGCGC 1

RESULT 169
AX630410
LOCUS      AX630410      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7451 from Patent WO02053774.
ACCESSION  AX630410
VERSION     AX630410.1 GI:28458448
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7451 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
    ||||| |||||
Db 1 CACGCAGTGGC 11

RESULT 170
AX630906/c
LOCUS      AX630906      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7947 from Patent WO02053774.
ACCESSION  AX630906
VERSION     AX630906.1 GI:28458946
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7947 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 5 GCCCGGCGGC 15
Db 11 GCCAGGCGCC 1

RESULT 171
AX630974
LOCUS AX630974 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8015 from Patent WO02053774.
ACCESSION AX630974
VERSION AX630974.1 GI:28459016
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8015 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
Db 1 CCCAACGCGCT 11

RESULT 172
AX631246
LOCUS AX631246 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8288 from Patent WO02053774.
ACCESSION AX631246
VERSION AX631246.1 GI:28459292
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8288 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCCCGGCGCGC 14
Db 1 GGCTGGGCGCG 11

RESULT 173
AX631370
LOCUS AX631370 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8412 from Patent WO02053774.

ACCESSION AX631370
VERSION AX631370.1 GI:28459416
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8412 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCCCGGCGCGC 14
Db 1 GGCCAGGCGGTG 11

RESULT 174
AX631647/c
LOCUS AX631647 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8689 from Patent WO02053774.
ACCESSION AX631647
VERSION AX631647.1 GI:28459723
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8689 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCCGCGCTGTGG 20
Db 11 GAGTGTCTGTGG 1

RESULT 175
AX631898
LOCUS AX631898 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8940 from Patent WO02053774.
ACCESSION AX631898
VERSION AX631898.1 GI:28460036
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 8940 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source     1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          3 TGGCCCGCGGC 13
            |||||
Db          1 TGACCGAGCGC 11

RESULT 176
AX632121/c
LOCUS       AX632121                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 9163 from Patent WO02053774.
ACCESSION  AX632121
VERSION    AX632121.1 GI:28467736
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 9163 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source     1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          10 GCGCGCTGTGG 20
            ||||||
Db          11 GAGCGCAGTGG 1

RESULT 177
AX632476
LOCUS       AX632476                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 9518 from Patent WO02053774.
ACCESSION  AX632476
VERSION    AX632476.1 GI:28468091
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 9518 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source     1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          10 GCGCGCTGTGG 20
            ||||||
Db          11 GAGCGCAGTGG 1

RESULT 178
AX632731/c
LOCUS       AX632731                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 9773 from Patent WO02053774.
ACCESSION  AX632731
VERSION    AX632731.1 GI:28468346
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 9773 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source     1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          10 GCGCGCTGTGG 20
            |||||
Db          11 GCGTGCAGTGG 1

RESULT 179
AR103254
LOCUS       AR103254                10 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6087170.
ACCESSION  AR103254
VERSION    AR103254.1 GI:12814842
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Kemble,G.William.
TITLE      VZV gene, mutant VZV and immunogenic compositions
JOURNAL    Patent: US 6087170-A 4 11-JUL-2000;
            Location/Qualifiers
FEATURES
  source     1. .10
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match  35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 GGCGCGCTG 17
            |||||||
Db          2 GGCGCGCCG 10

RESULT 180
AR490899
LOCUS       AR490899                10 bp      DNA      linear      PAT 15-MAY-2004
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AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 8940 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source     1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          5 GCCCGCGCGC 15
            |||||||
Db          1 GCCCGGTGCC 11

RESULT 178
AX632731/c
LOCUS       AX632731                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 9773 from Patent WO02053774.
ACCESSION  AX632731
VERSION    AX632731.1 GI:28468346
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 9773 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
  source     1. .11
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match  37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          10 GCGCGCTGTGG 20
            |||||
Db          11 GCGTGCAGTGG 1

RESULT 179
AR103254
LOCUS       AR103254                10 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6087170.
ACCESSION  AR103254
VERSION    AR103254.1 GI:12814842
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Kemble,G.William.
TITLE      VZV gene, mutant VZV and immunogenic compositions
JOURNAL    Patent: US 6087170-A 4 11-JUL-2000;
            Location/Qualifiers
FEATURES
  source     1. .10
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match  35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 GGCGCGCTG 17
            |||||||
Db          2 GGCGCGCCG 10

RESULT 180
AR490899
LOCUS       AR490899                10 bp      DNA      linear      PAT 15-MAY-2004
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DEFINITION Sequence 4 from patent US 6713296.
ACCESSION AR490899
VERSION AR490899.1 GI:47258429
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kemble,G.W.
TITLE VZV gene, mutant VZV and immunogenic compositions
JOURNAL Patent: US 6713296-A 4 30-MAR-2004;
MedImmune Vaccines, Inc.; Mountain View, CA
FEATURES
source
1. .10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 GCGCGCGCTG 17
|||||||
Db 2 GCGCGCGCCG 10
RESULT 181
AR033182/c
LOCUS AR033182 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5869250.
ACCESSION AR033182
VERSION AR033182.1 GI:5948787
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Cheng,X. and Juliano,R.L.
TITLE Method for the identification of peptides that recognize specific
JOURNAL DNA sequences
Patent: US 5869250-A 4 09-FEB-1999;
FEATURES Location/Qualifiers
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GCGCGCGCGC 12
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Db 9 GCGCGCGCGC 1
RESULT 182
AR071781/c
LOCUS AR071781 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 10 from patent US 5912147.
ACCESSION AR071781
VERSION AR071781.1 GI:7222669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 10 15-JUN-1999;
FEATURES Location/Qualifiers
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 CCGCGCGCGC 15
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Db 10 CCGCGCGCGC 2
RESULT 183
AR071786
LOCUS AR071786 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 15 from patent US 5912147.
ACCESSION AR071786
VERSION AR071786.1 GI:7222674
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 15 15-JUN-1999;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GCGCGCTGT 18
|||||||
Db 2 GCGCGCGGT 10
RESULT 184
AR071787
LOCUS AR071787 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 16 from patent US 5912147.
ACCESSION AR071787
VERSION AR071787.1 GI:7222675
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 16 15-JUN-1999;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 GCGCGCTGT 18
|||||||
Db 2 GCGCGCGGT 10
RESULT 185
AR105774
LOCUS AR105774 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 43 from patent US 6103244.
ACCESSION AR105774
VERSION AR105774.1 GI:12819839
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dörner,F., Scheiflinger,F., Falkner,F.Gunter. and Pfleiderer,M.
TITLE Methods for generating immune responses employing modified vaccinia of fowlpox viruses
JOURNAL Patent: US 6103244-A 43 15-AUG-2000;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CTGGCCCGG 10
|| |||||
Db 1 CTAGCCCGG 9
RESULT 186
AR107796
LOCUS AR107796 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 42 from patent US 6110667.
ACCESSION AR107796
VERSION AR107796.1 GI:12823283
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis
JOURNAL Patent: US 6110667-A 42 29-AUG-2000;
FEATURES Location/Qualifiers
source 1. .10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CTGGCCCGG 10
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Db 1 CTAGCCCGG 9
RESULT 187
BD083124
LOCUS BD083124 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083124
VERSION BD083124.1 GI:22628734
KEYWORDS JP 2001327293-A/45.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 45 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001327293-A/45
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI

NAGAI
PC C12N15/09,C07K16/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10
RESULT 188
BD091134
LOCUS BD091134 10 bp DNA linear PAT 27-AUG-2002
DEFINITION P53-induced apoptosis.
ACCESSION BD091134
VERSION BD091134.1 GI:22636744
KEYWORDS JP 2001523441-A/12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Vogelstein,B., Kinzler,K.W. and Polyak,K.
TITLE P53-induced apoptosis
JOURNAL Patent: JP 2001523441-A 12 27-NOV-2001;
THE JOHNS HOPKINS UNIVERSITY
COMMENT OS Homo sapiens (human)
PN JP 2001523441-A/12
PD 27-NOV-2001
PF 17-SEP-1998 JP 2000511894
PR 17-SEP-1997 US 60/059153,30-MAR-1998 US 60/079817 PI
BERT VOGELSTEIN,KENNETH W KINZLER,KORNELIA POLYAK PC
C12Q1/68,C07K16/32,C12P21/08//C12N15/09,C12N15/00 CC P53-induced
apoptosis
FH Key Location/Qualifiers
FT source 1. .10
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FEATURES Location/Qualifiers
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GCCCGCGCGC 13
|||||
Db 2 GCCCGCGCGC 10
RESULT 189
BD091134/c
LOCUS BD091134 10 bp DNA linear PAT 27-AUG-2002
DEFINITION P53-induced apoptosis.
ACCESSION BD091134
VERSION BD091134.1 GI:22636744
KEYWORDS JP 2001523441-A/12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;


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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      35.2%;   Score 7.4;   DB 1;   Length 10;
Best Local Similarity 88.9%;   Pred. No. 1.1e+02;
Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      8   CGGCGCGCT 16
        |||||||
Db      10   CGGCGCTCT 2

RESULT 193
BD166486
LOCUS      BD166486                10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166486
VERSION    BD166486.1   GI:27872298
KEYWORDS   JP 2002209591-A/31.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1   (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 31 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002209591-A/31
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO   PI
            YAMASHITA
            PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC C12P21/08,
            CC Human liver disease-expressing genes
            FH Key      Location/Qualifiers
            FT source   1..10
            FT          /organism='Homo sapiens (human)'.

FEATURES             Location/Qualifiers
     source           1..10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

Query Match      35.2%;   Score 7.4;   DB 1;   Length 10;
Best Local Similarity 88.9%;   Pred. No. 1.1e+02;
Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      7   CCGCGCGCC 15
        |||||||
Db      2   CCGCGGCC 10

RESULT 194
BD166500/c
LOCUS      BD166500                10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166500
VERSION    BD166500.1   GI:27872312
KEYWORDS   JP 2002209591-A/45.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1   (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 45 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002209591-A/45
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PD      30-JUL-2002
PF      19-JAN-2001 JP 2001012328
PI      KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO   PI
            YAMASHITA
            PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC C12P21/08,
            PC C12N15/00
            CC Human liver disease-expressing genes
            FH Key      Location/Qualifiers
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            FT          /organism='Homo sapiens (human)'.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32644"

Query Match      35.2%;   Score 7.4;   DB 1;   Length 10;
Best Local Similarity 88.9%;   Pred. No. 1.1e+02;
Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      6   CCCGCGCG 14
        |||||||
Db      10   CCCGCGCG 2

RESULT 195
BD166712/c
LOCUS      BD166712                10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166712
VERSION    BD166712.1   GI:27872524
KEYWORDS   JP 2002209591-A/257.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1   (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 257 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002209591-A/257
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO   PI
            YAMASHITA
            PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC C12P21/08,
            PC C12N15/00
            CC Human liver disease-expressing genes
            FH Key      Location/Qualifiers
            FT source   1..10
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FEATURES             Location/Qualifiers
     source           1..10
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Query Match      35.2%;   Score 7.4;   DB 1;   Length 10;
Best Local Similarity 88.9%;   Pred. No. 1.1e+02;
Matches      8;   Conservative      0;   Mismatches      1;   Indels      0;   Gaps      0;

QY      6   CCCGCGCG 14
        |||||||
Db      10   CCCGCGCG 2

RESULT 196
BD166714/c
LOCUS      BD166714                10 bp      DNA      linear      PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
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ACCESSION BD166714
VERSION BD166714.1 GI:27872526
KEYWORDS JP 2002209591-A/259.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 259 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/259
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGGCGCGCT 16
|||||
Db 10 CGGCGCTCT 2

RESULT 197
BD166826
LOCUS Human liver disease-expressing genes.
DEFINITION
ACCESSION BD166826
VERSION BD166826.1 GI:27872638
KEYWORDS JP 2002209591-A/371.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 371 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/371
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
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PC C12P21/08,
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CC Human liver disease-expressing genes
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CGGCGCGCT 16
|||||
Db 10 CGGCGCTCT 2

RESULT 197
BD166826
LOCUS Human liver disease-expressing genes.
DEFINITION
ACCESSION BD166826
VERSION BD166826.1 GI:27872638
KEYWORDS JP 2002209591-A/371.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 371 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/371
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCCGGCGCG 14
|||||
Db 2 CCAGGCGCG 10

RESULT 198
BD166993
LOCUS Human liver disease-expressing genes.
DEFINITION
ACCESSION BD166993
VERSION BD166993.1 GI:27872805
KEYWORDS JP 2002209591-A/538.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 538 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/538
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCCGGCGCG 14
|||||
Db 2 CCAGGCGCG 10

RESULT 199
BD167029
LOCUS Human liver disease-expressing genes.
DEFINITION
ACCESSION BD167029
VERSION BD167029.1 GI:27872841
KEYWORDS JP 2002209591-A/574.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 574 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/574
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA

PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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FT Location/Qualifiers
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 GCGCGGCTG 17
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Db 2 GACGCGCTG 10
RESULT 200
BD167035
LOCUS BD167035 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167035
VERSION BD167035.1 GI:27872847
KEYWORDS JP 2002209591-A/580.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 580 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/580
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 CCGCGCGCGC 15
| | | | | | | |
Db 2 CCGGCGCCC 10
RESULT 201
BD167212
LOCUS BD167212 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167212
VERSION BD167212.1 GI:27873024
KEYWORDS JP 2002209591-A/757.
SOURCE unidentified

ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 757 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/757
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10 /organism='Homo sapiens (human)'.
FT Location/Qualifiers
FEATURES
source 1..10 /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TGGCCCGGC 11
| | | | | | | |
Db 2 TGGCCAGGC 10
RESULT 202
BD238593/c
LOCUS BD238593 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238593
VERSION BD238593.1 GI:33048363
KEYWORDS JP 2002534056-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 11 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/11
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC

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C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCG 14
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Db 10 CCCGGCGGG 2

RESULT 203
BD240040/C
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240040
VERSION BD240040.1 GI:33049810
KEYWORDS JP 2002534056-A/1458.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1458 15-OCT-2002;
GENZYME CORP

OS Homo sapiens (human)
PN JP 2002534056-A/1458
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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/organism='Homo sapiens (human)'.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCG 14
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Db 10 CCCGGCGGG 2

RESULT 204
BD240685
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240685
VERSION BD240685.1 GI:33050455
KEYWORDS JP 2002534056-A/2103.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 2103 15-OCT-2002;
GENZYME CORP

OS Homo sapiens (human)
PN JP 2002534056-A/2103
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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Location/Qualifiers
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/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCGCTGTGG 20
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Db 2 GGGCTGTGG 10

RESULT 205
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCG 9
| | | | | | |
Db 9 GCTGGCCCG 1

RESULT 204
BD240685
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240685
VERSION BD240685.1 GI:33050455
KEYWORDS JP 2002534056-A/2103.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 2103 15-OCT-2002;
GENZYME CORP

OS Homo sapiens (human)
PN JP 2002534056-A/2103
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCGCTGTGG 20
| | | | | | |
Db 2 GGGCTGTGG 10

RESULT 205
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CQ759089 LOCUS CQ759089 10 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 1 from Patent WO2003106681.
ACCESSION CQ759089
VERSION CQ759089.1 GI:44849080
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Altan,O., Kurreck,J., Gruenweller,A. and Erdmann,V.
TITLE Antisense oligonucleotides against pimi
JOURNAL Patent: WO 2003106681-A 1 24-DEC-2003; Gruenenthal GmbH (DE)
FEATURES Location/Qualifiers
source 1..10
/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCCGCG 11
| | | | | | | |
Db 2 TTGCCCGCGC 10

RESULT 206
CQ772477/c LOCUS CQ772477 10 bp DNA linear PAT 04-MAR-2004
DEFINITION Sequence 78 from Patent WO2004011677.
ACCESSION CQ772477
VERSION CQ772477.1 GI:45126203
KEYWORDS
SOURCE Equid herpesvirus 1 (Equine herpesvirus 1)
ORGANISM Equid herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
REFERENCE 1
AUTHORS Davis Poynter,N., Nugent,J., Birch-Machin,I. and Allen,G.
TITLE Viral marker
JOURNAL Patent: WO 2004011677-A 78 05-FEB-2004; ANIMAL HEALTH TRUST (GB)
FEATURES Location/Qualifiers
source 1..10
/organism="Equid herpesvirus 1"
/mol_type="unassigned DNA"
/db_xref="taxon:10326"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCCGG 10
| | | | | | | |
Db 10 CTGGCTCGG 2

RESULT 207
CQ945058 LOCUS CQ945058 10 bp DNA linear PAT 01-DEC-2004
DEFINITION Sequence 205 from Patent WO2004099445.
ACCESSION CQ945058
VERSION CQ945058.1 GI:56294399
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1

AUTHORS Kahl,G., Winter,P., Krueger,D., Reich,S., Matsumura,H. and Terauchi,R.
TITLE Use of a type iii restriction enzyme to isolate identification tags comprising more than 25 nucleotides
JOURNAL Patent: WO 2004099445-A 205 18-NOV-2004; Iwate Prefectual Government (JP)
FEATURES Location/Qualifiers
source 1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Description of Artificial Sequence:Synthetic DNA (Tag Sequence)"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGCCCCGCGC 12
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Db 2 GGCGCGGCG 10

RESULT 208
CS128776/c LOCUS CS128776 10 bp DNA linear PAT 02-AUG-2005
DEFINITION Sequence 9 from Patent WO2005064015.
ACCESSION CS128776
VERSION CS128776.1 GI:71794797
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Khanuja,S.P.
JOURNAL Patent: WO 2005064015-A 9 14-JUL-2005; Council of Scientific and Industrial Research (IN)
FEATURES Location/Qualifiers
source 1..10
/organism="synthetic construct"
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/note="A primer used in RAPD for identifying plants having high content of artemisinin"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGCGCGCGC 15
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Db 9 CCGCGCTGC 1

RESULT 209
E39489 LOCUS E39489 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION E39489
VERSION E39489.1 GI:18621580
KEYWORDS JP 2000279181-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE Genes with human dendritic cell expression
JOURNAL Patent: JP 2000279181-A 22 10-OCT-2000; SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2000279181-A/22

PD 10-OCT-2000
PF 01-APR-1999 JP 1999095481
PR
PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
C12N15/09,C07K14/475,C07K16/18,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGGCCCGGC 11
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Db 2 TGGCCAGGC 10
RESULT 210
E54829
LOCUS Human normal liver cell expression genes. 10 bp DNA linear PAT 27-AUG-2002
DEFINITION E54829
ACCESSION E54829
VERSION E54829.1 GI:22556312
KEYWORDS JP 2001211883-A/181.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 181 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/181
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10
RESULT 211
AR222959
LOCUS Sequence 12 from patent US 6432640.
DEFINITION AR222959
ACCESSION AR222959
VERSION AR222959.1 GI:23330797
KEYWORDS
SOURCE Unknown.
Query Match 35.2%; Score 7.4; DB 1; Length 10;

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Polyak,K., Vogelstein,B. and Kinzler,K.W.
TITLE P53-induced apoptosis
JOURNAL Patent: US 6432640-A 12 13-AUG-2002;
The Johns Hopkins University; Baltimore, MD;
WOX;
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Location/Qualifiers
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GCCCGCGC 13
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Db 2 GCCCGCGC 10
RESULT 212
AR222959/c
LOCUS Sequence 12 from patent US 6432640. 10 bp DNA linear PAT 26-SEP-2002
DEFINITION AR222959
ACCESSION AR222959
VERSION AR222959.1 GI:23330797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Polyak,K., Vogelstein,B. and Kinzler,K.W.
TITLE P53-induced apoptosis
JOURNAL Patent: US 6432640-A 12 13-AUG-2002;
The Johns Hopkins University; Baltimore, MD;
WOX;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
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Query Match 35.2%; Score 7.4; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CGGCGCGCT 16
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Db 9 CGGCGGCT 1
RESULT 213
AR241748/c
LOCUS Sequence 36 from patent US 6472154. 10 bp DNA linear PAT 20-DEC-2002
DEFINITION AR241748
ACCESSION AR241748
VERSION AR241748.1 GI:27287560
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 36 29-OCT-2002;
Board of Regents, The University of Texas System; Austin, TX
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source
Location/Qualifiers
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/mol_type="genomic DNA"
Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGGCGC 13
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Db 9 GCCCGGCC 1

RESULT 214
AR241871/c
LOCUS AR241871 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 159 from patent US 6472154.
ACCESSION AR241871
VERSION AR241871.1 GI:27287683
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 159 29-OCT-2002;
Board of Regents, The University of Texas System; Austin, TX
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGGCGC 13
| | | | | | | |
Db 9 GCCCGGCC 1

RESULT 215
AR261814
LOCUS AR261814 10 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 240 from patent US 6322995.
ACCESSION AR261814
VERSION AR261814.1 GI:28072954
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hohmann,H.-P., Humbelin,M., van Loon,A. and Schurter,W.
TITLE Riboflavin production
JOURNAL Patent: US 6322995-A 240 27-NOV-2001;
F. Hoffmann-La Roche AG; Basel;
EPX;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCG 14
| | | | | | | |
Db 1 CCCAGCGCG 9

RESULT 216
AR261814/c
LOCUS AR261814 10 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 240 from patent US 6322995.
ACCESSION AR261814
VERSION AR261814.1 GI:28072954

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hohmann,H.-P., Humbelin,M., van Loon,A. and Schurter,W.
TITLE Riboflavin production
JOURNAL Patent: US 6322995-A 240 27-NOV-2001;
F. Hoffmann-La Roche AG; Basel;
EPX;
FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 CGCGCTGTG 19
| | | | | | | |
Db 9 CGCGCTGG 1

RESULT 217
AR310513/c
LOCUS AR310513 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6558940.
ACCESSION AR310513
VERSION AR310513.1 GI:31703523
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Alam,M., Sattar,A., Kumar,S., Samad,A., Dhawan,O.P.,
Khanuja,S.P.S., Shasany,A.K., Singh,S., Kumar,P.V.N.A., Khaliq,A.,
Zaim,M., Shahabuddin,S. and Trivedi,M.
TITLE Streptomyces strain with potential anti-microbial activity against
phytopathogenic fungi
JOURNAL Patent: US 6558940-A 3 06-MAY-2003;
Council of Scientific and Industrial Research;;
INX;
FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGCGCGC 15
| | | | | | | |
Db 9 CCGCGCTGC 1

RESULT 218
AR336888/c
LOCUS AR336888 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6566130.
ACCESSION AR336888
VERSION AR336888.1 GI:33722738
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 63 20-MAY-2003;
Henry M. Jackson Foundation for the Advancement of Military
Medicine; Rockville, MD

FEATURES source Location/Qualifiers
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGGC 11
| | | | | | | |
Db 10 TGGCCCGGC 2

RESULT 219
AR630140
LOCUS AR630140 10 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 194 from patent US 6838556.
ACCESSION AR630140
VERSION AR630140.1 GI:59762459
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Kim, M.Y. and Bruice, T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 194 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES source Location/Qualifiers
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
| | | | | | | |
Db 1 GGCGCGCGG 9

RESULT 220
AR630150
LOCUS AR630150 10 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 204 from patent US 6838556.
ACCESSION AR630150
VERSION AR630150.1 GI:59762479
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Kim, M.Y. and Bruice, T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 204 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES source Location/Qualifiers
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGCT 16
| | | | | | | |

Db 2 CCGCGCGCT 10

RESULT 221
AR630153/c
LOCUS AR630153 10 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 207 from patent US 6838556.
ACCESSION AR630153
VERSION AR630153.1 GI:59762485
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim, J.P., Starr, D.B., Tam, A.W., Laurance, M.E., Michelotti, E.F., Velligan, M.D., Latour, D.R., Thomas, R.L., Kongpachith, A., Sheppard, L.T., Kim, M.Y. and Bruice, T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 207 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES source Location/Qualifiers
1. .10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGT 18
| | | | | | | |
Db 9 GCGCGCTTT 1

RESULT 222
AX006877/c
LOCUS AX006877 10 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 30 from Patent WO0001832.
ACCESSION AX006877
VERSION AX006877.1 GI:9994892
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fenoll-Comes, C. and Munoz-Martin, M.D.
TITLE Inducible promoters
JOURNAL Patent: WO 0001832-A 30 13-JAN-2000;
FENOLL COMES CARMEN (ES); MUNOZ MARTIN MARIA DE LOS ANGE (ES); PLANT BIOSCIENCE LIMITED (GB)
FEATURES source Location/Qualifiers
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
| | | | | | | |
Db 10 CCGGCCCGG 2

RESULT 223
AX152364
LOCUS AX152364 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 279 from Patent WO0138577.
ACCESSION AX152364
VERSION AX152364.1 GI:14534015
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 279 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 GCGCTGTGG 20
| | | | | | | |
Db 2 GGGCTGTGG 10
RESULT 224
AX152365
LOCUS AX152365 Sequence 280 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION AX152365
ACCESSION AX152365
VERSION AX152365.1 GI:14534016
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 280 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 GCGCTGTGG 20
| | | | | | | |
Db 2 GGGCTGTGG 10
RESULT 225
AX152532/c
LOCUS AX152532 Sequence 447 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION AX152532
ACCESSION AX152532
VERSION AX152532.1 GI:14534183
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 447 31-MAY-2001;

FEATURES The Johns Hopkins University (US)
source Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 13 CGCTGTGGC 21
| | | | | | | |
Db 9 CGCTGGGC 1
RESULT 226
AX152671/c
LOCUS AX152671 Sequence 586 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION AX152671
ACCESSION AX152671
VERSION AX152671.1 GI:14534322
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 586 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 13 CGCTGTGGC 21
| | | | | | | |
Db 10 CGCAGTGGC 2
RESULT 227
AX153299/c
LOCUS AX153299 Sequence 1214 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION AX153299
ACCESSION AX153299
VERSION AX153299.1 GI:14534950
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1214 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 13 CGCTGTGGC 21
| | | | | | | |
Db 10 CGCAGTGGC 2

	Matches	8;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	3	TTGGCCCTCGGC	11							
Db	9	TTGGCCAGGC	1							

RESULT	228
AX153300/c	
LOCUS	AX153300
DEFINITION	Sequence 1215 from Patent WO0138577.
ACCESSION	AX153300
VERSION	AX153300.1 GI:14534951
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	1	Velculescu, V.E., Vogelstein, B. and Kinzler, K.W. Human transcriptomes Patent: WO 0138577-A 1215 31-MAY-2001; The Johns Hopkins University (US) Location/Qualifiers
AUTHORS		
TITLE		
JOURNAL		
FEATURES		

Query Match	35.2%	Score 7.4;	DB 1;	Length 10;
Best Local Similarity	88.9%;	Pred. No. 1.1e+02;		
Matches 8;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0;

RESULT 229					
AX153313					
LOCUS	AX153313	10 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 1228 from Patent WO0138577.				
ACCESSION	AX153313				
VERSION	AX153313.1	GI:14534964			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominoidea; Homo.				

REFERENCE	1	Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS		Human transcripts
TITLE		Patent: WO 0138577-A 1228 31-MAY-2001;
JOURNAL		The Johns Hopkins University (US)
FEATURES		Location/Qualifiers

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 230	ORGANISM
AX153314	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

LOCUS AX153314 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1229 from Patent WO0138577.
ACCESSION AX153314
VERSION AX153314.1 GI:14534965
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Human transcriptomes
TITLE
JOURNAL Patent: WO 0138577-A 1229 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. NO. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 231
AX153315
LOCUS AX153315 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1230 from Patent WO0138577.
ACCESSION AX153315
VERSION AX153315.1 GI:14534966
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

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Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TGCCCCGGC 11
        ||||| |||
Db      2 TGCCAGGC 10

```

RESULT	232
AX153316	
LOCUS	AX153316
DEFINITION	Sequence 1231 from Patent WO0138577.
ACCESSION	AX153316
VERSION	AX153316.1 GI:14534967
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1231 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10

RESULT 233
AX153317
LOCUS AX153317 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1232 from Patent WO0138577.
ACCESSION AX153317
VERSION AX153317.1 GI:14534968
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1232 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10

RESULT 234
AX153318
LOCUS AX153318 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1233 from Patent WO0138577.
ACCESSION AX153318
VERSION AX153318.1 GI:14534969
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1233 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10

RESULT 235
AX153319
LOCUS AX153319 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1234 from Patent WO0138577.
ACCESSION AX153319
VERSION AX153319.1 GI:14534970
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1234 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10

RESULT 236
AX224406
LOCUS AX224406 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 13 from Patent WO0160997.
ACCESSION AX224406
VERSION AX224406.1 GI:15554648
KEYWORDS .
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 13 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCG 9
|||||

Db 1 GCGGGCCCCG 9

RESULT 237
AX224406/c

LOCUS AX224406 10 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 13 from Patent WO0160997.

ACCESSION AX224406

VERSION AX224406.1 GI:15554648

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.

TITLE Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 13 23-AUG-2001;

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

source

1. .10

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.le+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9

Db 10 GCGGGCCCCG 2

RESULT 238
AX224408

LOCUS AX224408 10 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 15 from Patent WO0160997.

ACCESSION AX224408

VERSION AX224408.1 GI:15554650

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.

TITLE Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 15 23-AUG-2001;

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

source

1. .10

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.le+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9

Db 2 GCGGGCCCCG 10

RESULT 239
AX224412

LOCUS AX224412 10 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 19 from Patent WO0160997.

ACCESSION AX224412

VERSION AX224412.1 GI:15554654

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.

TITLE Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 19 23-AUG-2001;

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

source

1. .10

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.le+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9

Db 10 GCGGGCCCCG 2

RESULT 240
AX224412/c

LOCUS AX224412 10 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 19 from Patent WO0160997.

ACCESSION AX224412

VERSION AX224412.1 GI:15554654

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.

TITLE Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 19 23-AUG-2001;

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

source

1. .10

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.le+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9

Db 10 GCGGGCCCCG 2

RESULT 241
AX224413

LOCUS AX224413 10 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 20 from Patent WO0160997.

ACCESSION AX224413

VERSION AX224413.1 GI:15554655

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.

TITLE Male tissue-preferred regulatory region and method of using same

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.

TITLE Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 19 23-AUG-2001;

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

Location/Qualifiers

1. .10

/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.le+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9

Db 1 GCGGGCCCCG 9

RESULT 240
AX224412/c

LOCUS AX224412 10 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 19 from Patent WO0160997.

ACCESSION AX224412

VERSION AX224412.1 GI:15554654

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.

TITLE Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 19 23-AUG-2001;

PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

Location/Qualifiers

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/organism="Zea mays"

/mol_type="unassigned DNA"

/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.le+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9

Db 10 GCGGGCCCCG 2

RESULT 241
AX224413

LOCUS AX224413 10 bp DNA linear PAT 10-SEP-2001

DEFINITION Sequence 20 from Patent WO0160997.

ACCESSION AX224413

VERSION AX224413.1 GI:15554655

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.

TITLE Male tissue-preferred regulatory region and method of using same

JOURNAL Patent: WO 0160997-A 20 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
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1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCG 9
||| |||||
Db 1 GCGGGCCCG 9

RESULT 242
AX224413/c
LOCUS AX224413 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 20 from Patent WO0160997.
ACCESSION AX224413
VERSION AX224413.1 GI:15554655
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 20 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCG 9
||| |||||
Db 10 GCGGGCCCG 2

RESULT 243
AX224414
LOCUS AX224414 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 21 from Patent WO0160997.
ACCESSION AX224414
VERSION AX224414.1 GI:15554656
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 21 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCGCCGGCG 12
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Db 2 GCGCCGGCG 10

RESULT 244
AX224415/c
LOCUS AX224415 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 22 from Patent WO0160997.
ACCESSION AX224415
VERSION AX224415.1 GI:15554657
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 22 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCG 9
||| |||||
Db 9 GCGGGCCCG 1

RESULT 245
AX224416/c
LOCUS AX224416 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 23 from Patent WO0160997.
ACCESSION AX224416
VERSION AX224416.1 GI:15554658
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 23 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCG 9
||| |||||
Db 9 GCGGGCCCG 1

RESULT 246
AX224416/c
LOCUS AX224416 10 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 23 from Patent WO0160997.
ACCESSION AX224416
VERSION AX224416.1 GI:15554658
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L.
TITLE Male tissue-preferred regulatory region and method of using same
JOURNAL Patent: WO 0160997-A 23 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
1. .10
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCG 9
||| |||||
Db 9 GCGGGCCCG 1

RESULT 246

AX601650
LOCUS AX601650 10 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 32 from Patent WO02092825.
ACCESSION AX601650
VERSION AX601650.1 GI:28401695
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mikkelsen,J.G., Rasmussen,S.V., Duch,M., Pedersen,F.S. and Aagaard,L.
TITLE Improved vectors for gene therapy
JOURNAL Patent: WO 02092825-A 32 21-NOV-2002;
Aarhus University (DK)
FEATURES
source Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="palindrome at position 209-218 in Akv/AkvB"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9
|||||||
Db 1 GCTGGCCAG 9

RESULT 247
AX601650/c
LOCUS AX601650 10 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 32 from Patent WO02092825.
ACCESSION AX601650
VERSION AX601650.1 GI:28401695
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mikkelsen,J.G., Rasmussen,S.V., Duch,M., Pedersen,F.S. and Aagaard,L.
TITLE Improved vectors for gene therapy
JOURNAL Patent: WO 02092825-A 32 21-NOV-2002;
Aarhus University (DK)
FEATURES
source Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="palindrome at position 209-218 in Akv/AkvB"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9
|||||||
Db 1 GCTGGCCAG 9

RESULT 247
AX601650/c
LOCUS AX601650 10 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 32 from Patent WO02092825.
ACCESSION AX601650
VERSION AX601650.1 GI:28401695
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mikkelsen,J.G., Rasmussen,S.V., Duch,M., Pedersen,F.S. and Aagaard,L.
TITLE Improved vectors for gene therapy
JOURNAL Patent: WO 02092825-A 32 21-NOV-2002;
Aarhus University (DK)
FEATURES
source Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="palindrome at position 209-218 in Akv/AkvB"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCG 9
|||||||
Db 10 GCTGGCCAG 2

RESULT 248
AX958217
LOCUS AX958217 10 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 20 from Patent WO03046156.
ACCESSION AX958217
VERSION AX958217.1 GI:40785870
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified sequences.

REFERENCE 1
AUTHORS Claude,P.P.
TITLE Novel bacterial biomasses, method for obtaining same and uses thereof for bacterization of soils and crop residues
JOURNAL Patent: WO 03046156-A 20 05-JUN-2003;
Valbios (FR)
FEATURES
source Location/Qualifiers
1..10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Azobacter"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCCGGCGCG 14
|||||
Db 2 CCCAGCGCG 10

RESULT 249
AX958217/c
LOCUS AX958217 10 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 20 from Patent WO03046156.
ACCESSION AX958217
VERSION AX958217.1 GI:40785870
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Claude,P.P.
TITLE Novel bacterial biomasses, method for obtaining same and uses thereof for bacterization of soils and crop residues
JOURNAL Patent: WO 03046156-A 20 05-JUN-2003;
Valbios (FR)
FEATURES
source Location/Qualifiers
1..10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Azobacter"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 CGCGCTGTG 19
|||||||
Db 10 CGCGCTGGG 2

RESULT 250
BD007953/c
LOCUS BD007953 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007953
VERSION BD007953.1 GI:18636326
KEYWORDS JP 2001069993-A/229.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 229 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/229

PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
/organism='Homo sapiens (human)'.
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGC 11
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Db 9 TGGCCAGC 1

RESULT 251
BD007960/c
LOCUS 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007960
VERSION BD007960.1 GI:18636333
KEYWORDS JP 2001069993-A/236.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 236 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/236
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10
FT Location/Qualifiers
/organism='Homo sapiens (human)'.
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/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGC 14
|||||
Db 9 CCCGTGCG 1

RESULT 252
AX623125

LOCUS AX623125 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 166 from Patent WO02053774.
ACCESSION AX623125
VERSION AX623125.1 GI:28451066
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 166 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCG 10
|||||
Db 3 CTGGCCAGG 11

RESULT 253
AX630546
LOCUS 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7587 from Patent WO02053774.
ACCESSION AX630546
VERSION AX630546.1 GI:28458584
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 7587 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCG 10
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Db 3 CTGGCCAGG 11

RESULT 254
AR605251
LOCUS 11 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 42 from patent US 6818747.
ACCESSION AR605251
VERSION AR605251.1 GI:56656825
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)

AUTHORS Yao, Y. and Xu, H.
TITLE G.alpha.q protein variants and their use in the analysis and discovery of agonists and antagonists of chemosensory receptors
JOURNAL Patent: US 6818747-A 42 16-NOV-2004;
Senomyx, Inc.; La Jolla, CA
FEATURES
source
1. .11
/organism="unknown"
/mol_type="genomic DNA"
Query Match 35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 GGCGCGCTG 17
| | | | | | |
Db 1 GGCGCGCCG 9
RESULT 255
CQ766499/c
LOCUS CQ766499 12 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 460 from Patent WO2004005547.
ACCESSION CQ766499
VERSION CQ766499.1 GI:44908759
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weinzierl, R.
TITLE Method
JOURNAL Patent: WO 2004005547-A 460 15-JAN-2004;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source
1. .12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HS motif"
Query Match 35.2%; Score 7.4; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CTGGCCCGG 10
| | | | | | |
Db 9 CGGGCCCGG 1
RESULT 256
CQ786323/c
LOCUS CQ786323 16 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 131 from Patent WO2004020668.
ACCESSION CQ786323
VERSION CQ786323.1 GI:45721425
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Nakamura, Y. and Katagiri, T.
TITLE Method for treating synovial sarcoma
JOURNAL Patent: WO 2004020668-A 131 11-MAR-2004;
Oncotherapy Science, Inc. (JP); The University of Tokyo (JP)
FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: synthetic oligonucleotide"

Query Match 34.3%; Score 7.2; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 GCGCGCTGTGGC 21
| | | | | | |
Db 16 GCGCGCCGGCC 5
RESULT 257
AR086219
LOCUS AR086219 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 40 from patent US 5985558.
ACCESSION AR086219
VERSION AR086219.1 GI:10012985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean, N.M., McKay, R., Miraglia, L. and Baker, B.
TITLE Antisense oligonucleotide compositions and methods for the inhibition of c-Jun and c-Fos
JOURNAL Patent: US 5985558-A 40 16-NOV-1999;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 34.3%; Score 7.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 8 CGCGCGCTGTG 19
| | | | | | |
Db 5 CAGCGCGCCGG 16
RESULT 258
AR176785
LOCUS AR176785 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 40 from patent US 6312900.
ACCESSION AR176785
VERSION AR176785.1 GI:17919140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean, N.M., McKay, R., Miraglia, L. and Baker, B.
TITLE Antisense oligonucleotide compositions and methods for the modulation of activating protein 1
JOURNAL Patent: US 6312900-A 40 06-NOV-2001;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 34.3%; Score 7.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 3.4e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 8 CGCGCGCTGTG 19
| | | | | | |
Db 5 CAGCGCGCCGG 16
RESULT 259
E54824
LOCUS E54824 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION E54824
VERSION E54824.1 GI:225556307

```
KEYWORDS      JP 2001211883-A/176.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1 (bases 1 to 10)
AUTHORS      Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE        Human normal liver cell expression genes
JOURNAL      Patent: JP 2001211883-A 176 07-AUG-2001;
              SCIENCE & TECH AGENCY
COMMENT      OS Homo sapiens (human)
              PN JP 2001211883-A/176
              PD 07-AUG-2001
              PF 31-JAN-2000 JP 2000023170
              PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
              YAMASHITA
              PC C12N15/09, C07K16/18, C12P21/02, C12N15/00
              CC
FEATURES      FH Key Location/Qualifiers.
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                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGC 11
    |||||
Db 4 GCCCGGC 10

RESULT 260
A05335/c
LOCUS      A05335 Synthetic NarI restriction site. 10 bp DNA linear PAT 04-MAY-1993
DEFINITION A05335
ACCESSION  A05335
VERSION    A05335.1 GI:345064
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 10)
AUTHORS   .
TITLE     A PROCESS FOR PREPARING A PROTEIN OR POLYPEPTIDE, A DNA SEQUENCE
          CODING FOR THE POLYPEPTIDE, A MICROORGANISM CONTAINING THE DNA
          SEQUENCE AS WELL AS THE POLYPEPTIDE AND ITS USE AS A PHARMACEUTICAL
          PREPARATION
JOURNAL    Patent: WO 8810299-A 2 29-DEC-1988;
FEATURES   Location/Qualifiers
          source 1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGCGC 13
    |||||
Db 9 CCGGCGC 3

RESULT 261
AR036559
LOCUS      AR036559 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5872235.
ACCESSION  AR036559
VERSION    AR036559.1 GI:5953227
```

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KEYWORDS      .
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 10)
AUTHORS      Chen,L.BO., Bao,S. and Liu,Y.
TITLE        Nucleic acids encoding tumor marker
JOURNAL      Patent: US 5872235-A 12 16-FEB-1999;
              Location/Qualifiers
              source 1..10
                  /organism="unknown"
                  /mol_type="unassigned DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGC 11
    |||||
Db 2 GCCCGGC 8

RESULT 262
AR071790/c
LOCUS      AR071790 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 19 from patent US 5912147.
ACCESSION  AR071790
VERSION    AR071790.1 GI:7222678
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Stoler,D., Basik,M. and Anderson,G.
TITLE      Rapid means of quantitating genomic instability
JOURNAL    Patent: US 5912147-A 19 15-JUN-1999;
              Location/Qualifiers
              source 1..10
                  /organism="unknown"
                  /mol_type="unassigned DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGGCGC 15
    |||||
Db 10 GGCGGCGC 4

RESULT 263
AR071791
LOCUS      AR071791 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 20 from patent US 5912147.
ACCESSION  AR071791
VERSION    AR071791.1 GI:7222679
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Stoler,D., Basik,M. and Anderson,G.
TITLE      Rapid means of quantitating genomic instability
JOURNAL    Patent: US 5912147-A 20 15-JUN-1999;
              Location/Qualifiers
              source 1..10
                  /organism="unknown"
                  /mol_type="unassigned DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 10 GCGCGCT 16
Db 4 GCGCGCT 10

RESULT 264
AR071792
LOCUS AR071792 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 21 from patent US 5912147.
ACCESSION AR071792
VERSION AR071792.1 GI:7222680
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 21 15-JUN-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCGCGCT 16
Db 4 GCGCGCT 10

RESULT 265
AR092694
LOCUS AR092694 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 6 from patent US 5998193.
ACCESSION AR092694
VERSION AR092694.1 GI:10019446
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL Patent: US 5998193-A 6 07-DEC-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
Db 4 CTGTGGC 10

RESULT 266
AR092718/c
LOCUS AR092718 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 30 from patent US 5998193.
ACCESSION AR092718
VERSION AR092718.1 GI:10019470
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)

AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL Patent: US 5998193-A 30 07-DEC-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
Db 8 GCTGGCC 2

RESULT 267
AR098900/c
LOCUS AR098900 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 36 from patent US 6077685.
ACCESSION AR098900
VERSION AR098900.1 GI:12808666
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 36 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
Db 10 CTGTGGC 4

RESULT 268
AR106678
LOCUS AR106678 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 6 from patent US 6107078.
ACCESSION AR106678
VERSION AR106678.1 GI:12821208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL Patent: US 6107078-A 6 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
Db 4 CTGTGGC 10

RESULT 269
AR106678/c
LOCUS AR106678 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 6 from patent US 6107078.
ACCESSION AR106678
VERSION AR106678.1 GI:12821208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL Patent: US 6107078-A 6 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 269
AR106702/c
LOCUS          AR106702          10 bp      DNA          PAT 14-FEB-2001
DEFINITION     Sequence 30 from patent US 6107078.
ACCESSION      AR106702
VERSION        AR106702.1  GI:12821232
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Keese,P., Stapper,M. and Perriman,R.
TITLE         Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
              embedded ribozymes and compositions thereof
JOURNAL        Patent: US 6107078-A 30 22-AUG-2000;
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match    33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCC 7
        |||||||
Db      8 GCTGGCC 2

RESULT 270
AR107780
LOCUS          AR107780          10 bp      DNA          PAT 14-FEB-2001
DEFINITION     Sequence 26 from patent US 6110667.
ACCESSION      AR107780
VERSION        AR107780.1  GI:12823267
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE         Processes, apparatus and compositions for characterizing nucleotide
              sequences based on K-tuple analysis
JOURNAL        Patent: US 6110667-A 26 29-AUG-2000;
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match    33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCC 7
        |||||||
Db      8 GCTGGCC 2

RESULT 271
AR107802
LOCUS          AR107802          10 bp      DNA          PAT 14-FEB-2001
DEFINITION     Sequence 48 from patent US 6110667.
ACCESSION      AR107802
VERSION        AR107802.1  GI:12823289
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE         Processes, apparatus and compositions for characterizing nucleotide
```

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sequences based on K-tuple analysis
JOURNAL        Patent: US 6110667-A 48 29-AUG-2000;
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match    33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 GCTGTGG 20
        |||||||
Db      4 GCTGTGG 10

RESULT 272
AR107825
LOCUS          AR107825          10 bp      DNA          PAT 14-FEB-2001
DEFINITION     Sequence 71 from patent US 6110667.
ACCESSION      AR107825
VERSION        AR107825.1  GI:12823312
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE         Processes, apparatus and compositions for characterizing nucleotide
              sequences based on K-tuple analysis
JOURNAL        Patent: US 6110667-A 71 29-AUG-2000;
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match    33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCC 7
        |||||||
Db      1 GCTGGCC 7

RESULT 273
AR172413
LOCUS          AR172413          10 bp      DNA          PAT 17-DEC-2001
DEFINITION     Sequence 10 from patent US 6303308.
ACCESSION      AR172413
VERSION        AR172413.1  GI:17911904
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS       Halle,J.-P., Regenbogen,J. and Goppelt,A.
TITLE         Cloning vectors and their preparation and use for mRNA expression
              pattern analysis
JOURNAL        Patent: US 6303308-A 10 16-OCT-2001;
FEATURES       Location/Qualifiers
               source
               1. .10
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match    33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches        7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCGCGC 15
        |||||||
Db      2 GGCGCGC 8
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RESULT 274	AR172413/c	AR172413	Sequence 10 from patent US 6303308.	10 bp	DNA	linear	PAT 17-DEC-2001
LOCUS							
DEFINITION							
ACCESSION		AR172413					
VERSION		AR172413.1	GI:17911904				
KEYWORDS							
SOURCE		Unknown.					
ORGANISM		Unknown.					
REFERENCE		Unclassified.					
AUTHORS		1 (bases 1 to 10)					
TITLE		Halle,J.-P., Regenbogen,J. and Goppelt,A.					
JOURNAL		Cloning vectors and their preparation and use for mRNA expression					
FEATURES		pattern analysis					
source		Patent: US 6303308-A 10 16-OCT-2001;					
		Location/Qualifiers					
		1..10					
		/organism="unknown"					
		/mol_type="unassigned DNA"					
Query Match		33.3%;	Score 7;	DB 1;	Length 10;		
Best Local Similarity		100.0%;	Pred. No. 1.5e+02;				
Matches		7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY		9 GGCGGCGC 15					
Db		9 GGCGGCGC 3					
RESULT 275	BD065207	BD065207	Characterization of the yeast transcriptome.	10 bp	DNA	linear	PAT 27-AUG-2002
LOCUS							
DEFINITION							
ACCESSION		BD065207					
VERSION		BD065207.1	GI:22610810				
KEYWORDS		JP 2001509017-A/143.					
SOURCE		Saccharomyces cerevisiae (baker's yeast)					
ORGANISM		Saccharomyces cerevisiae					
REFERENCE		Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;					
AUTHORS		Saccharomycetales; Saccharomycetaceae; Saccharomyces.					
TITLE		1 (bases 1 to 10)					
JOURNAL		Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.					
COMMENT		Characterization of the yeast transcriptome					
		Patent: JP 2001509017-A 143 10-JUL-2001;					
		THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE					
		OS Saccharomyces cerevisiae (yeast)					
		PN JP 2001509017-A/143					
		PD 10-JUL-2001					
		PF 22-JAN-1998 JP 1998532117					
		PR 23-JAN-1997 US 60/035917					
		PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC					
		C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC					
		Characterization of the yeast transcriptome					
		FH Key					
		FT source					
		1..10					
		/organism='Saccharomyces cerevisiae (yeast)'					
FEATURES		Location/Qualifiers					
source		1..10					
		/organism="Saccharomyces cerevisiae"					
		/mol_type="genomic DNA"					
		/db_xref="taxon:4932"					
Query Match		33.3%;	Score 7;	DB 1;	Length 10;		
Best Local Similarity		100.0%;	Pred. No. 1.5e+02;				
Matches		7;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY		13 CGCTGTG 19					
Db		4 CGCTGTG 10					
RESULT 276							

BD083127	LOCUS	BD083127	Human matured/activated dendritic cell expression genes.	10 bp	DNA	linear	PAT 27-AUG-2002
BD083127	DEFINITION						
BD083127	ACCESSION						
BD083127.1	VERSION	GI:22628737					
JP 2001327293-A/48.	KEYWORDS						
Homo sapiens (human)	SOURCE						
Homo sapiens	ORGANISM						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	REFERENCE	1 (bases 1 to 10)					
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.	AUTHORS						
Human matured/activated dendritic cell expression genes	TITLE						
Patent: JP 2001327293-A 48 27-NOV-2001;	JOURNAL						
JAPAN SCIENCE AND TECHNOLOGY CORP	COMMENT						
OS Homo sapiens (human)							
PN JP 2001327293-A/48							
PD 27-NOV-2001							
PF 22-MAY-2000 JP 2000150562							
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI							
NAGAI							
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00							
CC							
FH	Key	Location/Qualifiers.					
source	1..10						
	/organism="Homo sapiens"						
	/mol_type="genomic DNA"						
	/db_xref="taxon:9606"						
Query Match	33.3%;	Score 7;					DB 1; Length 10;
Best Local Similarity	100.0%;	Pred. No. 1.5e+02;					
Matches	7; Conservative	0; Mismatches					0; Indels 0; Gaps 0;
Qy	15 CTGTGGC	21					
Db	2 CTGTGGC	8					
RESULT 277	BD083229						
LOCUS	BD083229	Human matured/activated dendritic cell expression genes.	10 bp	DNA	linear	PAT 27-AUG-2002	
DEFINITION							
ACCESSION	BD083229						
VERSION	BD083229.1	GI:22628839					
JP 2001327293-A/150.	KEYWORDS						
Homo sapiens (human)	SOURCE						
Homo sapiens	ORGANISM						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	REFERENCE	1 (bases 1 to 10)					
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.	AUTHORS						
Human matured/activated dendritic cell expression genes	TITLE						
Patent: JP 2001327293-A 150 27-NOV-2001;	JOURNAL						
JAPAN SCIENCE AND TECHNOLOGY CORP	COMMENT						
OS Homo sapiens (human)							
PN JP 2001327293-A/150							
PD 27-NOV-2001							
PF 22-MAY-2000 JP 2000150562							
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI							
NAGAI							
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00							
CC							
FH	Key	Location/Qualifiers.					
source	1..10						
	/organism="Homo sapiens"						
	/mol_type="genomic DNA"						
	/db_xref="taxon:9606"						
Query Match	33.3%;	Score 7;					DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0;

QY 15 CTGTGGC 21
|||||||

Db 2 CTGTGGC 8

RESULT 278
BD083293
LOCUS BD083293 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Human matured/activated dendritic cell expression genes.
ACCESSION BD083293
VERSION BD083293.1 GI:22628903
KEYWORDS JP 2001327293-A/214.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.
TITLE Human matured/activated dendritic cell expression genes
JOURNAL Patent: JP 2001327293-A 214 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001327293-A/214
PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC

FH Key Location/Qualifiers.

FEATURES
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
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Db 3 GCTGGCC 9

RESULT 279
BD161461
LOCUS BD161461 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161461
VERSION BD161461.1 GI:27867219
KEYWORDS JP 2002186482-A/283.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 283 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/283
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human activated Th1 and Th2 cell expression genes FH Key

Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.
FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
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Db 3 GGCGCGC 9

RESULT 280
BD161461/C
LOCUS BD161461 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161461
VERSION BD161461.1 GI:27867219
KEYWORDS JP 2002186482-A/283.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 283 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002186482-A/283
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human activated Th1 and Th2 cell expression genes FH Key

Location/Qualifiers
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FT Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
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Db 10 GGCGCGC 4

RESULT 281
BD161467
LOCUS BD161467 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161467
VERSION BD161467.1 GI:27867225
KEYWORDS JP 2002186482-A/289.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 10)

AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 289 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/289
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers 1. .10
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FT /organism='Homo sapiens (human)'.
FEATURES source
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GGCGCGC 15
|||||||
Db 3 GGCGCGC 9
RESULT 282
BD161475/c
LOCUS BD161475 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161475
VERSION BD161475.1 GI:27867233
KEYWORDS JP 2002186482-A/297.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 297 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/297
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers 1. .10
FT source
FT /organism='Homo sapiens (human)'.
FEATURES source
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GCTGTGG 20
|||||||
Db 7 GCTGTGG 1
RESULT 283
BD166636/c

LOCUS BD166636 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166636
VERSION BD166636.1 GI:27872448
KEYWORDS JP 2002209591-A/181.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 181 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/181
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1. .10
FT /organism='Homo sapiens (human)'.
FEATURES source
Location/Qualifiers
1. .10
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 GCGCTGT 18
|||||||
Db 7 GCGCTGT 1
RESULT 284
BD166798/c
LOCUS BD166798 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166798
VERSION BD166798.1 GI:27872610
KEYWORDS JP 2002209591-A/343.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 343 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/343
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1. .10
FT /organism='Homo sapiens (human)'.
FEATURES source
Location/Qualifiers
1. .10
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/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
|||||||
Db 7 GCTGGCC 1

RESULT 285
BD166944/c
LOCUS BD166944 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166944
VERSION BD166944.1 GI:27872756
KEYWORDS JP 2002209591-A/489.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 489 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/489
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1. .10
/organism='Homo sapiens (human)'.
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
|||||||
Db 7 GCTGGCC 1

RESULT 286
BD166997/c
LOCUS BD166997 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166997
VERSION BD166997.1 GI:27872809
KEYWORDS JP 2002209591-A/542.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 542 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/542
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1. .10
/organism='Homo sapiens (human)'.
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1. .10
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
|||||||
Db 7 GCTGGCC 1

RESULT 287
BD167054/c
LOCUS BD167054 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167054
VERSION BD167054.1 GI:27872866
KEYWORDS JP 2002209591-A/599.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 599 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/599
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1. .10
/organism='Homo sapiens (human)'.
FEATURES
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1. .10
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTGGCCC 8
|||||||
Db 9 CTGGCCC 3

RESULT 288
BD225345/c
LOCUS BD225345 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for the identification of lung tumor cells.
ACCESSION BD225345

VERSION BD225345.1 GI:33035115
 KEYWORDS JP 2002509707-A/27.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
 TITLE Compositions and methods for the identification of lung tumor cells
 JOURNAL Patent: JP 2002509707-A 27 02-APR-2002;
 GENZYME CORP
 OS Artificial Sequence
 PN JP 2002509707-A/27
 PD 02-APR-2002
 PF 30-MAR-1999 JP 2000541180
 PR 31-MAR-1998 US 60/080037
 PI GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
 C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
 C12N1/19,
 PC C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
 G01N33/566//
 PC A61K45/00,A61P9/00,A61P35/00,C12N15/00,C12N5/00 CC
 Compositions and methods for the identification of lung tumor cells
 FH Key Location/Qualifiers
 FT source 1..10
 FT Location/Qualifiers
 /organism='Artificial Sequence'.
 FEATURES source
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 33.3%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 CTGTGGC 21
 |||||
 Db 9 CTGTGGC 3
 RESULT 289
 BD238618
 LOCUS
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD238618
 VERSION BD238618.1 GI:33048388
 KEYWORDS JP 2002534056-A/36.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 10)
 Roberts,B.L. and Shankara,S.
 Preparation and use of superior vaccines
 Patent: JP 2002534056-A 36 15-OCT-2002;
 GENZYME CORP
 OS Homo sapiens (human)
 PN JP 2002534056-A/36
 PD 15-OCT-2002
 PF 18-JUN-1999 JP 2000554749
 PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
 19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
 19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
 19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
 19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
 19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
 19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
 19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
 19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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 19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS,SRINIVAS SHANKARA
 PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
 C12N1/19,
 PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
 G01N37/00,
 PC C12N15/00,C12N5/00,C12N15/00
 CC Preparation and use of superior vaccines
 FH Key Location/Qualifiers
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 FT Location/Qualifiers
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 Query Match 33.3%; Score 7; DB 1; Length 10;
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTGGCC 7
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 Db 3 GCTGGCC 9
 RESULT 290
 BD238881
 LOCUS
 DEFINITION Preparation and use of superior vaccines.
 ACCESSION BD238881
 VERSION BD238881.1 GI:33048651
 KEYWORDS JP 2002534056-A/299.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 10)
 Roberts,B.L. and Shankara,S.
 Preparation and use of superior vaccines
 Patent: JP 2002534056-A 299 15-OCT-2002;
 GENZYME CORP
 OS Homo sapiens (human)
 PN JP 2002534056-A/299
 PD 15-OCT-2002
 PF 18-JUN-1999 JP 2000554749
 PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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 19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
 19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
 19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
 19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
 19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
 19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
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 19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090045 PR
 08-DEC-1998 US 60/111715
 PI BRUCE L ROBERTS,SRINIVAS SHANKARA
 PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
 C12N1/19,
 PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
 G01N37/00,
 PC C12N15/00,C12N5/00,C12N15/00
 CC Preparation and use of superior vaccines
 FH Key Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

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FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 CGCTGTG 19
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Db 1 CGCTGTG 7
RESULT 291
BD239109/c
LOCUS BD239109 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239109
VERSION BD239109.1 GI:33048879
KEYWORDS JP 2002534056-A/527.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 527 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/527
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1. .10
/organism='Homo sapiens (human)'.
FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
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Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 CGCTGTG 19
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Db 1 CGCTGTG 7
RESULT 291
BD239109/c
LOCUS BD239109 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239109
VERSION BD239109.1 GI:33048879
KEYWORDS JP 2002534056-A/527.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 527 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/527
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
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19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
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FH Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
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Db 9 CTGTGGC 3
RESULT 292
BD239284
LOCUS BD239284 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239284
VERSION BD239284.1 GI:33049054
KEYWORDS JP 2002534056-A/702.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 702 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/702
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1. .10
/organism='Homo sapiens (human)'.
FEATURES
source
1. .10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GCCCGGC 11
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Db 4 GCCCGGC 10
RESULT 293
BD239353
LOCUS BD239353 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239353
VERSION BD239353.1 GI:33049123
KEYWORDS JP 2002534056-A/771.

19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
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Db 10 GCTGTGG 4

RESULT 296
BD240122/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240122
VERSION BD240122.1 GI:33049892
KEYWORDS JP 2002534056-A/1540.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1540 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1540
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

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source
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
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Db 10 GCTGTGG 4

RESULT 296
BD240122/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240122
VERSION BD240122.1 GI:33049892
KEYWORDS JP 2002534056-A/1540.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1540 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1540
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines

FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.

FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
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Db 7 GCTGGCC 1

RESULT 297
BD240437/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240437
VERSION BD240437.1 GI:33050207
KEYWORDS JP 2002534056-A/1855.
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1855 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1855
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
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Db 7 GCTGGCC 1

RESULT 297
BD240437/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240437
VERSION BD240437.1 GI:33050207
KEYWORDS JP 2002534056-A/1855.
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1855 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1855
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines


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Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCC 7
      |||||
Db      3 GCTGGCC 9

RESULT 304
CS106787
LOCUS      CS106787      10 bp      DNA      linear      PAT 10-JUN-2005
DEFINITION      Sequence 5 from Patent WO2005042781.
ACCESSION      CS106787
VERSION      CS106787.1 GI:67513715
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Smith,D.R., Malek,J.A. and Mckernan,K.J.
TITLE      Methods for producing a paired tag from a nucleic acid sequence and
methods of use thereof
JOURNAL      Patent: WO 2005042781-A 5 12-MAY-2005;
Agencourt Bioscience Corporation (US)
FEATURES      Location/Qualifiers
source      1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ASCII Linker - top strand"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCGCGC 15
      |||||
Db      1 GGCGCGC 7

RESULT 305
CS106787/c
LOCUS      CS106787      10 bp      DNA      linear      PAT 10-JUN-2005
DEFINITION      Sequence 5 from Patent WO2005042781.
ACCESSION      CS106787
VERSION      CS106787.1 GI:67513715
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Smith,D.R., Malek,J.A. and Mckernan,K.J.
TITLE      Methods for producing a paired tag from a nucleic acid sequence and
methods of use thereof
JOURNAL      Patent: WO 2005042781-A 5 12-MAY-2005;
Agencourt Bioscience Corporation (US)
FEATURES      Location/Qualifiers
source      1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ASCII Linker - top strand"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCGCGC 15
      |||||
Db      1 GGCGCGC 7

RESULT 306
CS106788
LOCUS      CS106788      10 bp      DNA      linear      PAT 10-JUN-2005
DEFINITION      Sequence 6 from Patent WO2005042781.
ACCESSION      CS106788
VERSION      CS106788.1 GI:67513716
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Smith,D.R., Malek,J.A. and Mckernan,K.J.
TITLE      Methods for producing a paired tag from a nucleic acid sequence and
methods of use thereof
JOURNAL      Patent: WO 2005042781-A 6 12-MAY-2005;
Agencourt Bioscience Corporation (US)
FEATURES      Location/Qualifiers
source      1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ASCII Linker - bottom strand"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCGCGC 15
      |||||
Db      1 GGCGCGC 7

RESULT 307
CS106788/c
LOCUS      CS106788      10 bp      DNA      linear      PAT 10-JUN-2005
DEFINITION      Sequence 6 from Patent WO2005042781.
ACCESSION      CS106788
VERSION      CS106788.1 GI:67513716
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Smith,D.R., Malek,J.A. and Mckernan,K.J.
TITLE      Methods for producing a paired tag from a nucleic acid sequence and
methods of use thereof
JOURNAL      Patent: WO 2005042781-A 6 12-MAY-2005;
Agencourt Bioscience Corporation (US)
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Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCGCGC 15
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Db      8 GGCGCGC 2

RESULT 308
E59637
LOCUS      E59637      10 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION      Cloning vector for mRNA-expressing pattern analysis, and
preparation and use thereof.
ACCESSION      E59637
VERSION      E59637.1 GI:13019440
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KEYWORDS JP 1999346790-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Yorun,P.H., Johannes,R. and Andreas,G.
TITLE Cloning vector for mRNA-expressing pattern analysis, and preparation and use thereof
JOURNAL Patent: JP 1999346790-A 10 21-DEC-1999;
COMMENT SWITCH BIOTECH GMBH
OS Unidentified
PN JP 1999346790-A/10
PD 21-DEC-1999
PF 17-MAY-1999 JP 1999136298
PR 18-MAY-1998 DE 19822287.4
PI YORUN PATER HARE,JOHANNES REGENBORGEN,ANDREAS GOPPERUTO PC
C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .10
FT /organism='Unidentified'.
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 GGCGCGC 15
Db 2 GGCGCGC 8
RESULT 309
E59637/c
LOCUS E59637 10 bp DNA linear PAT 18-JUN-2001
DEFINITION Cloning vector for mRNA-expressing pattern analysis, and preparation and use thereof.
ACCESSION E59637
VERSION E59637.1 GI:13019440
KEYWORDS JP 1999346790-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Yorun,P.H., Johannes,R. and Andreas,G.
TITLE Cloning vector for mRNA-expressing pattern analysis, and preparation and use thereof
JOURNAL Patent: JP 1999346790-A 10 21-DEC-1999;
COMMENT SWITCH BIOTECH GMBH
OS Unidentified
PN JP 1999346790-A/10
PD 21-DEC-1999
PF 17-MAY-1999 JP 1999136298
PR 18-MAY-1998 DE 19822287.4
PI YORUN PATER HARE,JOHANNES REGENBORGEN,ANDREAS GOPPERUTO PC
C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
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FT /organism='Unidentified'.
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 GGCGCGC 15
Db 2 GGCGCGC 8

Qy 9 GGCGCGC 15
Db 9 GGCGCGC 3
RESULT 310
E64716/c
LOCUS E64716 10 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for distinguishing rice variety.
ACCESSION E64716
VERSION E64716.1 GI:18623011
KEYWORDS JP 2000287691-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Otsubo,K., Nakamura,S., Teshima,H., Okatome,H. and Kawasaki,S.
TITLE Method for distinguishing rice variety
JOURNAL Patent: JP 2000287691-A 2 17-OCT-2000;
COMMENT NATL FOOD RES INST,KENICHI OTSUBO,HIDECHIKA TESHIMA,HIROSHI OKATOME
OS Oryza sativa L. (rice)
PN JP 2000287691-A/2
PD 17-OCT-2000
PF 09-APR-1999 JP 1999102709
PR
PI KENICHI OTSUBO,SUMIKO NAKAMURA,HIDECHIKA TESHIMA, PI HIROSHI OKATOME,
PI SHINJI KAWASAKI
PC C12N15/09,C12Q1/68,G01N33/10,C12N15/00
CC
FH Key Location/Qualifiers
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FT /organism='Oryza sativa L. (rice)'.
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source Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 GCTGTGG 20
Db 7 GCTGTGG 1
RESULT 311
I12013/c
LOCUS I12013 10 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 5 from Patent US 5418150.
ACCESSION I12013
VERSION I12013.1 GI:909454
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Topal,M.D. and Conrad,M.J.
TITLE Method of cleaving DNA
JOURNAL Patent: US 5418150-A 5 23-MAY-1995;
FEATURES
source Location/Qualifiers
1. .10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 CCGCGC 13

Db 7 CCGCGGC 1
|||||
RESULT 312
I79740/c
LOCUS I79740 10 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 36 from patent US 5707863.
ACCESSION I79740
VERSION I79740.1 GI:3208030
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor gene merlin
JOURNAL Patent: US 5707863-A 36 13-JAN-1998;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTGTGGC 21
|||||
Db 10 CTGTGGC 4
RESULT 313
I86912/c
LOCUS I86912 10 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5702931.
ACCESSION I86912
VERSION I86912.1 GI:3206630
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Andrews,W.H., Morser,M.J. and Vilander,L.R.
TITLE Mutagenesis methods and compositions
JOURNAL Patent: US 5702931-A 1 30-DEC-1997;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GGCGGC 15
|||||
Db 9 GGCGGC 3
RESULT 314
AR202187
LOCUS AR202187 10 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6361974.
ACCESSION AR202187
VERSION AR202187.1 GI:20256726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M., Djavakhishvili,T.David. and Frey,G.Johann.
TITLE Exonuclease-mediated nucleic acid reassembly in directed evolution

JOURNAL Patent: US 6361974-A 6 26-MAR-2002;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 CGCGCTG 17
|||||
Db 1 CGCGCTG 7
RESULT 315
AR254267/c
LOCUS AR254267 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 13 from patent US 6479731.
ACCESSION AR254267
VERSION AR254267.1 GI:27303040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Valent,B.S. and Bryan,G.T.
TITLE Pi-ta gene conferring fungal disease resistance to plants
JOURNAL Patent: US 6479731-A 13 12-NOV-2002;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 GCGCTGT 18
|||||
Db 7 GCGCTGT 1
RESULT 316
AR303347/c
LOCUS AR303347 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 72 from patent US 6544736.
ACCESSION AR303347
VERSION AR303347.1 GI:31692123
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 72 08-APR-2003;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GCTGTGG 20
|||||

Db 10 GCTGTGG 4

RESULT 317
AR303679
LOCUS AR303679 10 bp DNA PAT 12-JUN-2003
DEFINITION Sequence 404 from patent US 6544736.
ACCESSION AR303679
VERSION AR303679.1 GI:31692455
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 404 08-APR-2003;
Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo; JPX;

FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTG 19
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Db 4 CGCTGTG 10

RESULT 318
AR306871/c
LOCUS AR306871 10 bp DNA PAT 12-JUN-2003
DEFINITION Sequence 23 from patent US 6551476.
ACCESSION AR306871
VERSION AR306871.1 GI:31697271
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Scherba,E.S.
TITLE Noble-metal coated inert anode for aluminum production
JOURNAL Patent: US 6551476-A 23 22-APR-2003;
FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||||
Db 7 GCTGTGG 1

RESULT 319
AR336879/c
LOCUS AR336879 10 bp DNA PAT 17-AUG-2003
DEFINITION Sequence 54 from patent US 6566130.
ACCESSION AR336879
VERSION AR336879.1 GI:33722729
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M.
TITLE Exonuclease-mediated nucleic acid reassembly in directed evolution
JOURNAL Patent: US 6635449-A 6 21-OCT-2003;
Diversa Corporation; San Diego, CA

REFERENCE 1 (bases 1 to 10)
AUTHORS Srivastava,S.; Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 54 20-MAY-2003;
Henry M. Jackson Foundation for the Advancement of Military Medicine; Rockville, MD

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
|||||||
Db 7 GCTGGCC 1

RESULT 320
AR351736
LOCUS AR351736 10 bp DNA PAT 17-AUG-2003
DEFINITION Sequence 1278 from patent US 6588746.
ACCESSION AR351736
VERSION AR351736.1 GI:33753532
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet material
JOURNAL Patent: US 6588746-A 1278 08-JUL-2003;
NexPress Solutions LLC; Rochester, NY; DEX;

FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||||
Db 4 GCTGTGG 10

RESULT 321
AR410161
LOCUS AR410161 10 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6635449.
ACCESSION AR410161
VERSION AR410161.1 GI:40161386
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M.
TITLE Exonuclease-mediated nucleic acid reassembly in directed evolution
JOURNAL Patent: US 6635449-A 6 21-OCT-2003;
Diversa Corporation; San Diego, CA

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
Db 1 CGCGCTG 7

RESULT 322
AR477264 LOCUS AR477264 10 bp DNA PAT 14-MAY-2004
DEFINITION Sequence 5 from patent US 6696275.
ACCESSION AR477264
VERSION AR477264.1 GI:47234597
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M. and Frey,G.J.
TITLE End selection in directed evolution
JOURNAL Patent: US 6696275-A 5 24-FEB-2004;
Diversa Corporation; San Diego, CA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
Db 1 CGCGCTG 7

RESULT 323
AR489166 LOCUS AR489166 10 bp DNA PAT 15-MAY-2004
DEFINITION Sequence 6 from patent US 6709841.
ACCESSION AR489166
VERSION AR489166.1 GI:47256094
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M.
TITLE Exonuclease-mediated gene assembly in directed evolution
JOURNAL Patent: US 6709841-A 6 23-MAR-2004;
Diversa Corporation; San Diego, CA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
Db 1 CGCGCTG 7

RESULT 324
AR490750 LOCUS AR490750 10 bp DNA PAT 15-MAY-2004
DEFINITION Sequence 10 from patent US 6713279.
ACCESSION AR490750
VERSION AR490750.1 GI:47258162
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M. and Frey,G.J.
TITLE End selection in directed evolution
JOURNAL Patent: US 6713279-A 10 30-MAR-2004;
Diversa Corporation; San Diego, CA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
Db 1 CGCGCTG 7

RESULT 325
AR568611 LOCUS AR568611 10 bp DNA PAT 14-DEC-2004
DEFINITION Sequence 6 from patent US 6740506.
ACCESSION AR568611
VERSION AR568611.1 GI:56568059
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Short,J.M. and Frey,G.J.
TITLE End selection in directed evolution
JOURNAL Patent: US 6740506-A 6 25-MAY-2004;
Diversa Corporation; San Diego, CA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
Db 1 CGCGCTG 7

RESULT 326
AR630143 LOCUS AR630143 10 bp DNA PAT 14-FEB-2005
DEFINITION Sequence 197 from patent US 6838556.
ACCESSION AR630143
VERSION AR630143.1 GI:59762465
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 197 04-JAN-2005;
GeneLabs Technologies, Inc.; Redwood City, CA
FEATURES
source 1..10
/organism="unknown"
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Query Match 33.3%; Score 7; DB 1; Length 10;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCGCGCT 16
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Db 1 GCGCGCT 7

RESULT 327
AR630149/c
LOCUS AR630149 10 bp DNA PAT 14-FEB-2005
DEFINITION Sequence 203 from patent US 6838556.
ACCESSION AR630149
VERSION AR630149.1 GI:59762477
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 203 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
FEATURES
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/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCGCGCT 16
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Db 10 GCGCGCT 4

RESULT 328
AR642556/c
LOCUS AR642556 10 bp DNA PAT 20-APR-2005
DEFINITION Sequence 29 from patent US 6864052.
ACCESSION AR642556
VERSION AR642556.1 GI:62779710
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE Enhanced sequencing by hybridization using pools of probes
JOURNAL Patent: US 6864052-A 29 08-MAR-2005;
Callida Genomics, Inc.; Sunnyvale, CA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
| | | | | | |
Db 10 CTGTGGC 4

RESULT 329
AR642557/c
LOCUS AR642557 10 bp DNA PAT 20-APR-2005
DEFINITION Sequence 30 from patent US 6864052.
ACCESSION AR642557

VERSION AR642557.1 GI:62779711
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE Enhanced sequencing by hybridization using pools of probes
JOURNAL Patent: US 6864052-A 30 08-MAR-2005;
Callida Genomics, Inc.; Sunnyvale, CA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
| | | | | | |
Db 9 CTGTGGC 3

RESULT 330
AR642558/c
LOCUS AR642558 10 bp DNA PAT 20-APR-2005
DEFINITION Sequence 31 from patent US 6864052.
ACCESSION AR642558
VERSION AR642558.1 GI:62779712
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE Enhanced sequencing by hybridization using pools of probes
JOURNAL Patent: US 6864052-A 31 08-MAR-2005;
Callida Genomics, Inc.; Sunnyvale, CA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
| | | | | | |
Db 8 CTGTGGC 2

RESULT 331
AR642559/c
LOCUS AR642559 10 bp DNA PAT 20-APR-2005
DEFINITION Sequence 32 from patent US 6864052.
ACCESSION AR642559
VERSION AR642559.1 GI:62779713
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.
TITLE Enhanced sequencing by hybridization using pools of probes
JOURNAL Patent: US 6864052-A 32 08-MAR-2005;
Callida Genomics, Inc.; Sunnyvale, CA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
| | | | |
Db 7 CTGTGGC 1

RESULT 332
AX009254
LOCUS AX009254 10 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 10 from Patent EP0965642.
ACCESSION AX009254
VERSION AX009254.1 GI:9996585
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Goppelt,A.D., Halle,J.P. and Regenbogen,J.D.
TITLE Cloning vector, its production and use for the analysis of mrna
expression pattern
JOURNAL Patent: EP 0965642-A 10 22-DEC-1999;
SWITCH BIOTECH GMBH (DE)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
| | | | |
Db 2 GGCGCGC 8

RESULT 333
AX009254/c
LOCUS AX009254 10 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 10 from Patent EP0965642.
ACCESSION AX009254
VERSION AX009254.1 GI:9996585
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Goppelt,A.D., Halle,J.P. and Regenbogen,J.D.
TITLE Cloning vector, its production and use for the analysis of mrna
expression pattern
JOURNAL Patent: EP 0965642-A 10 22-DEC-1999;
SWITCH BIOTECH GMBH (DE)
FEATURES
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1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
| | | | |
Db 9 GGCGCGC 3

RESULT 334
AX147040

LOCUS AX147040 10 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 1 from Patent WO0136482.
ACCESSION AX147040
VERSION AX147040.1 GI:14346308
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Enikolopov,G.N. and Mignone,J.
TITLE Transgenic mice expressing fluorescent protein under the control of
the nestin promoter
JOURNAL Patent: WO 0136482-A 1 25-MAY-2001;
COLD SPRING HARBOR LABORATORY (US)
FEATURES
source
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Linker"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
| | | | |
Db 2 GGCGCGC 8

RESULT 335
AX147040/c
LOCUS AX147040 10 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 1 from Patent WO0136482.
ACCESSION AX147040
VERSION AX147040.1 GI:14346308
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Enikolopov,G.N. and Mignone,J.
TITLE Transgenic mice expressing fluorescent protein under the control of
the nestin promoter
JOURNAL Patent: WO 0136482-A 1 25-MAY-2001;
COLD SPRING HARBOR LABORATORY (US)
FEATURES
source
1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Linker"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
| | | | |
Db 9 GGCGCGC 3

RESULT 336
AX152322
LOCUS AX152322 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 237 from Patent WO0138577.
ACCESSION AX152322
VERSION AX152322.1 GI:14533973
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 237 31-MAY-2001;
          The Johns Hopkins University (US)
FEATURES
    source
      1 .10
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 4 GCTGGCC 10

RESULT 337
AX152346/c
LOCUS AX152346 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 261 from Patent WO0138577.
ACCESSION AX152346
VERSION AX152346.1 GI:14533997
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 261 31-MAY-2001;
          The Johns Hopkins University (US)
FEATURES
    source
      1 .10
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCGGCGC 13
Db 10 CCGGCGC 4

RESULT 338
AX152392/c
LOCUS AX152392 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 307 from Patent WO0138577.
ACCESSION AX152392
VERSION AX152392.1 GI:14534043
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 307 31-MAY-2001;
          The Johns Hopkins University (US)
FEATURES
    source
      1 .10
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
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          Hominidae; Homo.
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 339
AX152393/c
LOCUS AX152393 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 308 from Patent WO0138577.
ACCESSION AX152393
VERSION AX152393.1 GI:14534044
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 308 31-MAY-2001;
          The Johns Hopkins University (US)
FEATURES
    source
      1 .10
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCC 7
Db 7 GCTGGCC 1

RESULT 340
AX152609
LOCUS AX152609 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 524 from Patent WO0138577.
ACCESSION AX152609
VERSION AX152609.1 GI:14534260
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 524 31-MAY-2001;
          The Johns Hopkins University (US)
FEATURES
    source
      1 .10
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
Db 15 CTGTGGC 21
```

Db 4 CTGTGGC 10

RESULT 341
AX152706/c

LOCUS AX152706 10 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 621 from Patent WO0138577.

ACCESSION AX152706

VERSION AX152706.1 GI:14534357

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.

TITLE Human transcriptomes

JOURNAL Patent: WO 0138577-A 621 31-MAY-2001;

The Johns Hopkins University (US)

FEATURES

source

1. .10

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCC 8

Db

7 CTGGCCC 1

RESULT 342
AX153150/c

LOCUS AX153150 10 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 1065 from Patent WO0138577.

ACCESSION AX153150

VERSION AX153150.1 GI:14534801

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.

TITLE Human transcriptomes

JOURNAL Patent: WO 0138577-A 1065 31-MAY-2001;

The Johns Hopkins University (US)

FEATURES

source

1. .10

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCCG 10

Db

7 GGCCCCG 1

RESULT 343
AX153156

LOCUS AX153156 10 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 1071 from Patent WO0138577.

ACCESSION AX153156

VERSION AX153156.1 GI:14534807

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.

TITLE Human transcriptomes

JOURNAL Patent: WO 0138577-A 1071 31-MAY-2001;

The Johns Hopkins University (US)

FEATURES

Location/Qualifiers

1. .10

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7

Db

4 GCTGGCC 10

RESULT 344
AX153227

LOCUS AX153227 10 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 1142 from Patent WO0138577.

ACCESSION AX153227

VERSION AX153227.1 GI:14534878

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.

TITLE Human transcriptomes

JOURNAL Patent: WO 0138577-A 1142 31-MAY-2001;

The Johns Hopkins University (US)

FEATURES

Location/Qualifiers

1. .10

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGGCC 13

Db

3 CCGGGCC 9

RESULT 345
AX153234

LOCUS AX153234 10 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 1149 from Patent WO0138577.

ACCESSION AX153234

VERSION AX153234.1 GI:14534885

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.

TITLE Human transcriptomes

JOURNAL Patent: WO 0138577-A 1149 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCCCGGC 11
|||||
Db 4 GCCCGGC 10

RESULT 346
AX302590
LOCUS AX302590 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 108 from Patent WO0175177.
ACCESSION AX302590
VERSION AX302590.1 GI:17383117
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 108 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES Location/Qualifiers
source 1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CGCGCTG 17
|||||
Db 3 CGCGCTG 9

RESULT 347
AX391509
LOCUS AX391509 10 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 3 from Patent EP1184462.
ACCESSION AX391509
VERSION AX391509.1 GI:19700117
KEYWORDS .
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1
AUTHORS Fan,F.G., He,Y.G., Huang,J.G., Jiang,X.G., Mcdevitt,D.G.,
Rosenberg,M.G. and St John,A.G.
TITLE Identification of targets of antimicrobial compounds
JOURNAL Patent: EP 1184462-A 3 06-MAR-2002;
SmithKline Beecham Corporation (US) ; SMITHKLINE BEECHAM PLC (GB)

FEATURES Location/Qualifiers
source 1..10
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CGCGCTG 17
|||||
Db 3 CGCGCTG 9

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCGGC 15
|||||
Db 1 GGCGGC 7

RESULT 348
AX391509/c
LOCUS AX391509 10 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 3 from Patent EP1184462.
ACCESSION AX391509
VERSION AX391509.1 GI:19700117
KEYWORDS .
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1
AUTHORS Fan,F.G., He,Y.G., Huang,J.G., Jiang,X.G., Mcdevitt,D.G.,
Rosenberg,M.G. and St John,A.G.
TITLE Identification of targets of antimicrobial compounds
JOURNAL Patent: EP 1184462-A 3 06-MAR-2002;
SmithKline Beecham Corporation (US) ; SMITHKLINE BEECHAM PLC (GB)

FEATURES Location/Qualifiers
source 1..10
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCGGC 15
|||||
Db 8 GGCGGC 2

RESULT 349
AX391511
LOCUS AX391511 10 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 5 from Patent EP1184462.
ACCESSION AX391511
VERSION AX391511.1 GI:19700119
KEYWORDS .
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.

REFERENCE 1
AUTHORS Fan,F.G., He,Y.G., Huang,J.G., Jiang,X.G., Mcdevitt,D.G.,
Rosenberg,M.G. and St John,A.G.
TITLE Identification of targets of antimicrobial compounds
JOURNAL Patent: EP 1184462-A 5 06-MAR-2002;
SmithKline Beecham Corporation (US) ; SMITHKLINE BEECHAM PLC (GB)

FEATURES Location/Qualifiers
source 1..10
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCGGC 15
|||||
Db 3 GGCGGC 9

RESULT 350
AX391511/c
LOCUS AX391511 10 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 5 from Patent EP1184462.

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ACCESSION      AX391511
VERSION        AX391511.1  GI:19700119
KEYWORDS
SOURCE         Staphylococcus aureus
ORGANISM       Staphylococcus aureus
REFERENCE      1
AUTHORS        Fan,F.G., He,Y.G., Huang,J.G., Jiang,X.G., Mcdevitt,D.G.,
                Rosenberg,M.G. and St John,A.G.
TITLE          Identification of targets of antimicrobial compounds
JOURNAL        Patent: EP 1184462-A 5 06-MAR-2002;
                SmithKline Beecham Corporation (US) ; SMITHKLINE BEECHAM PLC (GB)
FEATURES
  source
    1..10
      /organism="Staphylococcus aureus"
      /mol_type="unassigned DNA"
      /db_xref="taxon:1280"

  Query Match      33.3%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred.No.1.5e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
    |||||
Db 10 GGCGCGC 4

RESULT 351
LOCUS      AX667829
DEFINITION Sequence 1278 from Patent WO242459. linear PAT 26-MAR-2003
ACCESSION  AX667829
VERSION    AX667829.1 GI:29291366
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

REFERENCE  1
AUTHORS    Liu,Q.
TITLE      Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL    Patent: WO 0242459-A 1278 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES
  source
    1..10
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="example target DNA"

  Query Match      33.3%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred.No.1.5e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
    |||||
Db 4 GCTGTGG 10

RESULT 352
LOCUS      AX753482
DEFINITION Sequence 27 from Patent EP1310556. linear PAT 23-JUN-2003
ACCESSION  AX753482
VERSION    AX753482.1 GI:32166242
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.

REFERENCE  1
AUTHORS    Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE      Composition and methods for the identification of lung tumor cells
JOURNAL    Patent: EP 1310556-A 27 14-MAY-2003;
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GENZYME CORPORATION (US)
Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

  Query Match      33.3%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred.No.1.5e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
    |||||
Db 9 CTGTGGC 3

RESULT 353
LOCUS      AX958222
DEFINITION Sequence 25 from Patent WO03046156. linear PAT 08-JAN-2004
ACCESSION  AX958222
VERSION    AX958222.1 GI:40785875
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified sequences.

REFERENCE  1
AUTHORS    Claude,P.P.
TITLE      Novel bacterial biomasses, method for obtaining same and uses
            thereof for bacterization of soils and crop residues
JOURNAL    Patent: WO 03046156-A 25 05-JUN-2003;
            Valbios (FR)
FEATURES
  source
    1..10
      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"
      /note="Azobacter"

  Query Match      33.3%; Score 7; DB 1; Length 10;
  Best Local Similarity 100.0%; Pred.No.1.5e+02;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCGCG 14
    |||||
Db 3 CGGCGCG 9

RESULT 354
LOCUS      BD007778
DEFINITION LPS activated human monocyte expressing genes. linear PAT 31-JAN-2002
ACCESSION  BD007778
VERSION    BD007778.1 GI:18636151
KEYWORDS   JP 2001069993-A/54.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 10)
            Matsushima,K., Hashimoto,S. and Suzuki,T.
            LPS activated human monocyte expressing genes
            Patent: JP 2001069993-A 54 21-MAR-2001;
            JAPAN SCIENCE AND TECHNOLOGY CORP
            OS Homo sapiens (human)
            PN JP 2001069993-A/54
            PD 21-MAR-2001
            PF 28-APR-2000 JP 2000131079
            PR
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
            Cl2N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
            A61P29/00,
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PC      A61P31/00,C12P21/08,C12N15/00
CC
FH      Key      Location/Qualifiers
FT      source    1..10
FT
FEATURES
    source        Location/Qualifiers
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
Db      2 CTGTGGC 8

RESULT 355
BD007922/c
LOCUS      10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007922
VERSION BD007922.1 GI:18636295
KEYWORDS JP 2001069993-A/198.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 198 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/198
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH      Key      Location/Qualifiers
FT      source    1..10
FT
FEATURES
    source        Location/Qualifiers
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTGGCCC 8
Db      7 CTGGCCC 1

RESULT 356
BD007966
LOCUS      10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007966
VERSION BD007966.1 GI:18636339
KEYWORDS JP 2001069993-A/242.
SOURCE Homo sapiens (human)
```

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 242 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/242
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH      Key      Location/Qualifiers
FT      source    1..10
FT
FEATURES
    source        Location/Qualifiers
    1..10
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCCCGGC 11
Db      4 GCCCGGC 10

Search completed: May 10, 2006, 10:44:15
Job time : 0.001 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:47:25 ; Search time 0.001 Seconds
(without alignments)
88.242 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336

Perfect score: 21

Sequence: 1 gctggccggcgctgtggc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 194 seqs, 2101 residues

Total number of hits satisfying chosen parameters: 388

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 221 summaries

Database : pubmaindb1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	14.4	68.6	20	1	US-10-430-196-40 Sequence 40, Appl
C 3	12.8	61.0	17	1	US-09-827-395A-739 Sequence 739, Appl
C 4	12.8	61.0	17	1	US-10-430-882-739 Sequence 739, Appl
C 5	12.4	59.0	17	1	US-09-827-395A-442 Sequence 442, Appl
C 6	12.4	59.0	17	1	US-09-827-395A-443 Sequence 443, Appl
C 7	12.4	59.0	17	1	US-10-430-882-442 Sequence 442, Appl
C 8	12.4	59.0	17	1	US-10-430-882-443 Sequence 443, Appl
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10	12.2	58.1	17	1	US-09-930-423-389 Sequence 389, Appl
11	12.2	58.1	17	1	US-09-895-040A-61 Sequence 389, Appl
12	10.4	49.5	14	1	US-09-745-237A-389 Sequence 14, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 40, Application US/09923517
; Publication No. US20020039741A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; ; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517
; FILING DATE: 07-Aug-2001
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
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Best Local Similarity 93.8%; Pred. No. 7.6;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCCGGCGCGCTGTGGC 21
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; Sequence 40, Application US/10430196
; Publication No. US20030194738A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/430,196
; FILING DATE: 05-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517A
; FILING DATE: 07-Aug-2001
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 40:
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; LENGTH: 20
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; STRANDEDNESS: Single
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; Sequence 739, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
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; ORGANISM: Homo sapiens
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; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; 
```

; NUMBER OF SEQ ID NOS: 2617
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 739
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
US-10-430-882-739

Query Match 61.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCCCGCGCGCTGT 18
| | | | | | | | | |
Db 17 TTGCCCGCGGGCTGT 2

RESULT 5
US-09-827-395A-442/c
 ; Sequence 442, Application US/09827395A
 ; Publication No. US20030113891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Lawrence Blatt
 ; APPLICANT: James McSwiggen
 ; APPLICANT: Bharat Chowrira
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
 ; FILE REFERENCE: MBHB00-878-C (400/017)
 ; CURRENT APPLICATION NUMBER: US/09/827,395A
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/780,533
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 2617
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 442
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
US-09-827-395A-442

Query Match 59.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGCTGT 18
| | | | | | | | | |
Db 17 GCCCGCGGGCTGT 4

RESULT 6
US-09-827-395A-443/c
 ; Sequence 443, Application US/09827395A
 ; Publication No. US20030113891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Lawrence Blatt
 ; APPLICANT: James McSwiggen
 ; APPLICANT: Bharat Chowrira
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
 ; FILE REFERENCE: MBHB00-878-C (400/017)
 ; CURRENT APPLICATION NUMBER: US/09/827,395A
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/780,533
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 2617
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 443
 ; LENGTH: 17
 ; TYPE: RNA

; ORGANISM: Homo sapiens
US-09-827-395A-443

Query Match 59.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGCTGT 18
| | | | | | | | | |
Db 16 GCCCGCGGGCTGT 3

RESULT 7
US-10-430-882-442/c
 ; Sequence 442, Application US/10430882
 ; Publication No. US20030203870A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Lawrence Blatt
 ; APPLICANT: James McSwiggen
 ; APPLICANT: Bharat Chowrira
 ; APPLICANT: Peter Haerberli
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
 ; FILE REFERENCE: MBHB00-878-H (400/112)
 ; CURRENT APPLICATION NUMBER: US/10/430,882
 ; CURRENT FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: 09/827,395
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/780,533
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: PCT/US01/04273
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: PCT/US02/10512
 ; PRIOR FILING DATE: 2002-04-03
 ; NUMBER OF SEQ ID NOS: 2617
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 442
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
US-10-430-882-442

Query Match 59.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGCTGT 18
| | | | | | | | | |
Db 17 GCCCGCGGGCTGT 4

RESULT 8
US-10-430-882-443/c
 ; Sequence 443, Application US/10430882
 ; Publication No. US20030203870A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Lawrence Blatt
 ; APPLICANT: James McSwiggen
 ; APPLICANT: Bharat Chowrira
 ; APPLICANT: Peter Haerberli
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
 ; FILE REFERENCE: MBHB00-878-H (400/112)
 ; CURRENT APPLICATION NUMBER: US/10/430,882
 ; CURRENT FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: 09/827,395
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 09/780,533
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: PCT/US01/04273
 ; PRIOR FILING DATE: 2001-02-09

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; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-443

Query Match          59.0%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 17;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCCCGGCGCGCTGT 18
Db      16 GCCCGGCGGCTGT 3

RESULT 9
US-09-895-040A-61
; Sequence 61, Application US/09895040A
; Patent No. US20020123474A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Ji, Yonggang
; TITLE OF INVENTION: HUMAN GTP-RHO BINDING PROTEIN 2
; FILE REFERENCE: AEOMICA-11
; CURRENT APPLICATION NUMBER: US/09/895,040A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 61
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-040A-61

Query Match          58.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 GCCCGGCGCGCTGTGC 21
Db      1 GACCGACGCGCTGTGC 17

RESULT 10
US-09-930-423-389
; Sequence 389, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 389
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-389

Query Match          58.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 20;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCTGGCCCGCGCGCTG 17
Db      1 GCUGGCCACAGGCCCCUG 17

RESULT 11
US-09-745-237A-389
; Sequence 389, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 389
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-389

Query Match          58.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 20;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCTGGCCCGCGCGCTG 17
Db      1 GCUGGCCACAGGCCCCUG 17

RESULT 12
US-10-402-099-14
; Sequence 14, Application US/10402099
; Publication No. US20030220287A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, M. Ian
; APPLICANT: Mohuczy, Dagmara
; TITLE OF INVENTION: Antisense Nucleic Acids
; FILE REFERENCE: 5853-235
; CURRENT APPLICATION NUMBER: US/10/402,099
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-402-099-14

Query Match          49.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 33;
```


Matches	11;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	2	CTGGCCCCGGCGC 13							
Db	3	CTTGCCCCGGCGC 14							
RESULT 13									
US-10-666-205-43									
; Sequence 43, Application US/10666205									
; Publication No. US20040157305A1									
; GENERAL INFORMATION:									
; APPLICANT: Stampfer, Wolfgang									
; APPLICANT: Kosjek, Birgit									
; APPLICANT: Kroutil, Wolfgang									
; APPLICANT: Faber, Kurt									
; APPLICANT: Niehaus, Frank									
; APPLICANT: Eck, Juergen									
; TITLE OF INVENTION: Alcohol dehydrogenases with increased solvent and temperature sta									
; FILE REFERENCE: HL/95-22634/CIP									
; CURRENT APPLICATION NUMBER: US/10/666,205									
; CURRENT FILING DATE: 2003-09-18									
; PRIOR APPLICATION NUMBER: PCT/EP03/02439									
; PRIOR FILING DATE: March 10, 2003									
; NUMBER OF SEQ ID NOS: 51									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 43									
; LENGTH: 14									
; TYPE: DNA									
; ORGANISM: Artificial Sequence									
; FEATURE:									
; OTHER INFORMATION: Sequence used as potential probe for identifying Rhodococcus rub									
; OTHER INFORMATION: r DSM 14855 alcohol dehydrogenase A gene									
US-10-666-205-43									
Query Match	46.7%;	Score 9.8;	DB 1;	Length 14;					
Best Local Similarity	84.6%;	Pred. No. 50;							
Matches	11;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	GCTGGCCCCGGCGC 13							
Db	1	GCCGCCCGCGCGC 13							
RESULT 14									
US-09-990-762-97/c									
; Sequence 97, Application US/09990762									
; Patent No. US20020119498A1									
; GENERAL INFORMATION:									
; APPLICANT: JOUNG, J. KEITH									
; APPLICANT: MILLER, JEFFREY									
; APPLICANT: PABO, CARL O.									
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS									
; FILE REFERENCE: MTV-030.02 (20021-3002)									
; CURRENT APPLICATION NUMBER: US/09/990,762									
; CURRENT FILING DATE: 2001-11-14									
; PRIOR APPLICATION NUMBER: 09/858,852									
; PRIOR FILING DATE: 2001-05-16									
; PRIOR APPLICATION NUMBER: 60/204,509									
; PRIOR FILING DATE: 2000-05-16									
; NUMBER OF SEQ ID NOS: 97									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 97									
; LENGTH: 12									
; TYPE: DNA									
; ORGANISM: Artificial Sequence									
; FEATURE:									
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative									
; OTHER INFORMATION: nucleotide sequence									
US-09-990-762-97									
Query Match	44.8%;	Score 9.4;	DB 1;	Length 12;					
Best Local Similarity	90.9%;	Pred. No. 38;							

Matches	10;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	5	GCCCCGGCGCGC 15							
Db	11	GCCCCAGCGGC 1							
RESULT 15									
US-10-257-017B-290182									
; Sequence 290182, Application US/10257017B									
; Publication No. US20040241651A1									
; GENERAL INFORMATION:									
; APPLICANT: Alexander Olek									
; APPLICANT: Christian Piepenbrock									
; APPLICANT: Kurt Berlin									
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin									
; TITLE OF INVENTION: methylations									
; FILE REFERENCE: E01/1193/WO									
; CURRENT APPLICATION NUMBER: US/10/257,017B									
; CURRENT FILING DATE: 2002-10-07									
; PRIOR APPLICATION NUMBER: DE 10019173.8									
; PRIOR FILING DATE: 2000-04-07									
; NUMBER OF SEQ ID NOS: 382046									
; SEQ ID NO 290182									
; LENGTH: 12									
; TYPE: DNA									
; ORGANISM: Artificial Sequence									
; FEATURE:									
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014238									
US-10-257-017B-290182									
Query Match	44.8%;	Score 9.4;	DB 1;	Length 12;					
Best Local Similarity	90.9%;	Pred. No. 38;							
Matches	10;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	10	GCGCGCTGTGG 20							
Db	1	GCGCGCGGTGG 11							
RESULT 16									
US-10-257-017B-304177									
; Sequence 304177, Application US/10257017B									
; Publication No. US20040241651A1									
; GENERAL INFORMATION:									
; APPLICANT: Alexander Olek									
; APPLICANT: Christian Piepenbrock									
; APPLICANT: Kurt Berlin									
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin									
; TITLE OF INVENTION: methylations									
; FILE REFERENCE: E01/1193/WO									
; CURRENT APPLICATION NUMBER: US/10/257,017B									
; CURRENT FILING DATE: 2002-10-07									
; PRIOR APPLICATION NUMBER: DE 10019173.8									
; PRIOR FILING DATE: 2000-04-07									
; NUMBER OF SEQ ID NOS: 382046									
; SEQ ID NO 304177									
; LENGTH: 12									
; TYPE: DNA									
; ORGANISM: Artificial Sequence									
; FEATURE:									
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020811									
US-10-257-017B-304177									
Query Match	44.8%;	Score 9.4;	DB 1;	Length 12;					
Best Local Similarity	90.9%;	Pred. No. 38;							
Matches	10;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	9	GCGCGCTGTG 19							
Db	1	GCGCGTTGTG 11							

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RESULT 17
US-10-257-017B-321157/c
; Sequence 321157, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 321157
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030082
US-10-257-017B-321157

Query Match          44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      9 GGCGCGCTGTG 19
      ||||| |||||
Db      12 GGCGCGATGTG 2

RESULT 18
US-10-915-233-97/c
; Sequence 97, Application US/10915233
; Publication No. US20050064477A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/10/915,233
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/09/990,762
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 97
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: nucleotide sequence
US-10-915-233-97

Query Match          44.8%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 38;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      5 GCCCGCGCGCG 15
      ||||| |||||
Db      11 GCCCAGCGCGC 1

RESULT 19
US-09-825-805-161
```

```
; Sequence 161, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MBHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 161
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-161

Query Match          44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 50;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCGGC 11
      ||:|||| |||||
Db      3 GCUGGCUCGCGC 13

RESULT 20
US-10-257-017B-66113/c
; Sequence 66113, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 66113
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017381
US-10-257-017B-66113

Query Match          44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      6 CCCGGCGCGCT 16
      ||||| |||||
Db     12 CCCGACGCGCT 2

RESULT 21
US-10-257-017B-66114
; Sequence 66114, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 66114
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0017381
US-10-257-017B-66114

Query Match      44.8%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCCGGCGCGCT 16
      ||||| |||||
Db     2 CCCGACGCGCT 12

RESULT 22
US-10-033-145-250/c
; Sequence 250, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-250

Query Match      42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCGCGCGCTG 17
      ||||| |||||
Db     9 GCGCGCGCTG 1

RESULT 23
US-10-330-627-903/c
; Sequence 903, Application US/10330627
; Publication No. US20030175771A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 903
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-903

Query Match      42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCGCGCGCTG 17
      ||||| |||||
Db     9 GCGCGCGCTG 1

RESULT 24
US-10-330-627-1410
; Sequence 1410, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1410
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1410

Query Match      42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTGGCCCGG 10
      ||||| |||||
Db     1 CTGGCCCGG 9

RESULT 25
US-10-330-627-1411
; Sequence 1411, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1411
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1411

Query Match          42.9%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTGGCCCGG 10
      |||||
Db       1 CTGGCCCGG 9

RESULT 26
US-10-978-283-13
; Sequence 13, Application US/10978283
; Publication No. US20050239734A1
; GENERAL INFORMATION:
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Vollmer, Jorg
; APPLICANT: Krieg, Arthur M
; APPLICANT: Noll, Bernhard O
; TITLE OF INVENTION: C-CLASS OLIGONUCLEOTIDE ANALOGS WITH ENHANCED IMMUNOSTIMULATORY
; TITLE OF INVENTION: POTENCY
; FILE REFERENCE: C1041.70034US01
; CURRENT APPLICATION NUMBER: US/10/978,283
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/516,913
; PRIOR FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-978-283-13

Query Match          42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCGCGCTG 17
      |||||
Db       1 GGCGCGCTG 9

RESULT 27
US-10-053-526A-9/c
; Sequence 9, Application US/10053526A
; Publication No. US20030003547A1
; GENERAL INFORMATION:
; APPLICANT: INSTITUT CURIE; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (C.N.R.S.);
; APPLICANT: MUSEUM NATIONAL D'HISTOIRE NATURELLE; INSTITUT NATIONAL DE LA SANTE ET DE
; APPLICANT: RECHERCHE MEDICALE (INSERM)
; APPLICANT: Dutreix, Marie
; APPLICANT: Sun, Jian-Sheng
; APPLICANT: Biet, Elodie
; APPLICANT: Maurisse, Rosalie
; APPLICANT: Feugeas, Jean-Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EFFECTING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 3754/OK213
; CURRENT APPLICATION NUMBER: US/10/053,526A
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/IB01/00749
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: EP 00401218.3
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-053-526A-9

Query Match          41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCTGGCCCGCG 12
      |||||
Db       12 GCTGGCCACGCG 1

RESULT 28
US-10-836-670-14/c
; Sequence 14, Application US/10836670
; Publication No. US20040235031A1
; GENERAL INFORMATION:
; APPLICANT: Schultz, Gregory Scott
; APPLICANT: Lewin, Alfred Samuel
; APPLICANT: Blalock, Timothy D.
; TITLE OF INVENTION: ANTI-SCARRING RIBOZYMES AND METHODS
; FILE REFERENCE: 5853-303
; CURRENT APPLICATION NUMBER: US/10/836,670
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Human adenovirus type 1
US-10-836-670-14

Query Match          41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GCCCGCGCGCGCT 16
      |||||
Db       12 GCCTGGAGCGCT 1

RESULT 29
US-10-033-145-39/c
; Sequence 39, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-39

Query Match          40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



```
QY      1 GCTGGCCCCG 10
      |||||
Db      10 GCTGGCCCCG 1

RESULT 30
US-10-140-763A-6/c
; Sequence 6, Application US/10140763A
; Publication No. US20030104420A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Methods and Compositions for Modulating
; FILE REFERENCE: SIER-012
; CURRENT APPLICATION NUMBER: US/10/140,763A
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,641
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-140-763A-6

Query Match      40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTGGCCCCG 10
      |||||
Db      10 GCTGGCCCCG 1

RESULT 31
US-10-330-627-718
; Sequence 718, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 718
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-718

Query Match      40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GCGCGCTGTG 19
      |||||
Db      1 GGGCGCTGTG 10

RESULT 32
US-10-091-281-362
; Sequence 362, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
```

```
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 362
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative EBOX/MYCMAX.03 motif
US-10-091-281-362

Query Match      40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCCGGCGCGC 14
      |||
Db      1 GCCAGCGCGC 10

RESULT 33
US-10-356-792-20/c
; Sequence 20, Application US/10356792
; Publication No. US20030215842A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej
; APPLICANT: Schweikhardt, Gary
; TITLE OF INVENTION: METHOD FOR THE ANALYSIS OF CYTOSINE METHYLATION PATTERNS
; FILE REFERENCE: 47675-33
; CURRENT APPLICATION NUMBER: US/10/356,792
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 60/352,944
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: AP-PCR Primer CG4
US-10-356-792-20

Query Match      40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCCGGCGCGC 15
      |||
Db      10 CGCGGCGCGC 1

RESULT 34
US-10-293-222-326
; Sequence 326, Application US/10293222
; Publication No. US2004003932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
```

;
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-326

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGTG 19
| | | | | | | |
Db 1 GGGCGCTGTG 10

RESULT 35
US-10-418-414-4/c
; Sequence 4, Application US/10418414
; Publication No. US20040072202A1
; GENERAL INFORMATION:
; APPLICANT: McGall, Glenn Hugh
; Miyada, Charles Garrett
; Cronin, Maureen T.
; Tan, Jennifer Dee
; Chee, Mark
; TITLE OF INVENTION: Modified Nucleic Acid Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/418,414
; FILING DATE: 22-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/608,691
; FILING DATE: 29-Jun-2000
; APPLICATION NUMBER: US/08/630,427
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/440,742
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: WO PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 16528X-012510
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-418-414-4

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 14
| | | | | | | |
Db 10 GCGCGCGCGC 1

RESULT 36
US-10-816-079-20
; Sequence 20, Application US/10816079
; Publication No. US2004016527A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Beaudry, Gary A
; APPLICANT: Madden, Stephen L
; APPLICANT: Bertelsen, Arthur H
; TITLE OF INVENTION: Composition and Methods for the Identification of Lung Tumor
; TITLE OF INVENTION: Cells
; FILE REFERENCE: GAO129C2
; CURRENT APPLICATION NUMBER: US/10/816,079
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: 09/663,516
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/080,037
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SAGE tag
US-10-816-079-20

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCCCGCGC 12
| | | | | | | |
Db 1 TGGCCCGCAG 10

RESULT 37
US-10-713-381-11/c
; Sequence 11, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays

US-10-713-381-11

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
| | | | | | | |
Db 10 CGGGCCCGGC 1

RESULT 38

US-10-713-381-14
; Sequence 14, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713.381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-14

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
| | | | | | | |
Db 1 CGGGCCCGGC 10

RESULT 39

US-10-487-934-245
; Sequence 245, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-245

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGG 10
| | | | | | | |
Db 1 GCTGGCCCGG 10

RESULT 40

US-10-487-934-266
; Sequence 266, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-266

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGTG 19
| | | | | | | |
Db 1 GGGCGCTGTG 10

RESULT 41

US-10-602-494-359/c
; Sequence 359, Application US/10602494
; Publication No. US20040265833A1
; GENERAL INFORMATION:
; APPLICANT: Cathy Lofton-Day
; APPLICANT: Andrew Sledziewski
; APPLICANT: Jeff Thomas
; APPLICANT: Robert W. Day
; APPLICANT: Lori Tonnes-Priddy
; APPLICANT: Karen Cardon
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of colorectal cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-45
; CURRENT APPLICATION NUMBER: US/10/602,494
; CURRENT FILING DATE: 2003-06-23
; NUMBER OF SEQ ID NOS: 385
; SEQ ID NO 359
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-602-494-359

Query Match 40.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCGC 15
| | | | | | | |
Db 10 CGCGCGCGC 1

RESULT 42

US-10-055-728-11
; Sequence 11, Application US/10055728
; Publication No. US20030170720A1
; GENERAL INFORMATION:
; APPLICANT: van der Kuyt, Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
; FILE REFERENCE: 5244US (REN/P55190US00)
; CURRENT APPLICATION NUMBER: US/10/055,728
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,722
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 0120373.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TAG sequence Hs183
US-10-055-728-11

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
|||||||
Db 2 CTGGCCCAGC 11

RESULT 43
US-10-310-677-11
; Sequence 11, Application US/10310677
; Publication No. US20030219772A1
; GENERAL INFORMATION:
; APPLICANT: Kuyt v.d., Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: Means and methods for treatment evaluation
; FILE REFERENCE: P55190US10
; CURRENT APPLICATION NUMBER: US/10/310,677
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: EP 01203703.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/325,722
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TAG sequence
; OTHER INFORMATION: Hs183
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
US-10-310-677-11

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
|||||||
Db 2 CTGGCCCAGC 11

RESULT 44
US-10-450-797-217/c
; Sequence 217, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-217

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGG 10
|||||||
Db 10 GCTGGCCCAG 1

RESULT 45
US-10-450-797-440
; Sequence 440, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 440
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-440

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGGC 11
|||||||
Db 2 CTGGCCCAGC 11

RESULT 46
US-10-450-797-1314/c
; Sequence 1314, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:


```
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1314
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1314

Query Match          40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 54;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCCCGGCGCG 14
      |||||
Db     11 GCCCGGCGGG 2

RESULT 47
US-09-990-762-97
; Sequence 97, Application US/09990762
; Patent No. US20020119498A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/09/990,762
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
US-09-990-762-97

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 GCGCGCTGTG 19
      |||||
Db     11 GCGCGCTGGG 10

RESULT 48
US-10-915-233-97
; Sequence 97, Application US/10915233
; Publication No. US20050064477A1
; GENERAL INFORMATION:
; APPLICANT: JOUNG, J. KEITH
; APPLICANT: MILLER, JEFFREY
; APPLICANT: PABO, CARL O.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INTERACTION TRAP ASSAYS
```

```
; FILE REFERENCE: MTV-030.02 (20021-3002)
; CURRENT APPLICATION NUMBER: US/10/915,233
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/09/990,762
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/858,852
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/204,509
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: nucleotide sequence
US-10-915-233-97

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 GCGCGCTGTG 19
      |||||
Db     11 GCGCGCTGGG 10

RESULT 49
US-09-263-959-437/c
; Sequence 437, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 437:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-437

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 CTGGCCCGGC 11
      ||||| |||
Db     11 CTGGCCTGGC 2

RESULT 50
US-09-949-041A-50/c
; Sequence 50, Application US/09949041A
; Publication No. US20030104387A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Meng
; APPLICANT: Woo, Hok
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Rif
; TITLE OF INVENTION: Resistance
; FILE REFERENCE: fp4637
; CURRENT APPLICATION NUMBER: US/09/949,041A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-949-041A-50

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 GCGCTGTGGC 21
      ||||| |||
Db     11 GCGCTGGGC 2

RESULT 51
US-10-403-232-144/c
; Sequence 144, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Qiudeng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 144
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-403-232-144

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 GCGCGCTGT 18
      ||||| |||
Db     12 GCGCGCCCGT 3

RESULT 52
US-10-257-017B-284862/c
; Sequence 284862, Application US/10257017B
; Publication No. US20040241651A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 284862
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012030
US-10-257-017B-284862

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 GCGCTGTGGC 21
      ||||| |||||
Db     11 GCGCGGTGGC 2

RESULT 53
US-10-257-017B-322854/c
; Sequence 322854, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322854
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322854

Query Match      40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCCCGCGCGC 14
      ||||| |||||
Db     10 GCCCGCCGCG 1

RESULT 54
US-10-257-017B-322859/c
; Sequence 322859, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322859
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322859

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGGCGCG 14
    ||||| |||||
Db 10 GCCCGCGCG 1

RESULT 55
US-10-257-017B-359284/c
; Sequence 359284, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359284
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC00008283
US-10-257-017B-359284

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 CGCGTGTGG 20
    ||||| |||||
Db 12 CGCGTTGTGG 3

RESULT 56
US-10-257-017B-376667/c
; Sequence 376667, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376667
; LENGTH: 12
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC00007696
US-10-257-017B-376667

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GCGCGCTGTG 19
    ||||| |||||
Db 10 GCGCGATGTG 1

RESULT 57
US-10-732-620-110/c
; Sequence 110, Application US/10732620
; Publication No. US20050032186A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Shin, Hyun-Chul
; APPLICANT: Kwon, Heung-Sun
; TITLE OF INVENTION: REGULATORY ZINC FINGER PROTEINS
; FILE REFERENCE: 12279-009001
; CURRENT APPLICATION NUMBER: US/10/732,620
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: US 60/431,892
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-732-620-110

Query Match          40.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCGC 15
    ||||| |||||
Db 12 CCCGGCCCCG 3

RESULT 58
US-10-033-145-273
; Sequence 273, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-033-145-273

Query Match          38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGG 20
```

Db 1 CGCTGTGG 8
|||||
RESULT 59
US-10-033-145-1876/c
; Sequence 1876, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1876
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1876

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
|||||
Db 9 GCTGGCCC 2

RESULT 60
US-10-713-381-17/c
; Sequence 17, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-17

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCCCGGC 11
|||||
Db 9 GGCCCGGC 2

RESULT 61
US-10-487-934-173
; Sequence 173, Application US/10487934
; Publication No. US20040265824A1

; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-173

Query Match 38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGG 20
|||||
Db 1 CGCTGTGG 8

RESULT 62
US-09-984-292-42/c
; Sequence 42, Application US/09984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-09-984-292-42

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCGCGC 15
|||||
Db 9 CGGCGCGC 2

RESULT 63
US-09-989-497-42/c
; Sequence 42, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE


```
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-09-989-497-42

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGCGCGC 15
      |||||
Db      9 CGGCGCGC 2

RESULT 64
US-09-249-155-6
; Sequence 6, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-6

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCCC 8
      |||||
Db      1 GCTGGCCC 8

RESULT 65
US-09-249-155-170
; Sequence 170, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
```

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; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-170

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTGGCCC 8
      |||||
Db      1 GCTGGCCC 8

RESULT 66
US-10-318-031-13/c
; Sequence 13, Application US/10318031
; Publication No. US20030220479A1
; GENERAL INFORMATION:
; APPLICANT: LI, XIAODONG
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: ADLER, JON ELLIOTT
; TITLE OF INVENTION: CHIMERIC Gal5 VARIANTS AND THEIR USE IN THE ANALYSIS AND
; TITLE OF INVENTION: DISCOVERY OF MODULATORS OF G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 100337.54104US
; CURRENT APPLICATION NUMBER: US/10/318,031
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 09/989,497
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/339,466
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: AscI site oligonucleotide
US-10-318-031-13

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGCGCGC 15
      |||||
Db      9 CGGCGCGC 2

RESULT 67
US-10-314-322-6
; Sequence 6, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
```

; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-6

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
|||||||
Db 1 GCTGGCCC 8

RESULT 68
US-10-314-322-170
; Sequence 170, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-170

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
|||||||
Db 1 GCTGGCCC 8

RESULT 69
US-10-314-322-305
; Sequence 305, Application US/10314322
; Publication No. US20030229911A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing

; FILE REFERENCE: 000486.00016
; CURRENT APPLICATION NUMBER: US/10/314,322
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-305

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGGC 21
|||||||
Db 1 GCTGTGGC 8

RESULT 70
US-10-450-797-1415
; Sequence 1415, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1415
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1415

Query Match 38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCC 8
|||||||
Db 4 GCTGGCCC 11

RESULT 71
US-10-633-531-13/c
; Sequence 13, Application US/10633531
; Publication No. US20050033021A1
; GENERAL INFORMATION:
; APPLICANT: LI, XIAODONG
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: ADLER, JON ELLIOTT
; TITLE OF INVENTION: CHIMERIC Gal5 VARIANTS AND THEIR USE IN THE ANALYSIS AND
; TITLE OF INVENTION: DISCOVERY OF MODULATORS OF G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 100337.54270US

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; CURRENT APPLICATION NUMBER: US/10/633,531
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 09/989,497
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/339,466
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: AscI site oligonucleotide
US-10-633-531-13

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGCGCGC 15
Db      9 CGGCGCGC 2

RESULT 72
US-10-952-773-42/c
; Sequence 42, Application US/10952773
; Publication No. US20050136512A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/10/952,773
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-10-952-773-42

Query Match      38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 71;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGCGCGC 15
Db      9 CGGCGCGC 2

RESULT 73
US-10-403-232-144
; Sequence 144, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Qiudeng
```

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; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 144
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-403-232-144

Query Match      38.1%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CGGCGCGC 15
Db      4 CGGCGCGC 11

RESULT 74
US-09-291-129-16/c
; Sequence 16, Application US/09291129
; Patent No. US2001001449A1
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Canter, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; TITLE OF INVENTION: BIOELECTRIC MICROCHIP
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/09/291,129
; CURRENT FILING DATE: 1999-04-12
; EARLIER APPLICATION NUMBER: US 09/030,156
; EARLIER FILING DATE: 1998-02-25
; EARLIER APPLICATION NUMBER: US 08/986,065
; EARLIER FILING DATE: 1997-12-05
; EARLIER APPLICATION NUMBER: US 08/859,644
; EARLIER FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US 08/725,976
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: US 08/708,262
; EARLIER FILING DATE: 1996-09-06
; EARLIER APPLICATION NUMBER: US 08/534,454
; EARLIER FILING DATE: 1995-09-27
; EARLIER APPLICATION NUMBER: US 08/304,657
; EARLIER FILING DATE: 1994-09-09
; EARLIER APPLICATION NUMBER: US 08/271,882
; EARLIER FILING DATE: 1994-07-07
; EARLIER APPLICATION NUMBER: US 08/146,504
; EARLIER FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
US-09-291-129-16

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches      9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CTGGCCCGCGC 12
Db      11 CTGGACAGGCG 1
```

RESULT 75
US-10-245-206-16/c
; Sequence 16, Application US/10245206
; Publication No. US20030073122A1
; GENERAL INFORMATION:
; APPLICANT: Nerenberg, Michael I.
; APPLICANT: Canter, David M.
; APPLICANT: Radtkey, Ray R.
; TITLE OF INVENTION: METHODS FOR DETERMINATION OF SINGLE
; TITLE OF INVENTION: NUCLEIC ACID POLYMORPHISMS USING A
; TITLE OF INVENTION: BIOELECTRIC MICROCHIP
; FILE REFERENCE: 240/240
; CURRENT APPLICATION NUMBER: US/10/245,206
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/291,129
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 09/030,156
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: US 08/986,065
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: US 08/859,644
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 08/725,976
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: US 08/708,262
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: US 08/534,454
; PRIOR FILING DATE: 1995-09-27
; PRIOR APPLICATION NUMBER: US 08/304,657
; PRIOR FILING DATE: 1994-09-09
; PRIOR APPLICATION NUMBER: US 08/271,882
; PRIOR FILING DATE: 1994-07-07
; PRIOR APPLICATION NUMBER: US 08/146,504
; PRIOR FILING DATE: 1993-11-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
US-10-245-206-16

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTGGCCCGCG 12
||| |
Db 11 CTGGACAGCG 1

RESULT 76
US-10-266-138B-11
; Sequence 11, Application US/10266138B
; Publication No. US20030152964A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: METHODS OF IDENTIFYING PHOTODAMAGE USING GENE
; FILE REFERENCE: J6664US(ED;EP/JVT)seq13Sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/266,138B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/338,272
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq.# 61 of
; OTHER INFORMATION: Table I
US-10-266-138B-11

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
||| |
Db 1 CCCAACGCGCT 11

RESULT 77
US-10-265-509B-11
; Sequence 11, Application US/10265509B
; Publication No. US20030170739A1
; GENERAL INFORMATION:
; APPLICANT: IOBST, Susanne T
; APPLICANT: SCHILLING, Kurt M
; APPLICANT: BOYD, Charles
; APPLICANT: URSCHITZ, Johann
; TITLE OF INVENTION: GENE EXPRESSION FOR ANALYZING PHOTODAMAGE
; FILE REFERENCE: J6663US(ED;EP/JVT)seq13Sep'02;51-84
; CURRENT APPLICATION NUMBER: US/10/265,509B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/337,856
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Seq.# 61 of
; OTHER INFORMATION: Table I
US-10-265-509B-11

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
||| |
Db 1 CCCAACGCGCT 11

RESULT 78
US-10-084-839-3364/c
; Sequence 3364, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.

; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsatska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3364
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3364

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGGCGCGC 15
| | | | | | | |
Db 11 GCCCGGGGTGC 1

RESULT 79
US-10-450-797-76
; Sequence 76, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-76

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCCGGCGCGCT 16
| | | | | | | |
Db 1 CCAGGCACGCT 11

RESULT 80
US-10-450-797-124/c
; Sequence 124, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-124

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
| | | | | | | |
Db 11 GAGCGCAGTGG 1

RESULT 81
US-10-450-797-579
; Sequence 579, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 579
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-579

Query Match 37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCCGGCGCG 14
| | | | | | | |
Db 1 GGCCCTGAGCG 11

RESULT 82
US-10-450-797-851/c
; Sequence 851, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 851

```

; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-851

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
Db 11 CTCGCTGGGGC 1

RESULT 83
US-10-450-797-1173/c
; Sequence 1173, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1173
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1173

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GCGCGCTGTGG 20
Db 11 GCGTGCAGTGG 1

RESULT 84
US-10-754-408-8
; Sequence 8, Application US/10754408
; Publication No. US20040203035A1
; GENERAL INFORMATION:
; APPLICANT: Mast, Andrea L.
; APPLICANT: Dorn, Erin
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Accola, Molly
; APPLICANT: Wigdal, Susan S.
; TITLE OF INVENTION: Connexin Allele Detection Assays
; FILE REFERENCE: FORS-08724
; CURRENT APPLICATION NUMBER: US/10/754,408
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-754-408-8

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
Db 11 CGCGCCGAGGC 11

RESULT 85
US-10-754-408-8/c
; Sequence 8, Application US/10754408
; Publication No. US20040203035A1
; GENERAL INFORMATION:
; APPLICANT: Mast, Andrea L.
; APPLICANT: Dorn, Erin
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Accola, Molly
; APPLICANT: Wigdal, Susan S.
; TITLE OF INVENTION: Connexin Allele Detection Assays
; FILE REFERENCE: FORS-08724
; CURRENT APPLICATION NUMBER: US/10/754,408
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-754-408-8

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCCGCGCGCG 14
Db 11 GCCTCGCGCGCG 1

RESULT 86
US-09-827-395A-739
; Sequence 739, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 739
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-739

Query Match      37.1%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGCCCGCGCGCGC 15
Db 5 GGCCCGCGCGCGC 15
```

```

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 CGCGCTGTGGC 21
Db 1 CGCGCCGAGGC 11

RESULT 85
US-10-754-408-8/c
; Sequence 8, Application US/10754408
; Publication No. US20040203035A1
; GENERAL INFORMATION:
; APPLICANT: Mast, Andrea L.
; APPLICANT: Dorn, Erin
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Accola, Molly
; APPLICANT: Wigdal, Susan S.
; TITLE OF INVENTION: Connexin Allele Detection Assays
; FILE REFERENCE: FORS-08724
; CURRENT APPLICATION NUMBER: US/10/754,408
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-754-408-8

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 81;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCCGCGCGCG 14
Db 11 GCCTCGCGCGCG 1

RESULT 86
US-09-827-395A-739
; Sequence 739, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 739
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-739

Query Match      37.1%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGCCCGCGCGCGC 15
Db 5 GGCCCGCGCGCGC 15
```

RESULT 87
US-10-430-882-739
; Sequence 739, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor (400/017)
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 739
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-739

Query Match 37.1%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGGC 15
||||| |||
Db 5 GCCCGCGCGGC 15

RESULT 88
US-09-827-395A-442
; Sequence 442, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor (400/017)
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 442
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-442

Query Match 37.1%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGGC 15
||||| |||

Db 7 GCCCGCGCGGC 17
RESULT 89
US-09-827-395A-443
; Sequence 443, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor (400/017)
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-443

Query Match 37.1%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGGC 15
||||| |||
Db 6 GCCCGCGCGGC 16

RESULT 90
US-10-430-882-442
; Sequence 442, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor (400/112)
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 442
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-442

Query Match 37.1%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
|||||
Db 7 GCCCGCGCGC 17

RESULT 91
US-10-430-882-443
; Sequence 443, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haeberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-H (400/112)
; CURRENT APPLICATION NUMBER: US/10/430,882
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 443
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-443

Query Match 37.1%; Score 7.8; DB 1; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.le+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGC 15
|||||
Db 6 GCCCGCGCGC 16

RESULT 92
US-09-154-750A-12
; Sequence 12, Application US/09154750A
; Publication No. US20020055097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCCCGCGC 13
|||||
Db 2 GCCCGCGC 10

RESULT 93
US-09-154-750A-12/c
; Sequence 12, Application US/09154750A
; Publication No. US20020055097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGCGCGGCT 16
|||||
Db 9 CGCGCGGCT 1

RESULT 94
US-09-538-456-3/c
; Sequence 3, Application US/09538456
; Patent No. US20020076802A1
; GENERAL INFORMATION:
; APPLICANT: Alam, Mansoor
; APPLICANT: Sattar, Abdul
; APPLICANT: Kumar, Sushu
; APPLICANT: Samad, Abdul
; APPLICANT: Dhawan, Om Prakash
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Singh, Seema
; APPLICANT: Kumar, Poovappallivadakethil Viswanathan Nair Ajay
; APPLICANT: Khalique, Abdul
; APPLICANT: Zaim, Mohammad
; APPLICANT: Shahabuddin, Saba
; APPLICANT: Trivedi, Mala
; TITLE OF INVENTION: A novel Streptomyces strain with potential anti-microbial
; FILE REFERENCE: 148920.00003
; CURRENT APPLICATION NUMBER: US/09/538,456
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Word-97
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-538-456-3

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
| | | | | | |
Db 9 CCGGCGTGC 1

RESULT 95
US-09-785-716A-6/c
; Sequence 6, Application US/09785716A
; Publication No. US20020184676P1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Singh, Maneesha
; APPLICANT: Singh, Ajay Pratap
; APPLICANT: Singh, Vandana
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Kuman, Sushil
; TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
; FILE REFERENCE: 41799/VGG/K375
; CURRENT APPLICATION NUMBER: US/09/785,716A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for RAPD profile
US-09-785-716A-6

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
| | | | | | |
Db 9 CCGGCGTGC 1

RESULT 96
US-09-799-880-6/c
; Sequence 6, Application US/09799880
; Publication No. US20030014799P1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastry, Kakaraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
; APPLICANT: Shasany, Ajit
; APPLICANT: Darokar, Mahendra
; APPLICANT: Khanuja, Suman
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAFAL'
; FILE REFERENCE: 2734-102
; CURRENT APPLICATION NUMBER: US/09/799,880
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-799-880-6

Query Match 35.2%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
| | | | | | |
Db 9 CCGGCGTGC 1

RESULT 97
US-09-915-063-1/c
; Sequence 1, Application US/09915063
; Publication No. US20030082544A1
; GENERAL INFORMATION:
; APPLICANT: Fors, Lance
; APPLICANT: Ganske, Rocky
; TITLE OF INVENTION: Methods and Systems for Validating Detection Assays, Developing
; TITLE OF INVENTION: Diagnostic DNA or RNA Analysis Products, and Increasing Revenue
; TITLE OF INVENTION: Margins from In-Vitro Diagnostic DNA or RNA Analysis Assays
; FILE REFERENCE: FORS-06467
; CURRENT APPLICATION NUMBER: US/09/915,063
; CURRENT FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: 60/304,521
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-915-063-1

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCG 14
| | | | | | |
Db 9 CTCGGCGCG 1

RESULT 98
US-09-929-135-1/c
; Sequence 1, Application US/09929135
; Publication No. US20030104470A1
; GENERAL INFORMATION:
; APPLICANT: Fors, Lance
; APPLICANT: Ganske, Rocky
; APPLICANT: Brower, Amy M.
; APPLICANT: Ziarno, Witold M.
; TITLE OF INVENTION: Electronic Medical Record, Library of Electronic Medical Records
; TITLE OF INVENTION: Polymorphism Data, and Computer Systems and Methods for Use Ther
; FILE REFERENCE: FORS-06443
; CURRENT APPLICATION NUMBER: US/09/929,135
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-929-135-1

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCG 14
| | | | | | |
Db 9 CTCGGCGCG 1


```

; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 279
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-279

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      12 GCGCTGTGG 20
      | ||||| |||
Db      2 GGGCTGTGG 10

RESULT 104
US-10-330-627-280
; Sequence 280, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-280

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      12 GCGCTGTGG 20
      | ||||| |||
Db      2 GGGCTGTGG 10

RESULT 105
US-10-330-627-447/c
; Sequence 447, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-447

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      12 GCGCTGTGG 20
      | ||||| |||
Db      2 GGGCTGTGG 10

RESULT 106
US-10-330-627-586/c
; Sequence 586, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 586
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-586

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      13 CGCTGTGGC 21
      ||||| |||
Db      9 CGCTGGGC 1

RESULT 107
US-10-330-627-1214/c
; Sequence 1214, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1214
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1214

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      3 TGGCCCGGC 11
      ||||| |||
Db      9 TGGCCAGGC 1

RESULT 108
US-10-330-627-1215/c
```

```

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      13 CGCTGTGGC 21
      ||||| |||
Db      9 CGCTGGGC 1

RESULT 106
US-10-330-627-586/c
; Sequence 586, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 586
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-586

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      13 CGCTGTGGC 21
      ||||| |||
Db      10 CGCAGTGGC 2

RESULT 107
US-10-330-627-1214/c
; Sequence 1214, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1214
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1214

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      3 TGGCCCGGC 11
      ||||| |||
Db      9 TGGCCAGGC 1

RESULT 108
US-10-330-627-1215/c
```

```
; Sequence 1215, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1215
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1215
```

```
Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 TGGCCCGGC 11
        ||||| |||
Db       9 TGGCCAGGC 1
```

RESULT 109

```
US-10-330-627-1228
; Sequence 1228, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1228
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1228
```

```
Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 TGGCCCGGC 11
        ||||| |||
Db       2 TGGCCAGGC 10
```

RESULT 110

```
US-10-330-627-1229
; Sequence 1229, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
```

```
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1229
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1229
```

```
Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 TGGCCCGGC 11
        ||||| |||
Db       2 TGGCCAGGC 10
```

RESULT 111

```
US-10-330-627-1230
; Sequence 1230, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1230
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1230
```

```
Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 TGGCCCGGC 11
        ||||| |||
Db       2 TGGCCAGGC 10
```

RESULT 112

```
US-10-330-627-1231
; Sequence 1231, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1231
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1231
```

```
Query Match          35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
```


Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10

RESULT 113
US-10-330-627-1232
; Sequence 1232, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1232
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1232

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10

RESULT 114
US-10-330-627-1233
; Sequence 1233, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1233
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1233

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10

RESULT 115
US-10-330-627-1234
; Sequence 1234, Application US/10330627
; Publication No. US20030175771A1

; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1234
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1234

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGGCCCGGC 11
|||||
Db 2 TGGCCAGGC 10

RESULT 116
US-10-353-751-1/c
; Sequence 1, Application US/10353751
; Publication No. US20030219784A1
; GENERAL INFORMATION:
; APPLICANT: Ip, Hon S.
; APPLICANT: Ziarno, Witold A.
; APPLICANT: Donald, Glen
; TITLE OF INVENTION: Systems and Methods for Analysis of Agricultural Products
; FILE REFERENCE: FORS-07809
; CURRENT APPLICATION NUMBER: US/10/353,751
; CURRENT FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-353-751-1

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCCGGCGCG 14
|||||
Db 9 CTCGGCGCG 1

RESULT 117
US-10-321-039-753/c
; Sequence 753, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30

;
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 753
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-753

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCG 14
| | | | | | | |
Db 9 CTCGGCGCG 1

RESULT 118

US-10-418-414-21/c
; Sequence 21, Application US/10418414
; Publication No. US20040072202A1
; GENERAL INFORMATION:
; APPLICANT: McGall, Glenn Hugh
; Miyada, Charles Garrett
; Cronin, Maureen T.
; Tan, Jennifer Dee
; Chee, Mark
; TITLE OF INVENTION: Modified Nucleic Acid Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/418,414
; FILING DATE: 22-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/608,691
; FILING DATE: 29-Jun-2000
; APPLICATION NUMBER: US/08/630,427
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/440,742
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: WO PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 16528X-012510
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 10
OTHER INFORMATION: /note= "N = cytosine covalently modified
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-418-414-21

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCCGGCGCG 14
| | | | | | | |
Db 9 CGCGGCGCG 1

RESULT 119

US-10-418-414-27
; Sequence 27, Application US/10418414
; Publication No. US20040072202A1
; GENERAL INFORMATION:
; APPLICANT: McGall, Glenn Hugh
; Miyada, Charles Garrett
; Cronin, Maureen T.
; Tan, Jennifer Dee
; Chee, Mark
; TITLE OF INVENTION: Modified Nucleic Acid Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/418,414
; FILING DATE: 22-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/608,691
; FILING DATE: 29-Jun-2000
; APPLICATION NUMBER: US/08/630,427
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/440,742
; FILING DATE: 10-MAY-1995
; APPLICATION NUMBER: WO PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 16528X-012510
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /note= "N = guanine covalently modified
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-418-414-27

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CCCGCCGCGC 14
      | | | | | | |
Db      2 CGCGGCGCG 10

RESULT 120
US-10-434-479-63/c
; Sequence 63, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-63

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TGGCCCCGC 11
      | | | | | | |
Db      10 TGGCCCCGC 2

RESULT 121
US-10-401-753-5/c
; Sequence 5, Application US/10401753
; Publication No. US20040194175P1
; GENERAL INFORMATION:
; APPLICANT: LAL, Raj K et al
; TITLE OF INVENTION: A CITRAL RICH HIGH YIELDING LEMONGRASS PLANT 'NIMA' OF CYMBOPOGON
; TITLE OF INVENTION: FLEXUOSUS
; FILE REFERENCE: 2761-0167P
; CURRENT APPLICATION NUMBER: US/10/401,753
; CURRENT FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Random MAP primer
US-10-401-753-5

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CCGGCGCGC 15
      | | | | | | |
Db      9 CCGGCGGTGC 1

RESULT 122
US-10-401-691-6/c
; Sequence 6, Application US/10401691
; Publication No. US20040194176P1
; GENERAL INFORMATION:
; APPLICANT: KHANUJA, SUMAN PREET SINGH
; APPLICANT: SHASANY, AJIT KUMAR
; APPLICANT: YADAV, USHA
; APPLICANT: DHAWAN, SUNITA
; APPLICANT: DAROKAR, MAHENDRA PANDURANG
; APPLICANT: BAL, JANEK RAJ
; APPLICANT: GUPTA, SONI
; APPLICANT: PANDEY, SWETA
; APPLICANT: SINGH, ANIL KUMAR
; APPLICANT: BANSAL, RAVI PRAKASH
; APPLICANT: LAL, RAJ KISHORI
; APPLICANT: DHAWAN, OM PARKESH
; APPLICANT: NAQVI, ALI ARIF
; APPLICANT: KALRA, ALOK
; APPLICANT: KRISHNA, ALOK
; APPLICANT: TOMAR, VIRENDRA KUMAR SINGH
; TITLE OF INVENTION: MINT PLANT 'KUSHAL' FOR LATE TRANSPLANTING
; FILE REFERENCE: 056859-0184
; CURRENT APPLICATION NUMBER: US/10/401,691
; CURRENT FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
US-10-401-691-6

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CCGGCGCGC 15
      | | | | | | |
Db      9 CCGGCGGTGC 1

RESULT 123
US-10-404-304-5/c
; Sequence 5, Application US/10404304
; Publication No. US20040199969P1
; GENERAL INFORMATION:
; APPLICANT: Lal, Raj Kishori
; APPLICANT: Singh, Nilakshi
; APPLICANT: Mishra, Hari Om
; APPLICANT: Sharma, Jawahar Ram
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Khanuja, Suman Preet Singh
```

;
; TITLE OF INVENTION: EARLY MATURING, HIGH YIELDING PSYLLIUM (PLANTAGO OVATA F.)
; FILE REFERENCE: 11378.48US01
; CURRENT APPLICATION NUMBER: US/10/404,304
; CURRENT FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers
US-10-404-304-5

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
|||
Db 9 CCGGCGTGC 1

RESULT 124

US-10-713-381-13
; Sequence 13, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-13

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCCG 9
|||
Db 1 GCGGGCCCCG 9

RESULT 125

US-10-713-381-13/c
; Sequence 13, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14

;
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-13

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCCG 9
|||
Db 10 GCGGGCCCCG 2

RESULT 126

US-10-713-381-15
; Sequence 15, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-15

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCCG 9
|||
Db 2 GCGGGCCCCG 10

RESULT 127

US-10-713-381-19
; Sequence 19, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19

Db 2 GCGCCGCCG 10
||| ||| ||
RESULT 132
US-10-713-381-22/c
; Sequence 22, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-22
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCTGGCCCCG 9
||| ||| ||
Db 9 GCGGGCCCCG 1
RESULT 133
US-10-713-381-23/c
; Sequence 23, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; TITLE OF INVENTION: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-23
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCTGGCCCCG 9
||| ||| ||
Db 9 GCGGGCCCCG 1
RESULT 134

US-10-478-014-32
; Sequence 32, Application US/10478014
; Publication No. US20040248083A1
; GENERAL INFORMATION:
; APPLICANT: Aarhus Universitet
; APPLICANT: Finn Skou Pedersen
; APPLICANT: Jacob Giehm Mikkelsen
; APPLICANT: Soren Vestergaards Rasmussen
; APPLICANT: Mogens Ouch
; APPLICANT: Lars Aagaard
; TITLE OF INVENTION: Improved Vectors for Gene Therapy
; FILE REFERENCE: P32171 PC 01
; CURRENT APPLICATION NUMBER: US/10/478,014
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: PA 2001 00789
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: palindrome at position 209-218 in Akv/AkvB
US-10-478-014-32
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCTGGCCCCG 9
||| ||| ||
Db 1 GCTGGCCAG 9
RESULT 135
US-10-478-014-32/c
; Sequence 32, Application US/10478014
; Publication No. US20040248083A1
; GENERAL INFORMATION:
; APPLICANT: Aarhus Universitet
; APPLICANT: Finn Skou Pedersen
; APPLICANT: Jacob Giehm Mikkelsen
; APPLICANT: Soren Vestergaards Rasmussen
; APPLICANT: Mogens Ouch
; APPLICANT: Lars Aagaard
; TITLE OF INVENTION: Improved Vectors for Gene Therapy
; FILE REFERENCE: P32171 PC 01
; CURRENT APPLICATION NUMBER: US/10/478,014
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: PA 2001 00789
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: palindrome at position 209-218 in Akv/AkvB
US-10-478-014-32
Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCTGGCCCCG 9
||| ||| ||
Db 10 GCTGGCCAG 2
RESULT 136
US-10-487-934-236/c

```
; Sequence 236, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-487-934-236

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      3 TGGCCCGGC 11
Db      9 TGGCCAGGC 1

RESULT 137
US-10-487-934-237/c
; Sequence 237, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-487-934-237

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      3 TGGCCCGGC 11
Db      9 TGGCCAGGC 1

RESULT 138
US-10-626-832-234/c
; Sequence 234, Application US/10626832
; Publication No. US2005003342A1
; GENERAL INFORMATION:
; APPLICANT: Davis Poynter, Nick
; APPLICANT: Nugent, Josephine
```

```
; APPLICANT: Birch-Machin, Ian
; APPLICANT: Allen, George P
; TITLE OF INVENTION: Viral Marker
; FILE REFERENCE: 620-262
; CURRENT APPLICATION NUMBER: US/10/626,832
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,576
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Equine herpesvirus 1
; US-10-626-832-234

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      2 CTGGCCCGC 10
Db      10 CTGGCTCGG 2

RESULT 139
US-10-647-114-13/c
; Sequence 13, Application US/10647114
; Publication No. US20050050593A1
; GENERAL INFORMATION:
; APPLICANT: GUPTA, ANIL KUMAR
; APPLICANT: KHANUJA, SUMAN PREET SINGH
; APPLICANT: GUPTA, MADAN MOHAN
; APPLICANT: SHASANY, AJIT KUMAR
; APPLICANT: JAIN, NEERAJ
; APPLICANT: VERMA, RAM KISHOR
; APPLICANT: DAROKAR, MAHENDRA PANDURANG
; APPLICANT: BAGCHI, GURU DAS
; APPLICANT: KUMAR, SUSHIL
; TITLE OF INVENTION: HIGH HERB, PHYLLANTHIN AND HYPOPHYLLANTHIN YIELDING
; TITLE OF INVENTION: CULTIVAR OF PHYLLANTHUS AMARUS 'CIM-JEEVAN'
; FILE REFERENCE: 056859-0188
; CURRENT APPLICATION NUMBER: US/10/647,114
; CURRENT FILING DATE: 2003-08-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
; US-10-647-114-13

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      7 CCGGCGCGC 15
Db      9 CCGGCGGTGC 1

RESULT 140
US-10-639-682-6/c
; Sequence 6, Application US/10639682
; Publication No. US20050091705A1
; GENERAL INFORMATION:
; APPLICANT: LAL, RAJ KISHORI
; APPLICANT: KHANUJA, SUMAN PREET SINGH
; APPLICANT: AGNIHOTRI, ARUN KUMAR
; APPLICANT: MISRA, HARI OM
```

```
; APPLICANT: SHASANY, AJIT KUMAR
; APPLICANT: NAQVI, ALI ARIF
; APPLICANT: DHAWAN, OM PRAKASH
; APPLICANT: KALARA, ALOK
; APPLICANT: BAHL, JANAK RAJ
; APPLICANT: DAROKAR, MAHENDRA PANDURANG
; TITLE OF INVENTION: A HIGH ESSENTIAL OIL AND EUGENOL YIELDING CULTIVAR OF
; FILE REFERENCE: 056859-0187
; CURRENT APPLICATION NUMBER: US/10/639,682
; CURRENT FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-639-682-6
```

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
| | | | | | | |
Db 9 CCGGCGGTGC 1

```
RESULT 141
US-10-813-160-9/c
; Sequence 9, Application US/10813160
; Publication No. US20050142564A1
; GENERAL INFORMATION:
; APPLICANT: COUNCIL OF SCIENTIFIC & INDUSTRIAL RESEARCH
; APPLICANT: KHANUJA, Suman Preet Singh
; APPLICANT: PAUL, Shilpi
; APPLICANT: SHASANY, Ajit Kumar
; APPLICANT: DAROKAR, Mahendra Pandurang
; APPLICANT: SHUKLA, Ashutosh Kumar
; APPLICANT: GUPTA, Madan Mohan
; APPLICANT: KUMAR, Anuruddha
; TITLE OF INVENTION: PRIMERS AND A SCREENING METHOD FOR IDENTIFICATION OF ARTEMISININ
; TITLE OF INVENTION: PRODUCING PLANTS
; FILE REFERENCE: Q80746
; CURRENT APPLICATION NUMBER: US/10/813,160
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: PCT/IN03/00404
; PRIOR FILING DATE: 2003-09-29
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer MAP06
US-10-813-160-9
```

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
| | | | | | | |
Db 9 CCGGCGGTGC 1

RESULT 142
US-10-967-711-11/c
; Sequence 11, Application US/10967711

```
; Publication No. US20050186588A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Jarvis, Nancy
; APPLICANT: Roeven, Robert
; APPLICANT: Hall, Jeff G.
; APPLICANT: Allawi, Hatim T.
; TITLE OF INVENTION: Direct Nucleic Acid Detection in Bodily Fluids
; FILE REFERENCE: FORS-09661
; CURRENT APPLICATION NUMBER: US/10/967,711
; CURRENT FILING DATE: 2004-10-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-967-711-11
```

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCGGCGCGC 14
| | | | | | | |
Db 9 CTCGGCGCG 1

```
RESULT 143
US-10-811-244B-6/c
; Sequence 6, Application US/10811244B
; Publication No. US20050223447P1
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Paul, Shilipi
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Gupta, Anil Kumar
; APPLICANT: Darokar, Mahendra Pandurang
; TITLE OF INVENTION: HIGH ARTEMISININ YIELDING PLANT GENOTYPE 'CIM-AROGYA'
; FILE REFERENCE: U 015108-9
; CURRENT APPLICATION NUMBER: US/10/811,244B
; CURRENT FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: MAP Primer
US-10-811-244B-6
```

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CCGGCGCGC 15
| | | | | | | |
Db 9 CCGGCGGTGC 1

RESULT 144
US-11-035-899-386/c
; Sequence 386, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe

;
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 386:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 386:
US-11-035-899-386

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 CTGGCCCGG 10
Db 10 CTGGCCCTG 2

RESULT 145
US-11-035-899-387/c
; Sequence 387, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 387:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 387:
US-11-035-899-387

Query Match 35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 76;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGG 10
Db 9 CTGGCCCTG 1

RESULT 146
US-09-984-292-42
; Sequence 42, Application US/09984292
; Patent No. US20020128433A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-09-984-292-42

Query Match 35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
Db 1 GGCGCGCGG 9

Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
| | | | | | | |
Db 1 GGCGCGCCG 9

RESULT 149
US-10-633-531-13
; Sequence 13, Application US/10633531
; Publication No. US20050033021A1
; GENERAL INFORMATION:
; APPLICANT: LI, XIAODONG
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: ADLER, JON ELLIOTT
; TITLE OF INVENTION: CHIMERIC Gal5 VARIANTS AND THEIR USE IN THE ANALYSIS AND
; TITLE OF INVENTION: DISCOVERY OF MODULATORS OF G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 100337.54270US
; CURRENT APPLICATION NUMBER: US/10/633,531
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 09/989,497
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/339,466
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: AscI site oligonucleotide
US-10-633-531-13

Query Match 35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
| | | | | | | |
Db 1 GGCGCGCCG 9

RESULT 150
US-10-952-773-42
; Sequence 42, Application US/10952773
; Publication No. US20050136512A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/10/952,773
; PRIOR FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative

RESULT 147
US-09-989-497-42
; Sequence 42, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-09-989-497-42

Query Match 35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GGCGCGCTG 17
| | | | | | | |
Db 1 GGCGCGCCG 9

RESULT 148
US-10-318-031-13
; Sequence 13, Application US/10318031
; Publication No. US20030220479A1
; GENERAL INFORMATION:
; APPLICANT: LI, XIAODONG
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: ADLER, JON ELLIOTT
; TITLE OF INVENTION: CHIMERIC Gal5 VARIANTS AND THEIR USE IN THE ANALYSIS AND
; TITLE OF INVENTION: DISCOVERY OF MODULATORS OF G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 100337.54104US
; CURRENT APPLICATION NUMBER: US/10/318,031
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 09/989,497
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/339,466
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: AscI site oligonucleotide
US-10-318-031-13

Query Match 35.2%; Score 7.4; DB 1; Length 11;

```
; OTHER INFORMATION: oligonucleotide
US-10-952-773-42

Query Match      35.2%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 GCGCGCGCTG 17
      |||||
Db      1 GCGCGCGCG 9

RESULT 151
US-09-923-517-40
; Sequence 40, Application US/09923517
; Publication No. US20020039741A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-923-517-40

Query Match      34.3%; Score 7.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      8 CGGCGCGCTGTG 19
      |||||
Db      5 CAGCGCGCCGG 16

RESULT 152
US-10-430-196-40
; Sequence 40, Application US/10430196
; Publication No. US20030194738A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/430,196
; FILING DATE: 05-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517A
; FILING DATE: 07-Aug-2001
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-430-196-40

Query Match      34.3%; Score 7.2; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      8 CGGCGCGCTGTG 19
      |||||
Db      5 CAGCGCGCCGG 16

RESULT 153
US-09-942-487-3
; Sequence 3, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: McDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; TITLE OF INVENTION: ANTIMICROBIAL COMPOUNDS
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-942-487-3
```

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 GGCGCGC 15
        |||||
Db       1 GGCGCGC 7
```

RESULT 154

```
US-09-942-487-3/c
; Sequence 3, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
```

```
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: MCDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
```

US-09-942-487-3

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 GGCGCGC 15
        |||||
Db       8 GGCGCGC 2
```

RESULT 155

```
US-09-942-487-5
; Sequence 5, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
```

```
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: MCDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-942-487-5
```

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 GGCGCGC 15
        |||||
Db       3 GGCGCGC 9
```

RESULT 156

```
US-09-942-487-5/c
; Sequence 5, Application US/09942487
; Publication No. US20020086310A1
; GENERAL INFORMATION:
```

```
; APPLICANT: FAN, FRANK
; APPLICANT: HE, YIPING
; APPLICANT: HUANG, JIANZHONG
; APPLICANT: JIANG, XINHE
; APPLICANT: MCDEVITT, DAMIEN
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: ST. JOHN, ANNEMARIE
; TITLE OF INVENTION: IDENTIFICATION OF TARGETS OF
; FILE REFERENCE: P51167
; CURRENT APPLICATION NUMBER: US/09/942,487
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/229,965
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
```

US-09-942-487-5

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 GGCGCGC 15
        |||||
Db      10 GGCGCGC 4
```

RESULT 157

```
US-09-867-262-5
; Sequence 5, Application US/09867262
; Patent No. US20020119457A1
; GENERAL INFORMATION:
```

```
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DEVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
```



```
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-867-262-5

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CGCGCTG 17
      |||||
Db      1 CGCGCTG 7

RESULT 158
US-09-885-551A-6
; Sequence 6, Application US/09885551A
; Patent No. US20020146762A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/885,551A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-885-551A-6

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CGCGCTG 17
      |||||
Db      1 CGCGCTG 7

RESULT 159
US-09-990-186-1278
; Sequence 1278, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
```

```
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1278

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 GCTGTGG 20
      |||||
Db      4 GCTGTGG 10

RESULT 160
US-09-989-994-1278
; Sequence 1278, Application US/099899994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1278

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 GCTGTGG 20
      |||||
Db      4 GCTGTGG 10

RESULT 161
US-10-087-426-6
; Sequence 6, Application US/10087426
; Publication No. US20020142394A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
```

; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-087-426-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
|||||
Db 1 CGCGCTG 7

RESULT 162
US-10-033-145-36
; Sequence 36, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-36

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
|||||
Db 3 GCTGGCC 9

RESULT 163
US-10-033-145-299
; Sequence 299, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 299
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-299

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTG 19
|||||
Db 1 CGCTGTG 7

RESULT 164
US-10-033-145-527/c
; Sequence 527, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 527
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-527

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
|||||
Db 9 CTGTGGC 3

RESULT 165
US-10-033-145-702
; Sequence 702, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 702
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-702

Query Match 33.3%; Score 7; DB 1; Length 10;

```
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGC 11
   |||||
Db 4 GCCCGGC 10

RESULT 166
US-10-033-145-771
; Sequence 771, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 771
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-771

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGC 11
   |||||
Db 1 GCCCGGC 7

RESULT 167
US-10-033-145-1178/c
; Sequence 1178, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1178
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1178

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
   |||||
Db 8 GGCGCGC 2

RESULT 168
US-10-033-145-1502/c
; Sequence 1502, Application US/10033145
```

```
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1502
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1502

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
   |||||
Db 10 GCTGTGG 4

RESULT 169
US-10-033-145-1540/c
; Sequence 1540, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1540
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1540

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
   |||||
Db 7 GCTGGCC 1

RESULT 170
US-10-033-145-1855/c
; Sequence 1855, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
```

; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1855
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1855

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||
Db 9 GCTGTGG 3

RESULT 171

US-10-033-145-1872
; Sequence 1872, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C

; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1872
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1872

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCCCGGC 11
|||||
Db 2 GCCCGGC 8

RESULT 172

US-10-033-145-1908
; Sequence 1908, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C

; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1908
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1908

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||
Db 2 GCTGTGG 8

RESULT 173

US-10-033-145-2019
; Sequence 2019, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:

; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C

; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2019

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2019

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||
Db 1 GCTGTGG 7

RESULT 174

US-10-150-509-1
; Sequence 1, Application US/10150509
; Publication No. US20020178460A1
; GENERAL INFORMATION:

; APPLICANT: Enikolopov, Grigori N.
; APPLICANT: Mignone, John
; TITLE OF INVENTION: TRANSGENIC MICE EXPRESSING FLUORESCENT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 1314.1062-010

; CURRENT APPLICATION NUMBER: US/10/150,509
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US 09/444,335
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: PCT/US00/31150
; PRIOR FILING DATE: 2000-11-14

; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Linker
US-10-150-509-1

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
|||||
Db 2 GGCGCGC 8

RESULT 175

US-10-150-509-1/c
; Sequence 1, Application US/10150509
; Publication No. US20020178460A1
; GENERAL INFORMATION:
; APPLICANT: Enikolopov, Grigori N.
; APPLICANT: Mignone, John
; TITLE OF INVENTION: TRANSGENIC MICE EXPRESSING FLUORESCENT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 1314.1062-010
; CURRENT APPLICATION NUMBER: US/10/150,509
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US 09/444,335
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: PCT/US00/31150
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Linker
US-10-150-509-1

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
|||||||
Db 9 GGCGCGC 3

RESULT 176
US-10-094-146-21
; Sequence 21, Application US/10094146
; Publication No. US20020192755A1
; GENERAL INFORMATION:
; APPLICANT: FRANCIS, Kevin P.
; APPLICANT: DOYLE, Timothy C.
; APPLICANT: NAWOTKA, Kevin A.
; TITLE OF INVENTION: METHODS OF SCREENING FOR INTRODUCTION OF DNA INTO A
; TITLE OF INVENTION: TARGET CELL
; FILE REFERENCE: 9400-0015 / PXE-015.US
; CURRENT APPLICATION NUMBER: US/10/094,146
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/274,094
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/292,828
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Asc I linker
US-10-094-146-21

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
|||||||
Db 2 GGCGCGC 8

RESULT 177
US-10-094-146-21/c
; Sequence 21, Application US/10094146

; Publication No. US20020192755A1
; GENERAL INFORMATION:
; APPLICANT: FRANCIS, Kevin P.
; APPLICANT: DOYLE, Timothy C.
; APPLICANT: NAWOTKA, Kevin A.
; TITLE OF INVENTION: METHODS OF SCREENING FOR INTRODUCTION OF DNA INTO A
; TITLE OF INVENTION: TARGET CELL
; FILE REFERENCE: 9400-0015 / PXE-015.US
; CURRENT APPLICATION NUMBER: US/10/094,146
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/274,094
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/292,828
; PRIOR FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Asc I linker
US-10-094-146-21

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
|||||||
Db 9 GGCGCGC 3

RESULT 178
US-10-108-077-6
; Sequence 6, Application US/10108077
; Publication No. US20030036116A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTIO
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/108,077
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-108-077-6

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
|||||||
Db 1 CGCGCTG 7

RESULT 179
US-10-142-111-23/c
; Sequence 23, Application US/10142111
; Publication No. US20030101485A1

; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; TITLE OF INVENTION: CHEN, Jinqing
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/142,111
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-142-111-23

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCTGTGG 20
|||||
Db 7 GCTGTGG 1

RESULT 180
US-10-390-045-54/c
; Sequence 54, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: POYNUCLEOTIDE ARRAY
; CURRENT APPLICATION NUMBER: US/10/390,045
; CURRENT FILING DATE: 2003-03-18
; PRIOR FILING DATE: US/09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-390-045-54

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
|||||
Db 7 GCTGGCC 1

RESULT 181
US-10-330-627-237
; Sequence 237, Application US/10330627
; Publication No. US20030175771A1

; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 237
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-237

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
|||||
Db 4 GCTGGCC 10

RESULT 182
US-10-330-627-261/c
; Sequence 261, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-261

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGCGC 13
|||||
Db 10 CCGGCGC 4

RESULT 183
US-10-330-627-307/c
; Sequence 307, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564


```
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1071
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1071
```

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GCTGGCC 7
        |||||
Db       4 GCTGGCC 10
```

```
RESULT 189
US-10-330-627-1142
; Sequence 1142, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1142
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1142
```

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 CCGGCGC 13
        |||||
Db       3 CCGGCGC 9
```

```
RESULT 190
US-10-330-627-1149
; Sequence 1149, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1149
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1149
```

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GCCCGGC 11
        |||||
Db       4 GCCCGGC 10
```

```
RESULT 191
US-10-197-019-97/c
; Sequence 97, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MWH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-97
```

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GCTGGCC 7
        |||||
Db       7 GCTGGCC 1
```

```
RESULT 192
US-10-197-019-108/c
; Sequence 108, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MWH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-197-019-108
```

```
Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
```


Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGGCCC 8
| | | | |
Db 8 CTGGCCC 2

RESULT 193

US-10-257-021-108
; Sequence 108, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-108

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
| | | | |
Db 3 CGCGCTG 9

RESULT 194

US-10-403-232-143
; Sequence 143, Application US/10403232
; Publication No. US20030226164A1
; GENERAL INFORMATION:
; APPLICANT: Suttie, Janet Louise
; APPLICANT: Chilton, Mary-Dell
; APPLICANT: Que, Qiudeng
; APPLICANT: de Framond, Anic
; TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
; FILE REFERENCE: 70005USPS
; CURRENT APPLICATION NUMBER: US/10/403,232
; CURRENT FILING DATE: 2003-03-28
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 143
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-403-232-143

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCGCGC 15
| | | | |
Db 4 GGCGCGC 10

RESULT 195

US-10-422-523-28
; Sequence 28, Application US/10422523
; Publication No. US20040002103A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; TITLE OF INVENTION: SYNTHETIC LIGATION REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-15A US
; CURRENT APPLICATION NUMBER: US/10/422,523
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: 09/332,835
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-422-523-28

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
| | | | |
Db 1 CGCGCTG 7

RESULT 196

US-10-301-875A-10
; Sequence 10, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-10

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGCGCGC 13
| | | | |
Db 3 CCGCGCGC 9

RESULT 197

US-10-301-875A-11
; Sequence 11, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION

```
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-11

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CCGCGCG 13
      |||||
Db      3 CCGCGCG 9

RESULT 198
US-10-301-875A-19/c
; Sequence 19, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-19

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCGCGCG 14
      |||||
Db      7 CCGCGCG 1

RESULT 199
US-10-301-875A-20/c
; Sequence 20, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-20

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCGCGCG 14
      |||||
Db      7 CCGCGCG 1

RESULT 200
US-10-301-875A-21/c
; Sequence 21, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-21

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCGCGCG 14
      |||||
Db      7 CCGCGCG 1

RESULT 201
US-10-301-875A-27/c
; Sequence 27, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
```

US-10-301-875A-27

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCGGCGC 13
| | | | | | |
Db 9 CCGGCGC 3

RESULT 202

US-10-434-479-54/c
; Sequence 54, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-434-479-54

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCC 7
| | | | | | |
Db 7 GCTGGCC 1

RESULT 203

US-10-029-221C-5
; Sequence 5, Application US/10029221C
; Publication No. US20040152077A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; APPLICANT: DJAVAKHISHVILI, TSOTNE D.
; APPLICANT: FREY, GERHARD J.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-21
; CURRENT APPLICATION NUMBER: US/10/029,221C
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site

US-10-029-221C-5

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCGCTG 17
| | | | | | |
Db 1 CGCGCTG 7

RESULT 204

US-10-816-079-27/c
; Sequence 27, Application US/10816079
; Publication No. US20040166527A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Beaudry, Gary A
; APPLICANT: Madden, Stephen L
; APPLICANT: Bertelsen, Arthur H
; TITLE OF INVENTION: Composition and Methods for the Identification of Lung Tumor
; TITLE OF INVENTION: Cells
; FILE REFERENCE: GA0129C2
; CURRENT APPLICATION NUMBER: US/10/816,079
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: 09/663,516
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/080,037
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SAGE tag
US-10-816-079-27

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTGTGGC 21
| | | | | | |
Db 9 CTGTGGC 3

RESULT 205

US-10-631-544-6
; Sequence 6, Application US/10631544
; Publication No. US20040248143A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTI
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/631,544
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10

```

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-631-544-6

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CGCGCTG 17
Db      1 CGCGCTG 7

RESULT 206
US-10-487-934-119
; Sequence 119, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-119

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
Db      2 CTGTGGC 8

RESULT 207
US-10-487-934-185
; Sequence 185, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-185
```

```

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTGGCCC 8
Db      1 CTGGCCC 7

RESULT 208
US-10-487-934-186
; Sequence 186, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-186

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTGGCCC 8
Db      1 CTGGCCC 7

RESULT 209
US-10-398-271-14
; Sequence 14, Application US/10398271
; Publication No. US20050124010A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Fu, Pengcheng
; APPLICANT: Latterich, Martin
; APPLICANT: Wei, Jing
; APPLICANT: Levin, Michael
; TITLE OF INVENTION: WHOLE CELL ENGINEERING BY MUTAGENIZING A
; TITLE OF INVENTION: SUBSTANTIAL PORTION OF A STARTING GENOME, COMBINING
; TITLE OF INVENTION: MUTATIONS, AND OPTIONALLY REPEATING
; FILE REFERENCE: 09010-060US1
; CURRENT APPLICATION NUMBER: US/10/398,271
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: PCT/US01/31004
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/US01/19367
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/279,702
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/677,584
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
```


; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polynucleotide sequence of a restriction site
US-10-398-271-14

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CGCGCTG 17
|||
Db 1 CGCGCTG 7

RESULT 210

US-10-987-549-29/c

; Sequence 29, Application US/10987549
; Publication No. US20050191656A1

; GENERAL INFORMATION:

; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.

; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES

; FILE REFERENCE: 30311/35918

; CURRENT APPLICATION NUMBER: US/10/987,549

; CURRENT FILING DATE: 2004-11-12

; PRIOR APPLICATION NUMBER: US/09/479,608

; PRIOR FILING DATE: 2000-01-06

; PRIOR APPLICATION NUMBER: US 60/115,284

; PRIOR FILING DATE: 1999-01-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 29

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Hypothetical sequence

US-10-987-549-29

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
|||
Db 10 CTGTGGC 4

RESULT 211

US-10-987-549-30/c

; Sequence 30, Application US/10987549

; Publication No. US20050191656A1

; GENERAL INFORMATION:

; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.

; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES

; FILE REFERENCE: 30311/35918

; CURRENT APPLICATION NUMBER: US/10/987,549

; CURRENT FILING DATE: 2004-11-12

; PRIOR APPLICATION NUMBER: US/09/479,608

; PRIOR FILING DATE: 2000-01-06

; PRIOR APPLICATION NUMBER: US 60/115,284

; PRIOR FILING DATE: 1999-01-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 30

; LENGTH: 10

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-30

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
|||
Db 9 CTGTGGC 3

RESULT 212

US-10-987-549-31/c

; Sequence 31, Application US/10987549

; Publication No. US20050191656A1

; GENERAL INFORMATION:

; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.

; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES

; FILE REFERENCE: 30311/35918

; CURRENT APPLICATION NUMBER: US/10/987,549

; CURRENT FILING DATE: 2004-11-12

; PRIOR APPLICATION NUMBER: US/09/479,608

; PRIOR FILING DATE: 2000-01-06

; PRIOR APPLICATION NUMBER: US 60/115,284

; PRIOR FILING DATE: 1999-01-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 31

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Hypothetical sequence

US-10-987-549-31

Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTGTGGC 21
|||
Db 8 CTGTGGC 2

RESULT 213

US-10-987-549-32/c

; Sequence 32, Application US/10987549

; Publication No. US20050191656A1

; GENERAL INFORMATION:

; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.

; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES

; FILE REFERENCE: 30311/35918

; CURRENT APPLICATION NUMBER: US/10/987,549

; CURRENT FILING DATE: 2004-11-12

; PRIOR APPLICATION NUMBER: US/09/479,608

; PRIOR FILING DATE: 2000-01-06

; PRIOR APPLICATION NUMBER: US 60/115,284

; PRIOR FILING DATE: 1999-01-06

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 32

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; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-10-987-549-32

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTGTGGC 21
Db      7 CTGTGGC 1

RESULT 214
US-10-727-780A-443
; Sequence 443, Application US/10727780A
; Publication No. US20050233329A1
; GENERAL INFORMATION:
; APPLICANT: Vaish, Narendra
; APPLICANT: Zinnen, Shawn
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: Inhibition of Gene Expression Using Duplex Forming
; FILE REFERENCE: 03-1070 (400.139)
; CURRENT APPLICATION NUMBER: US/10/727,780A
; CURRENT FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 772
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 443
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-727-780A-443

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GGCCCCG 10
Db      1 GGCCCCG 7

RESULT 215
US-10-727-780A-443/c
; Sequence 443, Application US/10727780A
; Publication No. US20050233329A1
; GENERAL INFORMATION:
; APPLICANT: Vaish, Narendra
; APPLICANT: Zinnen, Shawn
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: Inhibition of Gene Expression Using Duplex Forming
; FILE REFERENCE: 03-1070 (400.139)
; CURRENT APPLICATION NUMBER: US/10/727,780A
; CURRENT FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 772
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 443
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-727-780A-443
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Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GGCCCCG 10
Db      10 GGCCCCG 4

RESULT 216
US-11-035-899-388/c
; Sequence 388, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 388:
US-11-035-899-388

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTGGCCC 8
Db      8 CTGGCCC 2

RESULT 217
US-11-035-899-389/c
; Sequence 389, Application US/11035899
```

```
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 389:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 389:
US-11-035-899-389

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CTGGCCC 8
      |||||
Db      7 CTGGCCC 1

RESULT 218
US-11-035-899-579
; Sequence 579, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
```

```
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 579:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 579:
US-11-035-899-579

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TGGCCCG 9
      |||||
Db      4 TGGCCCG 10

RESULT 219
US-11-035-899-580
; Sequence 580, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 580:
US-11-035-899-580

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TGGCCCG 9
      |||||
Db      3 TGGCCCG 9

RESULT 220
US-11-035-899-581
; Sequence 581, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 582:
US-11-035-899-582

Query Match      33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TGGCCCG 9
      |||||
Db      2 TGGCCCG 8

RESULT 221
US-11-035-899-582
; Sequence 582, Application US/11035899
; Publication No. US20050196412A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; Jennifer C. Learmont
; Dale A. McPhee
; Suzanne Crowe
; David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/035,899
; FILING DATE: 14-Jan-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,464
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 582:
US-11-035-899-582
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Query Match 33.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGCCCG 9
 |||||
Db 1 TGGCCCG 7

Search completed: May 10, 2006, 10:47:25
Job time : 0.001 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:49:30 ; Search time 0.001 Seconds
(without alignments)
19.992 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336
Perfect score: 21
Sequence: 1 gctggcccgcgctgtggc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 31 seqs, 476 residues

Total number of hits satisfying chosen parameters: 62

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 38 summaries

Database : pubnewdb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	71.4	18	1	US-10-310-914A-552603
C 2	14.8	70.5	20	1	US-10-310-914A-1289776
C 3	14	66.7	20	1	US-10-310-914A-539788
C 4	13.8	65.7	19	1	US-10-310-914A-174538
5	13.8	65.7	19	1	US-10-310-914A-490721
6	13.8	65.7	19	1	US-10-310-914A-559227
7	13.8	65.7	19	1	US-10-310-914A-710539
C 8	13.4	63.8	18	1	US-10-310-914A-232524
C 9	13.4	63.8	18	1	US-10-310-914A-708934
10	13.2	62.9	18	1	US-10-310-914A-474217
C 11	13.2	62.9	18	1	US-10-310-914A-1344026
C 12	12.8	61.0	18	1	US-10-310-914A-52923
C 13	12.8	61.0	18	1	US-10-310-914A-157006
C 14	12.8	61.0	18	1	US-10-310-914A-388441
C 15	12.8	61.0	18	1	US-10-310-914A-1179628
16	12.4	59.0	16	1	US-11-067-231-131
17	11.4	54.3	16	1	US-10-517-151-91
C 18	11.2	53.3	19	1	US-10-310-914A-490721
C 19	10.8	51.4	15	1	US-10-858-341-274
C 20	10.8	51.4	15	1	US-10-858-145-274
21	10	47.6	11	1	US-10-766-560-14
C 22	9.8	46.7	14	1	US-10-980-194-66
C 23	9	42.9	11	1	US-11-158-209-473
C 24	9	42.9	12	1	US-11-103-122-25
C 25	9	42.9	12	1	US-11-103-122-29
C 26	8.8	41.9	12	1	US-11-260-192-15
C 27	8.4	40.0	11	1	US-11-158-209-829
28	8.4	40.0	11	1	US-11-158-209-1161
29	8.4	40.0	18	1	US-10-310-914A-52923
30	8.2	39.0	15	1	US-10-858-341-274
31	8.2	39.0	15	1	US-10-858-145-274
C 32	8.2	39.0	19	1	US-10-310-914A-710539
33	8	38.1	10	1	US-10-993-514-36

C 34	8	38.1	11	1	US-11-227-086-42	Sequence 42, Appl
35	8	38.1	18	1	US-10-310-914A-388441	Sequence 388441,
36	7.8	37.1	11	1	US-11-158-209-841	Sequence 841, App
C 37	7.8	37.1	19	1	US-10-310-914A-559227	Sequence 559227,
C 38	7.4	35.2	10	1	US-10-913-792-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-310-914A-552603/c
; Sequence 552603, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 552603
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-552603

Query Match 71.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGCGC 15
|||||
Db 15 GCTGGCCCGCGCGC 1

RESULT 2
US-10-310-914A-1289776/c
; Sequence 1289776, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1289776
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1289776

Query Match 70.5%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCCGCGCGCTGTGGC 21
|||||
Db 20 GGCCTGGCGCGTGGC 3

RESULT 3
US-10-310-914A-539788/c
; Sequence 539788, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 539788
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-539788

Query Match 66.7%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTGGCCCCGCGC 14
 |||||
Db 17 GCTGGCCCCGCGC 4

RESULT 4
US-10-310-914A-174538/c
; Sequence 174538, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174538
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-174538

Query Match 65.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 3.2;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCCCGGCGCGCTGTGGC 21
 |||||
Db 18 GCCCGGCTCGCTGTCG 2

RESULT 5
US-10-310-914A-490721
; Sequence 490721, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490721
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-490721

Query Match 65.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 3.2;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCCCGGCGCGCTGTGGC 21
 |||||
Db 3 GCCCGGCGCGCGGGC 19

RESULT 6
US-10-310-914A-559227
; Sequence 559227, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 559227
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-559227

Query Match 65.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.2;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCCCGGCGCGCTGTGGC 21
 |||||
Db 1 GCCUGGCCCGCUGUGGC 17

RESULT 7
US-10-310-914A-710539
; Sequence 710539, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 710539
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-710539

Query Match 65.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 3.2;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCCCGGCGCGCTGTGGC 21
 |||||
Db 3 GCCCGGCGCGCUCGGC 19

RESULT 8
US-10-310-914A-232524/c
; Sequence 232524, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac

```

; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 232524
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-232524

Query Match      63.8%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.4;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GGCCCGGCGCGCTGT 18
      ||||| |||||
Db      18 GGCCCGGCGCGCTGT 4

RESULT 9
US-10-310-914A-708934/c
; Sequence 708934, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 708934
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-708934

Query Match      63.8%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 3.4;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GGCCCGGCGCGCTGT 18
      ||||| |||||
Db      18 GGCCCGGCGCGCTGT 4

RESULT 10
US-10-310-914A-474217
; Sequence 474217, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 474217
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-474217

Query Match      62.9%; Score 13.2; DB 1; Length 18;
```

```

Best Local Similarity 72.2%; Pred. No. 3.9;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 TGGCCCGGCGCGCTGTGG 20
      :||||| ||| |:| ||
Db      1 UGGCCCGGGGGCCCGCGG 18

RESULT 11
US-10-310-914A-1344026/c
; Sequence 1344026, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1344026
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1344026

Query Match      62.9%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.9;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GCTGGCCCGGCGCGCTGT 18
      || ||||| ||||| ||
Db      18 GCCGGCCCGGAGCGCAGT 1

RESULT 12
US-10-310-914A-52923/c
; Sequence 52923, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52923
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-52923

Query Match      61.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CTGGCCCGGCGCGCTG 17
      |||| | ||||| ||
Db      17 CTGACCGGCGCGCCG 2

RESULT 13
US-10-310-914A-157006/c
; Sequence 157006, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
```



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; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 157006
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-157006

Query Match          61.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCCGCGCGCTGTG 19
    ||||| ||||| |
Db 18 GGCCCGCGCGCTGAG 3

RESULT 14
US-10-310-914A-388441/c
; Sequence 388441, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 388441
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-388441

Query Match          61.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.8;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCCGCGCGCTGTG 19
    ||||| ||||| |
Db 18 GGCCCGCGCGCTGG 3

RESULT 15
US-10-310-914A-1179628/c
; Sequence 1179628, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1179628
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1179628

Query Match          61.0%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.8;
```

```

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCCCGCGCGCTGTGG 20
    ||||| ||||| |||
Db 17 GCCCGCGCGCTTTGG 2

RESULT 16
US-11-067-231-131
; Sequence 131, Application US/11067231
; Publication No. US20050272063A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Katagiri, Toyomasa
; APPLICANT: Fukukawa, Chikako
; TITLE OF INVENTION: METHOD FOR TREATING SYNOVIAL SARCOMA
; FILE REFERENCE: 1254-0272PUS1
; CURRENT APPLICATION NUMBER: US/11/067,231
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/407,506
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/486,195
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/JP03/10591
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: PCT/JP2004/002144
; PRIOR FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US 60/598,834
; PRIOR FILING DATE: 2004-08-05
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-11-067-231-131

Query Match          59.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 4.5;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGCGCGC 15
    ||||| ||||| |
Db 3 CCGCCCGCGCGCGC 16

RESULT 17
US-10-517-151-91
; Sequence 91, Application US/10517151
; Publication No. US20060019252A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Oncotherapy Science, Inc.
; APPLICANT: The University of Tokyo
; TITLE OF INVENTION: Genes and Polypeptides Relating to Hepatocellular or
; TITLE OF INVENTION: Colorectal Carcinoma
; FILE REFERENCE: 082379-000400US
; CURRENT APPLICATION NUMBER: US/10/517,151
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/386,985
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: WO PCT/JP03/07070
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial
```

```

; FEATURE:
; OTHER INFORMATION: an artificially synthesized S-oligonucleotide
US-10-517-151-91

Query Match      54.3%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 7.8;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CTGGCCCGCGCGC 14
      ||||| ||||| |||||
Db       3 CTGGTCCGCGCGC 15

RESULT 18
US-10-310-914A-490721/c
; Sequence 490721, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490721
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-490721

Query Match      53.3%; Score 11.2; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 GGCCCGCGCGCGCTGTG 19
      ||||| ||||| |||||
Db      19 GCCCGCGCGCGCGGG 4

RESULT 19
US-10-858-341-274/c
; Sequence 274, Application US/10858341
; Publication No. US20050287667A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnjad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09053
; CURRENT APPLICATION NUMBER: US/10/858,341
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-341-274

Query Match      51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 9.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CTGGCCCGCGCGC 15
      ||||| ||||| |||||
Db      15 CCGGCCCGCGCGC 2

RESULT 20
US-10-858-145-274/c
; Sequence 274, Application US/10858145
; Publication No. US20060073596A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnjad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: PRONAI-09054
; CURRENT APPLICATION NUMBER: US/10/858,145
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-145-274

Query Match      51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 9.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CTGGCCCGCGCGC 15
      ||||| ||||| |||||
Db      15 CCGGCCCGCGCGC 2

RESULT 21
US-10-766-560-14
; Sequence 14, Application US/10766560
; Publication No. US20050281837A1
; GENERAL INFORMATION:
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Bartoloni, Antonella
```

```

; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-341-274

Query Match      51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 9.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CTGGCCCGCGCGC 15
      ||||| ||||| |||||
Db      15 CCGGCCCGCGCGC 2

RESULT 20
US-10-858-145-274/c
; Sequence 274, Application US/10858145
; Publication No. US20060073596A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnjad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: PRONAI-09054
; CURRENT APPLICATION NUMBER: US/10/858,145
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-145-274

Query Match      51.4%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 9.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CTGGCCCGCGCGC 15
      ||||| ||||| |||||
Db      15 CCGGCCCGCGCGC 2

RESULT 21
US-10-766-560-14
; Sequence 14, Application US/10766560
; Publication No. US20050281837A1
; GENERAL INFORMATION:
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Bartoloni, Antonella
```

```

; TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE POLYPEPTIDES WITH ALTERED TOXICITY USEFUL
; TITLE OF INVENTION: PREPARATION OF AN ANTIPERTUSSIS VACCINE
; FILE REFERENCE: 002441.00076
; CURRENT APPLICATION NUMBER: US/10/766,560
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/261,668
; PRIOR FILING DATE: 1994-06-17
; PRIOR APPLICATION NUMBER: US 08/012,243
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/265,742
; PRIOR FILING DATE: 1988-11-01
; PRIOR APPLICATION NUMBER: ITALY 22481 A/87
; PRIOR FILING DATE: 1987-11-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Bordetella pertussis
US-10-766-560-14

Query Match      47.6%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CCGGCGCGCT 16
      |||||
Db      2 CCGGCGCGCT 11

RESULT 22
US-10-980-194-66/c
; Sequence 66, Application US/10980194
; Publication No. US20050250120A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BUCHRIESER-BROSCH, ROLAND
; APPLICANT: BILLAULT, ALAIN
; APPLICANT: GARNIER, THIERRY
; TITLE OF INVENTION: DELETED SEQUENCES IN M. BOVIS BCG/M. BOVIS OR M.
; TITLE OF INVENTION: TUBERCULOSIS, METHOD FOR DETECTING MYCOBACTERIA USING
; TITLE OF INVENTION: THESE SEQUENCES AND VACCINES
; FILE REFERENCE: 05394.0013-01000
; CURRENT APPLICATION NUMBER: US/10/980,194
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 09/936,523
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: PCT/FR00/00637
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 66
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-980-194-66

Query Match      46.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 13;
Matches 11; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY      2 CTGGCCCGCGCG 14
      |||||
Db      13 CCGGCCCGCGCGTG 1

RESULT 23
US-11-158-209-473/c
; Sequence 473, Application US/11158209
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; TITLE OF INVENTION: MODULAR DESIGN AND CONSTRUCTION OF NUCLEIC ACID
```

```

; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 473
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-473

Query Match      42.9%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GCGCGCGCTG 17
      |||||
Db      9 GCGCGCGCTG 1

RESULT 24
US-11-103-122-25/c
; Sequence 25, Application US/11103122
; Publication No. US20050282190A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Hua
; APPLICANT: Lis, John T.
; TITLE OF INVENTION: MODULAR DESIGN AND CONSTRUCTION OF NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, APTAMER-DERIVED NUCLEIC ACID CONSTRUCTS, RNA
; TITLE OF INVENTION: SCAFFOLDS, THEIR EXPRESSION, AND METHODS OF USE
; FILE REFERENCE: 19603/4491
; CURRENT APPLICATION NUMBER: US/11/103,122
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: 60/560,895
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: functional
; OTHER INFORMATION: element N3
US-11-103-122-25

Query Match      42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CGCTGTGGC 21
      |||||
Db      9 CGCTGTGGC 1

RESULT 25
US-11-103-122-29/c
; Sequence 29, Application US/11103122
; Publication No. US20050282190A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Hua
; APPLICANT: Lis, John T.
; TITLE OF INVENTION: MODULAR DESIGN AND CONSTRUCTION OF NUCLEIC ACID
```

; TITLE OF INVENTION: MOLECULES, APTAMER-DERIVED NUCLEIC ACID CONSTRUCTS, RNA
; FILE OF INVENTION: SCAFFOLDS, THEIR EXPRESSION, AND METHODS OF USE
; FILE REFERENCE: 19603/4491
; CURRENT APPLICATION NUMBER: US/11/103,122
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: 60/560,895
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: functional
; OTHER INFORMATION: element N3
US-11-103-122-29

Query Match 42.9%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGCTGTGGC 21
| | | | |
Db 9 CGCTGTGGC 1

RESULT 26
US-11-260-192-15/c
; Sequence 15, Application US/11260192
; Publication No. US20060067934A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; APPLICANT: GOODWIN, Raymond G.
; APPLICANT: BECKMANN, Patricia M.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
; FILE REFERENCE: A8466

; CURRENT APPLICATION NUMBER: US/11/260,192
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: US/10/420,785
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 09/758,124
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 08/953,268
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: US 08/555,629
; PRIOR FILING DATE: 1995-11-09
; PRIOR APPLICATION NUMBER: US 08/468,453
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/038,765
; PRIOR FILING DATE: 1993-03-13
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,241
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-Terminus of human TNF receptor including restriction
; OTHER INFORMATION: endonuclease cleavage sites
US-11-260-192-15

Query Match 41.9%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CCGGCGGCTGT 18
| | | | |
Db 12 CCGGCGAGTTGT 1

RESULT 27
US-11-158-209-829
; Sequence 829, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 829
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-829

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCGCTGTGGC 21
| | | | |
Db 2 GCGCTGTGGC 11

RESULT 28
US-11-158-209-1161
; Sequence 1161, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 1161
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-1161

Query Match 40.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTGGCCCGG 10
| | | | | | | |
Db 1 GGTGGCCCGG 10

RESULT 29
US-10-310-914A-52923
; Sequence 52923, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52923
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-52923

Query Match 40.0%; Score 8.4; DB 1; Length 18;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGGCGCGCTG 17
| | | | | | | |
Db 2 CGGCGCGCGG 11

RESULT 30
US-10-858-341-274
; Sequence 274, Application US/10858341
; Publication No. US20050287667A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnjad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene Expression
; FILE REFERENCE: PRONAI-09053
; CURRENT APPLICATION NUMBER: US/10/858,341
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-341-274

Query Match 39.0%; Score 8.2; DB 1; Length 15;
Best Local Similarity 76.9%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 GGCGCGCTGTGGC 21
| | | | | | | |
Db 1 GGCGCGCGGGCC 13

RESULT 31
US-10-858-145-274
; Sequence 274, Application US/10858145
; Publication No. US20060073596A1
; GENERAL INFORMATION:
; APPLICANT: Sheikhnjad, Reza
; APPLICANT: Sooch, Mina P.
; APPLICANT: Goodwin, Neal
; APPLICANT: Olson, David
; TITLE OF INVENTION: Methods and Compositions for the Inhibition of Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: PRONAI-09054
; CURRENT APPLICATION NUMBER: US/10/858,145
; CURRENT FILING DATE: 2004-06-01
; NUMBER OF SEQ ID NOS: 1439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 274
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)..(5)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7)..(7)
; OTHER INFORMATION: methylated C nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(13)
; OTHER INFORMATION: methylated C nucleotide
US-10-858-145-274

Query Match 39.0%; Score 8.2; DB 1; Length 15;
Best Local Similarity 76.9%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 GGCGCGCTGTGGC 21
| | | | | | | |
Db 1 GGCGCGCGGGCC 13

RESULT 32
US-10-310-914A-710539/c
; Sequence 710539, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 710539

```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-710539

Query Match          39.0%; Score 8.2; DB 1; Length 19;
Best Local Similarity 76.9%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTGGCCCGCGC 13
Db 13 GCGCGCCGGCGC 1

RESULT 33
US-10-993-514-36
; Sequence 36, Application US/10993514
; Publication No. US20050250122A1
; GENERAL INFORMATION:
; APPLICANT: Aerssens, Jeroen
; APPLICANT: Athanasiou, Maria
; APPLICANT: Brain, Carlos
; APPLICANT: Cohen, Nadine
; APPLICANT: Dain, Bradley
; APPLICANT: Denton, R. Rex
; APPLICANT: Judson, Richard S.
; APPLICANT: Ozdemir, Vural
; APPLICANT: Reed, Carol R.
; TITLE OF INVENTION: APOA4 Genetic Markers Associated with Progression of Alzheimer's
; TITLE OF INVENTION: Disease
; FILE REFERENCE: 2300.0080001
; CURRENT APPLICATION NUMBER: US/10/993,514
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: US 60/524,467
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer Extension Oligo for Detecting Alleles at PSS in
; OTHER INFORMATION: Haplotypes Comprising Preferred Embodiments of Progression
; OTHER INFORMATION: Markers I and Progression Markers II
US-10-993-514-36

Query Match          38.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCGCTGTG 19
Db 3 GCGCTGTG 10

RESULT 34
US-11-227-086-42/c
; Sequence 42, Application US/11227086
; Publication No. US20060084117A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: T1530-00214
; CURRENT APPLICATION NUMBER: US/11/227,086
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: 09/989,497
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
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; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 42
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
US-11-227-086-42

Query Match          38.1%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCGCGC 15
Db 9 CGGCGCGC 2

RESULT 35
US-10-310-914A-388441
; Sequence 388441, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 388441
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-388441

Query Match          38.1%; Score 8; DB 1; Length 18;
Best Local Similarity 68.8%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CCCGCGCGCTGTGGC 21
Db 3 CCCAGCGCCCGCGGCC 18

RESULT 36
US-11-158-209-841
; Sequence 841, Application US/11158209
; Publication No. US20060088852A1
; GENERAL INFORMATION:
; APPLICANT: Dirk Petersohn
; APPLICANT: Kordula Schlotmann
; APPLICANT: Thomas Gassenmeier
; APPLICANT: Olaf Holtkotter
; APPLICANT: Marcus Conradt
; APPLICANT: Kay Hofmann
; TITLE OF INVENTION: Method for Determining the Homeostasis of Hairy Skin
; FILE REFERENCE: H 05667 PCT
; CURRENT APPLICATION NUMBER: US/11/158,209
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: PCT/EP2003/014070
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 102 60 931.4-41
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 1335
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 841
```

```
;
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-158-209-841

Query Match      37.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 CCGGCGCGGCT 16
      ||| |||||
Db      1 CCCAACGCGCT 11

RESULT 37
US-10-310-914A-559227/c
; Sequence 559227, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 559227
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-559227

Query Match      37.1%; Score 7.8; DB 1; Length 19;
Best Local Similarity 81.8%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCTGGCCCCGCGC 11
      || ||||| |||
Db      11 GCGGGCCAGGC 1

RESULT 38
US-10-913-792-6/c
; Sequence 6, Application US/10913792
; Publication NO. US20060031957A1
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Lal, Raj Kishori
; APPLICANT: Agnihotri, Arun Kumar
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Misra, Hari Om
; APPLICANT: Dhawan, Om Parkash
; APPLICANT: Kalra, Alok
; APPLICANT: Singh, Aparbal
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Singh, Saudan
; APPLICANT: Patra, Dharani Dhar
; APPLICANT: Agarwal, Shilpi
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Gupta, Anil Kumar
; APPLICANT: Gupta, Moti Lal
; APPLICANT: Chandra, Ram
; TITLE OF INVENTION: DISTINCT TYPE CULTIVAR OF OCIMUM BASILICUM "CIM-SAUMYA"
; FILE REFERENCE: 11378.64US01
; CURRENT APPLICATION NUMBER: US/10/913,792
; CURRENT FILING DATE: 2004-08-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
```

```
;
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Operon Primer OPA 06
US-10-913-792-6

Query Match      35.2%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 CCGGCGCGC 15
      ||||| ||
Db      9 CCGGCGGTGC 1

Search completed: May 10, 2006, 10:49:31
Job time : 1 secs
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 10:46:22 ; Search time 0.001 Seconds
(without alignments)
331.422 Million cell updates/sec

Title: US-09-904-968A-1_DELETE_3336
Perfect score: 21
Sequence: 1 gctggccggcgctgtggc 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 741 seqs, 7891 residues

Total number of hits satisfying chosen parameters: 1482

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 813 summaries

Database : ngsdb1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.4	68.6	20	AAV69995	Mouse c-jun protei
C 2	12.8	61.0	17	ADL47206	Human NOGO recepto
3	12.8	61.0	17	ADM54550	Human GRID mRNA su
4	12.4	59.0	16	ADL91730	Collagen type IX a
C 5	12.4	59.0	17	ADL46910	Human NOGO recepto
C 6	12.4	59.0	17	ADL46909	Human NOGO recepto
7	12.2	58.1	17	AAT76338	Human fibronectin
8	12.2	58.1	17	AAV54140	Human fibronectin
9	12.2	58.1	17	AAA33584	Low adenosine anti
10	12.2	58.1	17	AAF19706	Human fibronectin
11	12.2	58.1	17	ADV02886	Human BACE NCH rib
12	12.2	58.1	17	ABS71913	Human GTP-Rho bind
13	12.2	58.1	17	ABZ95400	Human fibronectin
14	12.2	58.1	17	ABD19452	Human fibronectin
15	12	57.1	15	AAL39559	SSTR4 gene ASO pro
16	12	57.1	15	ABL45841	Human EDG6 gene al
17	11.8	56.2	15	AAF45245	IGFBP2 oligonucleo
18	11.4	54.3	16	ADH44902	Human APCDD1scram
C 19	11	52.4	15	AAQ57977	Sequence of portio
C 20	10.8	51.4	15	AAV02387	Pseudo-nitzschia p
21	10.8	51.4	15	AAF46831	IGFBP3 oligonucleo
22	10.8	51.4	15	AAF46943	IGFBP3 oligonucleo
23	10.8	51.4	15	AAF45244	IGFBP2 oligonucleo
24	10.8	51.4	15	AAF46942	IGFBP3 oligonucleo
25	10.8	51.4	15	AAF45246	IGFBP2 oligonucleo
26	10.8	51.4	15	AAF46830	IGFBP3 oligonucleo
C 27	10.8	51.4	15	AAS97374	PCR primer #1 for
28	10.4	49.5	13	AAT76242	Human IL6 receptor
29	10.4	49.5	13	AAX54032	Human IL-6 recepto
30	10.4	49.5	13	AAA33476	Low adenosine anti
31	10.4	49.5	13	AAF19598	Human IL6 receptor
32	10.4	49.5	13	ABZ95292	Human IL-6 recepto
33	10.4	49.5	13	ABD19276	Human IL6 receptor

34	10.4	49.5	14	1	AAF88189	Murine CSP-1 speci
35	10.4	49.5	14	1	AAF88184	Human CSP-1 derive
36	10.4	49.5	14	1	ADH02741	B. anthracis ATR/h
37	10.2	48.6	15	1	AAS97374	PCR primer #1 for
C 38	10	47.6	12	1	AAF60901	Conjugate forming
C 39	9.8	46.7	14	1	AAF62477	M tuberculosis alp
C 40	9.8	46.7	14	1	AAF24230	M. tuberculosis al
C 41	9.8	46.7	14	1	ADM58001	Asci reverse ligat
C 42	9.8	46.7	14	1	ADM67994	Oligonucleotide As
43	9.8	46.7	14	1	ADY85199	Alcohol dehydrogen
C 44	9.4	44.8	11	1	AAV54772	Endothelial nitric
C 45	9.4	44.8	11	1	AAA34219	Human adenosine re
C 46	9.4	44.8	11	1	AAF20341	Human endothelial
47	9.4	44.8	11	1	ABV69628	Human skin EST 741
C 48	9.4	44.8	11	1	ABV69375	Human skin EST 716
49	9.4	44.8	11	1	ABV68029	Human skin EST 581
C 50	9.4	44.8	11	1	ABZ96035	Human endothelial
C 51	9.4	44.8	11	1	ABD19675	Human endothelial
52	9.4	44.8	11	1	ADQ33478	Human facial skin-
C 53	9.4	44.8	12	1	ABI21184	Oligonucleotide pr
54	9.4	44.8	12	1	ABI04204	Oligonucleotide pr
55	9.4	44.8	12	1	ABH90189	Oligonucleotide pr
C 56	9.4	44.8	12	1	ADM67995	Oligonucleotide As
C 57	9.4	44.8	12	1	ADR44241	Human melanoma dif
58	9.4	44.8	13	1	ABC66097	Oligonucleotide SE
C 59	9.4	44.8	13	1	ABC66096	Oligonucleotide SE
60	9.4	44.8	13	1	ADV63462	Human Her2 class I
61	9.4	44.8	13	1	ADR33857	Human nicking agen
62	9.4	44.8	13	1	ADR33858	Human nicking agen
63	9.4	44.8	13	1	ADR33855	Human nicking agen
64	9.4	44.8	13	1	ADR33856	Human nicking agen
65	9.2	43.8	15	1	AAQ57977	Sequence of portio
C 66	9	42.9	10	1	AAZ77822	Human dendritic ce
C 67	9	42.9	10	1	AAS85441	Metastatic breast
C 68	9	42.9	10	1	AAZ84999	Metastatic breast
69	9	42.9	10	1	AAZ81584	Metastatic breast
70	9	42.9	10	1	AAH64571	Human ubiquitously
71	9	42.9	10	1	AAH64570	Human ubiquitously
C 72	9	42.9	10	1	AAH64063	Human ubiquitously
C 73	9	42.9	10	1	ABV78444	Human Th1 cell pre
74	9	42.9	10	1	ABK30052	Vancomycin-resista
C 75	9	42.9	11	1	ABV69619	Human skin EST 740
C 76	9	42.9	11	1	ADQ35656	Human hair-bearing
C 77	9	42.9	12	1	ABK29997	Hepatitis B virus
78	9	42.9	12	1	AEAI4698	Immunostimulatory
79	8.8	41.9	12	1	AAV65523	Primer pBS 777-23
C 80	8.8	41.9	12	1	ABK14022	DNA adaptor sequen
81	8.8	41.9	12	1	ABK14028	DNA sequence of a
C 82	8.8	41.9	12	1	ADG47248	Oligonucleotide us
C 83	8.8	41.9	12	1	ADU73707	Connective tissue
84	8.8	41.9	12	1	ADV92309	E. coli rRNA RT-PC
85	8.8	41.9	12	1	ADV92172	Universal bacteria
C 86	8.8	41.9	12	1	ADZ23854	Human SNP detectio
C 87	8.8	41.9	12	1	ADZ23918	Human SNP detectio
C 88	8.8	41.9	12	1	ADZ23906	Human SNP detectio
C 89	8.8	41.9	15	1	AAF45246	IGFBP2 oligonucleo
90	8.4	40.0	10	1	AAQ88580	Human mitochondria
C 91	8.4	40.0	10	1	AAQ32927	Sequence of first
C 92	8.4	40.0	10	1	AAQ32911	Sequence of a targ
93	8.4	40.0	10	1	AAQ32930	5' fluorescein-lab
94	8.4	40.0	10	1	AAZ07924	8-oxo-dGTPase onco
C 95	8.4	40.0	10	1	AAV54917	C/EBP-beta antisen
96	8.4	40.0	10	1	AAZ28340	Lung cancer indica
C 97	8.4	40.0	10	1	AAZ34364	Human adenosine re
C 98	8.4	40.0	10	1	AAZ77611	Human dendritic ce
99	8.4	40.0	10	1	AAZ85164	Metastatic breast
C 100	8.4	40.0	10	1	AAZ85539	Metastatic breast
101	8.4	40.0	10	1	AAZ81510	Metastatic breast
C 102	8.4	40.0	10	1	AAZ85260	Metastatic breast
C 103	8.4	40.0	10	1	AAZ83876	Metastatic breast
C 104	8.4	40.0	10	1	AAZ81514	Metastatic breast
C 105	8.4	40.0	10	1	AAZ74184	Human monocyte and
C 106	8.4	40.0	10	1	AAF20486	Human C/EBP polynu

107	8.4	40.0	10	1	AAH63878	Human ubiquitously
108	8.4	40.0	10	1	AAH28611	Human interleukin-
109	8.4	40.0	10	1	ABA06193	Human normal hepat
c 110	8.4	40.0	10	1	ABA06199	Human normal hepat
111	8.4	40.0	10	1	AAH76345	Z. mays Ms45 promo
c 112	8.4	40.0	10	1	AAH76342	Z. mays Ms45 promo
113	8.4	40.0	10	1	AAS98389	Galanin receptor g
114	8.4	40.0	10	1	AAD26098	Human apolipoprote
c 115	8.4	40.0	10	1	ABK95838	Solute Carrier Pam
116	8.4	40.0	10	1	AAD27548	Human p21WAF1 CCG
c 117	8.4	40.0	10	1	ABL52254	Human PHKG2 prefer
c 118	8.4	40.0	10	1	ABA03982	Human STK11 gene p
119	8.4	40.0	10	1	ABN87962	Human GSR preference
c 120	8.4	40.0	10	1	ABV84280	Human vesicle-asso
121	8.4	40.0	10	1	ABK23699	Transcript tag DNA
122	8.4	40.0	10	1	AAS19821	Oligonucleotide #1
c 123	8.4	40.0	10	1	AAS97347	Human CRYBB1 gene
124	8.4	40.0	10	1	ABL45887	Human EDG6 gene al
125	8.4	40.0	10	1	ABL45886	Human EDG6 gene al
c 126	8.4	40.0	10	1	ABK96167	Human CYP1A2 allele
127	8.4	40.0	10	1	ABK72637	Leukotriene B4 rec
c 128	8.4	40.0	10	1	ABI99149	Human PCDH2 ASO PC
c 129	8.4	40.0	10	1	ABK30048	Vancomycin-resista
130	8.4	40.0	10	1	AAD52054	Human CES2 gene po
131	8.4	40.0	10	1	ACA94662	DNA tag from human
132	8.4	40.0	10	1	ACA94641	DNA tag from human
c 133	8.4	40.0	10	1	AAD58325	GC4 primer used in
134	8.4	40.0	10	1	ADE14251	Optineurin promote
c 135	8.4	40.0	10	1	ABZ96180	Human C/EBP antise
c 136	8.4	40.0	10	1	ABZ23891	TERT minimal promo
c 137	8.4	40.0	10	1	ABD20089	Human C/EBPN DNA f
138	8.4	40.0	10	1	ADP54006	Oligonucleotide #3
c 139	8.4	40.0	10	1	ADW10554	Human genomic DNA
c 140	8.4	40.0	10	1	AEA52328	Prostate cancer ge
141	8.4	40.0	11	1	AAX54698	Muscarinic acetylch
142	8.4	40.0	11	1	AAX55034	C/EBP-beta antisen
c 143	8.4	40.0	11	1	AAX54916	C/EBP-beta antisen
144	8.4	40.0	11	1	AAA34145	Human adenosine re
c 145	8.4	40.0	11	1	AAA34363	Human adenosine re
146	8.4	40.0	11	1	AAF20481	Human muscarinic a
147	8.4	40.0	11	1	AAF20267	Human C/EBP polynu
148	8.4	40.0	11	1	AAF20603	Human C/EBP polynu
c 149	8.4	40.0	11	1	AAF20485	Human skin stress/
c 150	8.4	40.0	11	1	ABQ87559	Human skin stress/
151	8.4	40.0	11	1	ABQ86685	Human skin stress/
c 152	8.4	40.0	11	1	ABQ86462	Human skin EST 649
153	8.4	40.0	11	1	ABV62863	Human skin EST 758
c 154	8.4	40.0	11	1	ABV69801	Human skin EST 625
155	8.4	40.0	11	1	ABV68467	Human skin EST 674
156	8.4	40.0	11	1	ABV65097	Human skin EST 288
c 157	8.4	40.0	11	1	ABV62380	Human skin EST 166
c 158	8.4	40.0	11	1	ABV66009	Human skin EST 379
159	8.4	40.0	11	1	ABV70284	Human skin EST 807
160	8.4	40.0	11	1	ABV67796	Human skin EST 558
161	8.4	40.0	11	1	ABV68955	Human skin EST 674
c 162	8.4	40.0	11	1	ABV65076	Human skin EST 286
163	8.4	40.0	11	1	ABV68550	Human skin EST 633
164	8.4	40.0	11	1	AAI70947	Snap back stealth
165	8.4	40.0	11	1	ABQ81861	Kaposi's Sarcoma S
166	8.4	40.0	11	1	ABZ95961	Human muscarinic ac
c 167	8.4	40.0	11	1	ABZ96179	Human C/EBP antise
168	8.4	40.0	11	1	ABZ96297	Human C/EBP antise
169	8.4	40.0	11	1	ABD19413	Human muscarinic a
c 170	8.4	40.0	11	1	ABD20088	Human C/EBPN DNA f
171	8.4	40.0	11	1	ABD20206	Human C/EBPN DNA f
172	8.4	40.0	11	1	ADQ36344	Human hair-bearing
173	8.4	40.0	11	1	ADQ36012	Human hair-bearing
c 174	8.4	40.0	11	1	ADQ32141	Human facial skin-
175	8.4	40.0	11	1	ADQ34742	Human facial skin-
176	8.4	40.0	11	1	ADQ34850	Human facial skin-
177	8.4	40.0	11	1	ADQ34986	Human facial skin-
c 178	8.4	40.0	11	1	ADQ32364	Human facial skin-
179	8.4	40.0	11	1	ADQ32731	Human facial skin-
180	8.4	40.0	12	1	ADM67995	Oligonucleotide As
181	8.4	40.0	12	1	AAX55124	C/EBP-beta antisen
182	8.4	40.0	12	1	AAX55033	C/EBP-beta antisen
c 183	8.4	40.0	12	1	AAX54915	C/EBP-beta antisen
184	8.4	40.0	12	1	AAX54938	C/EBP-beta antisen
185	8.4	40.0	12	1	AAA34385	Human adenosine re
186	8.4	40.0	12	1	AAA34571	Human adenosine re
c 187	8.4	40.0	12	1	AAA34362	Human adenosine re
188	8.4	40.0	12	1	AAA34480	Human adenosine re
189	8.4	40.0	12	1	AAF20602	Human C/EBP polynu
c 190	8.4	40.0	12	1	AAF20484	Human C/EBP polynu
191	8.4	40.0	12	1	AAF20507	Human C/EBP polynu
192	8.4	40.0	12	1	AAF20693	Human C/EBP polynu
c 193	8.4	40.0	12	1	ABI22886	Oligonucleotide pr
c 194	8.4	40.0	12	1	ABH84869	Oligonucleotide pr
c 195	8.4	40.0	12	1	ABI59311	Oligonucleotide pr
c 196	8.4	40.0	12	1	ABI76694	Oligonucleotide pr
c 197	8.4	40.0	12	1	ABI22881	Oligonucleotide pr
c 198	8.4	40.0	12	1	ADC33639	M. tuberculosis PC
c 199	8.4	40.0	12	1	ADF42386	Oligonucleotide SE
200	8.4	40.0	12	1	ADF57536	PCR primer used in
201	8.4	40.0	12	1	ADG28788	Bacterial strain i
202	8.4	40.0	12	1	ABZ96296	Human C/EBP antise
203	8.4	40.0	12	1	ABZ96387	Human C/EBP antise
c 204	8.4	40.0	12	1	ABZ96178	Human C/EBP antise
205	8.4	40.0	12	1	ABZ96201	Human C/EBPN antise
206	8.4	40.0	12	1	ABD20205	Human C/EBPN DNA f
c 207	8.4	40.0	12	1	ABD20087	Human C/EBPN DNA f
208	8.4	40.0	12	1	ABD20296	Human C/EBPN DNA f
c 209	8.4	40.0	12	1	ADH70243	Human Vbeta gene r
c 210	8.4	40.0	12	1	ADP71002	Human VEGF-A promo
211	8.4	40.0	12	1	ADR05232	Wiltling bacterial-
212	8.4	40.0	12	1	ADZ39909	Primer used in bac
c 213	8.4	40.0	12	1	ADZ23856	Human SNP detectio
214	8.4	40.0	12	1	AEB31299	Mouse 18S rDNA com
215	8.4	40.0	12	1	AEB31301	Human 18S rDNA com
216	8.4	40.0	12	1	AEB31300	Rat 18S rDNA compl
217	8.4	40.0	14	1	ADM68001	Ascl reverse ligat
218	8.4	40.0	14	1	ADM67994	Oligonucleotide As
c 219	8.2	39.0	15	1	AAL39559	SSTR4 gene ASO pro
c 220	8	38.1	10	1	AAX54963	C/EBP-beta antisen
c 221	8	38.1	10	1	AAA34410	Human adenosine re
c 222	8	38.1	10	1	AAX79448	Human dendritic ce
223	8	38.1	10	1	AAX77845	Human dendritic ce
224	8	38.1	10	1	AAX81742	Metastatic breast
225	8	38.1	10	1	AAX84919	Metastatic breast
c 226	8	38.1	10	1	AAX85536	Metastatic breast
c 227	8	38.1	10	1	AAX85951	Metastatic breast
c 228	8	38.1	10	1	AAX85303	Metastatic breast
229	8	38.1	10	1	AAX81487	Metastatic breast
230	8	38.1	10	1	AAX82030	Metastatic breast
231	8	38.1	10	1	AAX81594	Metastatic breast
c 232	8	38.1	10	1	AAX81263	Metastatic breast
c 233	8	38.1	10	1	AAX83789	Metastatic breast
234	8	38.1	10	1	AAX84863	Metastatic breast
235	8	38.1	10	1	AAX79762	Human breast tumou
c 236	8	38.1	10	1	AAF20532	Human C/EBP polynu
c 237	8	38.1	10	1	AAS57287	Human CHRN2 allele
c 238	8	38.1	10	1	ABA06035	Human normal hepat
c 239	8	38.1	10	1	AAF37831	Yeast NORF gene SA
c 240	8	38.1	10	1	AAH76348	Z. mays Ms45 promo
241	8	38.1	10	1	AAS98367	Galanin receptor g
242	8	38.1	10	1	ABL52193	Human PER1 prefer
243	8	38.1	10	1	AAD25879	Primer #1 to detec
244	8	38.1	10	1	ABL42855	Human maturation/a
245	8	38.1	10	1	ABK12733	Oligonucleotide pr
246	8	38.1	10	1	ABK96054	Human LIPE gene po
c 247	8	38.1	10	1	AAD26166	Human endothelin 2
c 248	8	38.1	10	1	ABV84803	Human S-protein/so
c 249	8	38.1	10	1	ABV84905	Human S-protein/so
250	8	38.1	10	1	AAS19877	Oligonucleotide #5
251	8	38.1	10	1	AAS19891	Oligonucleotide #7
252	8	38.1	10	1	ABI99136	Human PCDH2 ASO PC

C 253	8	38.1	10	1	ABK30053	Vancomycin-resista
C 254	8	38.1	10	1	AAL39799	SMOH polymorphism
C 255	8	38.1	10	1	ADG28253	Human Myo/V1 prote
C 256	8	38.1	10	1	ADG28195	Human Myo/V1 prote
C 257	8	38.1	10	1	ADG28266	Human Myo/V1 prote
C 258	8	38.1	10	1	ADG28042	Human Myo/V1 prote
C 259	8	38.1	10	1	AAD47803	Human GNB3 gene po
C 260	8	38.1	10	1	ACA94569	DNA tag from human
C 261	8	38.1	10	1	ABZ96226	Human C/EBP antise
C 262	8	38.1	10	1	ABD20135	Human C/EBPN DNA f
C 263	8	38.1	10	1	ADK13021	Human glioma endot
C 264	8	38.1	10	1	ADS77995	Breast cancer dete
C 265	8	38.1	11	1	AAZ18995	Murine MRL SAGE ta
C 266	8	38.1	11	1	AAZ18860	Murine MRL SAGE ta
C 267	8	38.1	11	1	AAZ18696	Murine C57BL/6 SAG
C 268	8	38.1	11	1	AAX54962	C/EBP-beta antisen
C 269	8	38.1	11	1	AAX23380	HLA-A, HLA-B, HLA-
C 270	8	38.1	11	1	AAA34409	Human adenosine re
C 271	8	38.1	11	1	AAF20531	Human C/EBP polynu
C 272	8	38.1	11	1	ABQ87660	Human skin stress/
C 273	8	38.1	11	1	ABV69823	Human skin EST 760
C 274	8	38.1	11	1	ABV62316	Human skin EST 102
C 275	8	38.1	11	1	ABV67208	Human skin EST 499
C 276	8	38.1	11	1	ABV69737	Human skin EST 752
C 277	8	38.1	11	1	ABV68966	Human skin EST 675
C 278	8	38.1	11	1	ABV68820	Human skin EST 660
C 279	8	38.1	11	1	ABV62402	Human skin EST 188
C 280	8	38.1	11	1	ABV65601	Human skin EST 338
C 281	8	38.1	11	1	ABV68097	Human skin EST 588
C 282	8	38.1	11	1	ABV70503	Human skin EST 828
C 283	8	38.1	11	1	ABV63082	Human skin EST 868
C 284	8	38.1	11	1	ABV67604	Human skin EST 539
C 285	8	38.1	11	1	ABZ96225	Human C/EBP antise
C 286	8	38.1	11	1	ABD20134	Human C/EBPN DNA f
C 287	8	38.1	11	1	ADQ31967	Human facial skin-
C 288	8	38.1	11	1	ADQ33912	Human facial skin-
C 289	8	38.1	11	1	ADQ33912	Human facial skin-
C 290	8	38.1	11	1	ADQ33912	Human facial skin-
C 291	8	38.1	12	1	ADP425610	5' AscI site oligo
C 292	8	38.1	17	1	AAT76338	Oligonucleotide SE
C 293	8	38.1	17	1	AAX54140	Human fibronectin
C 294	8	38.1	17	1	AAA33584	Human fibronectin
C 295	8	38.1	17	1	AAF19706	Low adenosine anti
C 296	8	38.1	17	1	ABZ95400	Human fibronectin
C 297	8	38.1	17	1	ABD19452	Human fibronectin
C 298	7.8	37.1	11	1	AAX54772	Endothelial nitric
C 299	7.8	37.1	11	1	AAA34219	Human adenosine re
C 300	7.8	37.1	11	1	AAF20341	Human endothelial
C 301	7.8	37.1	11	1	ABV68029	Human skin EST 581
C 302	7.8	37.1	11	1	ABZ96035	Human endothelial
C 303	7.8	37.1	11	1	ABD19675	Human endothelial
C 304	7.8	37.1	11	1	ADQ33478	Human facial skin-
C 305	7.8	37.1	11	1	ABV68955	Human skin EST 674
C 306	7.8	37.1	11	1	ADQ34850	Human facial skin-
C 307	7.8	37.1	11	1	AAV61050	Nucleotide sequenc
C 308	7.8	37.1	11	1	AAV58720	Nucleotide sequenc
C 309	7.8	37.1	11	1	AAC38076	Human FXHL7 DNA fr
C 310	7.8	37.1	11	1	AAC65615	Multiplex analysis
C 311	7.8	37.1	11	1	AAD15332	Human allele speci
C 312	7.8	37.1	11	1	AAS15764	Allele-specific Fa
C 313	7.8	37.1	11	1	ABQ87418	Human skin stress/
C 314	7.8	37.1	11	1	ABQ86369	Human skin stress/
C 315	7.8	37.1	11	1	ABQ87096	Human skin stress/
C 316	7.8	37.1	11	1	ABQ86824	Human skin stress/
C 317	7.8	37.1	11	1	ABQ86321	Human skin stress/
C 318	7.8	37.1	11	1	ABV69665	Human skin EST 745
C 319	7.8	37.1	11	1	ABV67742	Human skin EST 552
C 320	7.8	37.1	11	1	ABV64310	Human skin EST 209
C 321	7.8	37.1	11	1	ABV64565	Human skin EST 235
C 322	7.8	37.1	11	1	ABV71376	Human skin EST 916
C 323	7.8	37.1	11	1	ABV66441	Human skin EST 422
C 324	7.8	37.1	11	1	ABV70902	Human skin EST 868
C 325	7.8	37.1	11	1	ABV71153	Human skin EST 893

C 326	7.8	37.1	11	1	ABV71986	Human skin EST 977
C 327	7.8	37.1	11	1	ABV66078	Human skin EST 386
C 328	7.8	37.1	11	1	ABV68518	Human skin EST 630
C 329	7.8	37.1	11	1	ABV68764	Human skin EST 655
C 330	7.8	37.1	11	1	ABV69433	Human skin EST 721
C 331	7.8	37.1	11	1	ABV70501	Human skin EST 828
C 332	7.8	37.1	11	1	ABV71731	Human skin EST 951
C 333	7.8	37.1	11	1	ABV63204	Human skin EST 990
C 334	7.8	37.1	11	1	ABV65801	Human skin EST 358
C 335	7.8	37.1	11	1	ABV69385	Human skin EST 717
C 336	7.8	37.1	11	1	ABV69394	Human skin EST 718
C 337	7.8	37.1	11	1	ABV69452	Human skin EST 723
C 338	7.8	37.1	11	1	ABV70625	Human skin EST 841
C 339	7.8	37.1	11	1	ABV62244	Human skin EST 30
C 340	7.8	37.1	11	1	ABV62740	Human skin EST 526
C 341	7.8	37.1	11	1	ABV63080	Human skin EST 866
C 342	7.8	37.1	11	1	ABV63955	Human skin EST 174
C 343	7.8	37.1	11	1	ABV66320	Human skin EST 410
C 344	7.8	37.1	11	1	ABV66933	Human skin EST 471
C 345	7.8	37.1	11	1	ABV68596	Human skin EST 638
C 346	7.8	37.1	11	1	ABV70229	Human skin EST 801
C 347	7.8	37.1	11	1	ABV63481	Human skin EST 126
C 348	7.8	37.1	11	1	ABV63732	Human skin EST 151
C 349	7.8	37.1	11	1	ABV65830	Human skin EST 361
C 350	7.8	37.1	11	1	ABV62808	Human skin EST 594
C 351	7.8	37.1	11	1	ABV70161	Human skin EST 794
C 352	7.8	37.1	11	1	ABV67671	Human skin EST 545
C 353	7.8	37.1	11	1	ABV68707	Human skin EST 649
C 354	7.8	37.1	11	1	ABV66603	Human skin EST 438
C 355	7.8	37.1	11	1	ADA25627	Allele-specific hu
C 356	7.8	37.1	11	1	ADH74993	Photodamage detect
C 357	7.8	37.1	11	1	ADM77004	Photodamage marker
C 358	7.8	37.1	11	1	ADZ99461	Human photodamage
C 359	7.8	37.1	11	1	ADQ36024	Human hair-bearing
C 360	7.8	37.1	11	1	ADQ32015	Human facial skin-
C 361	7.8	37.1	11	1	ADQ32041	Human facial skin-
C 362	7.8	37.1	11	1	ADQ32145	Human facial skin-
C 363	7.8	37.1	11	1	ADQ32181	Human facial skin-
C 364	7.8	37.1	11	1	ADQ34751	Human facial skin-
C 365	7.8	37.1	11	1	ADQ34112	Human facial skin-
C 366	7.8	37.1	11	1	ADT79188	Oligonucleotide #1
C 367	7.8	37.1	11	1	ADT79188	Oligonucleotide #1
C 368	7.8	37.1	12	1	AAAX55033	C/EBP-beta antisen
C 369	7.8	37.1	12	1	AAA34480	Human adenosine re
C 370	7.8	37.1	12	1	AAF20602	Human C/EBP polynu
C 371	7.8	37.1	12	1	ABZ96296	Human C/EBP antise
C 372	7.8	37.1	12	1	ABD20205	Human C/EBPN DNA f
C 373	7.8	37.1	15	1	ABL45841	Human EDG6 gene al
C 374	7.8	37.1	15	1	AAF45245	IGFBP2 oligonucleo
C 375	7.8	37.1	17	1	ADL47206	Human NOGO recepto
C 376	7.8	37.1	17	1	ADL46910	Human NOGO recepto
C 377	7.8	37.1	17	1	ADL46909	Human NOGO recepto
C 378	7.4	35.2	10	1	AD52054	Human CES2 gene po
C 379	7.4	35.2	10	1	AAZ82030	Metastatic breast
C 380	7.4	35.2	10	1	AAQ96791	HIV-1 NL4-3 nef ge
C 381	7.4	35.2	10	1	AAQ96790	HIV-1 NL4-3 nef ge
C 382	7.4	35.2	10	1	AAT29308	5'-primer for mamm
C 383	7.4	35.2	10	1	AAV38304	MDR Sp1 junction s
C 384	7.4	35.2	10	1	AAV35965	Primer used in RAP
C 385	7.4	35.2	10	1	AAV35949	Primer used in RAP
C 386	7.4	35.2	10	1	AAAX18606	p53 serial analysi
C 387	7.4	35.2	10	1	AAAX77471	US5912147 primer 1
C 388	7.4	35.2	10	1	AAAX77466	US5912147 primer 1
C 389	7.4	35.2	10	1	AAAX77472	US5912147 primer 1
C 390	7.4	35.2	10	1	AAAX54874	C/EBP-beta antisen
C 391	7.4	35.2	10	1	AAAX54736	Leukotriene C4 syn
C 392	7.4	35.2	10	1	AAAX86209	SAGE tag used to i
C 393	7.4	35.2	10	1	AAAX86209	SAGE tag used to i
C 394	7.4	35.2	10	1	AAAX43321	Human adenosine re
C 395	7.4	35.2	10	1	AAZ27583	Human dendritic ce
C 396	7.4	35.2	10	1	AAZ79675	Human dendritic ce
C 397	7.4	35.2	10	1	AAZ79030	Human dendritic ce
C 398	7.4	35.2	10	1	AAZ85628	Metastatic breast

C 399	7.4	35.2	10	1	AAZ82348	Metastatic breast
C 400	7.4	35.2	10	1	AAZ81963	Metastatic breast
C 401	7.4	35.2	10	1	AAZ85633	Metastatic breast
C 402	7.4	35.2	10	1	AAZ82808	Metastatic breast
C 403	7.4	35.2	10	1	AAZ82808	Metastatic breast
C 404	7.4	35.2	10	1	AAZ83553	Metastatic breast
C 405	7.4	35.2	10	1	AAZ86073	Metastatic breast
C 406	7.4	35.2	10	1	AAZ83525	Metastatic breast
C 407	7.4	35.2	10	1	AAZ85815	Metastatic breast
C 408	7.4	35.2	10	1	AAZ81985	Metastatic breast
C 409	7.4	35.2	10	1	AAZ84603	Metastatic breast
C 410	7.4	35.2	10	1	AAZ82759	Metastatic breast
C 411	7.4	35.2	10	1	AAZ81010	Metastatic breast
C 412	7.4	35.2	10	1	AAZ86217	Metastatic breast
C 413	7.4	35.2	10	1	AAZ81807	Metastatic breast
C 414	7.4	35.2	10	1	AAZ83555	Metastatic breast
C 415	7.4	35.2	10	1	AAZ83948	Metastatic breast
C 416	7.4	35.2	10	1	AAZ84942	Metastatic breast
C 417	7.4	35.2	10	1	AAZ86676	Metastatic breast
C 418	7.4	35.2	10	1	AAZ81145	Metastatic breast
C 419	7.4	35.2	10	1	AAZ85914	Metastatic breast
C 420	7.4	35.2	10	1	AAC73935	Human dendritic ce
C 421	7.4	35.2	10	1	AAZ79832	Human lung tumou
C 422	7.4	35.2	10	1	AAZ79759	Human breast tumou
C 423	7.4	35.2	10	1	AAC66345	Adaptor (Not I) Sa
C 424	7.4	35.2	10	1	AAF20443	Human C/EBP polyu
C 425	7.4	35.2	10	1	AAA89854	Adaptor -SmaI. Sy
C 426	7.4	35.2	10	1	AAA73207	Arbitrary primer 8
C 427	7.4	35.2	10	1	AAS12772	SmaI-adaptor DNA s
C 428	7.4	35.2	10	1	AAH63607	Human ubiquitously
C 429	7.4	35.2	10	1	AAH63746	Human ubiquitously
C 430	7.4	35.2	10	1	AAH64374	Human ubiquitously
C 431	7.4	35.2	10	1	AAH64390	Human ubiquitously
C 432	7.4	35.2	10	1	AAH63440	Human ubiquitously
C 433	7.4	35.2	10	1	AAH64391	Human ubiquitously
C 434	7.4	35.2	10	1	AAH63439	Human ubiquitously
C 435	7.4	35.2	10	1	AAH64389	Human ubiquitously
C 436	7.4	35.2	10	1	AAH64388	Human ubiquitously
C 437	7.4	35.2	10	1	AAH64393	Human ubiquitously
C 438	7.4	35.2	10	1	AAH64375	Human ubiquitously
C 439	7.4	35.2	10	1	AAH64392	Human ubiquitously
C 440	7.4	35.2	10	1	AAH64394	Human ubiquitously
C 441	7.4	35.2	10	1	AAS57313	Human CHRN2 allel
C 442	7.4	35.2	10	1	AAD20716	Primer #8 used to
C 443	7.4	35.2	10	1	AAD20716	Primer #8 used to
C 444	7.4	35.2	10	1	AAH32856	LPS activated huma
C 445	7.4	35.2	10	1	AAH32863	LPS activated huma
C 446	7.4	35.2	10	1	ABA06204	Human normal hepat
C 447	7.4	35.2	10	1	AAF41458	Yeast NORF gene SA
C 448	7.4	35.2	10	1	AAF42948	Yeast NORF gene SA
C 449	7.4	35.2	10	1	AAF41493	Yeast NORF gene SA
C 450	7.4	35.2	10	1	AAF42326	Yeast NORF gene SA
C 451	7.4	35.2	10	1	AAF34571	Yeast NORF gene SA
C 452	7.4	35.2	10	1	AAF37416	Yeast NORF gene SA
C 453	7.4	35.2	10	1	AAF42930	Yeast NORF gene SA
C 454	7.4	35.2	10	1	AAF35455	Yeast NORF gene SA
C 455	7.4	35.2	10	1	AAF43175	Yeast NORF gene SA
C 456	7.4	35.2	10	1	AAF43167	Yeast NORF gene SA
C 457	7.4	35.2	10	1	AAH76352	Z. mays Ms45 promo
C 458	7.4	35.2	10	1	AAH76350	Z. mays Ms45 promo
C 459	7.4	35.2	10	1	AAH76350	Z. mays Ms45 promo
C 460	7.4	35.2	10	1	AAH76346	Z. mays Ms45 promo
C 461	7.4	35.2	10	1	AAH76351	Z. mays Ms45 promo
C 462	7.4	35.2	10	1	AAH76354	Z. mays Ms45 promo
C 463	7.4	35.2	10	1	AAH76353	Z. mays Ms45 promo
C 464	7.4	35.2	10	1	AAH76344	Z. mays Ms45 promo
C 465	7.4	35.2	10	1	AAH76344	Z. mays Ms45 promo
C 466	7.4	35.2	10	1	AAH76344	Galanin receptor g
C 467	7.4	35.2	10	1	AAS98388	Galanin receptor g
C 468	7.4	35.2	10	1	AAS98391	Galanin receptor g
C 469	7.4	35.2	10	1	AAS98386	Galanin receptor g
C 470	7.4	35.2	10	1	ABK24232	Retinaldehyde-bind
C 471	7.4	35.2	10	1	AAS99949	Even-skipped homeo
C 472	7.4	35.2	10	1	AAS99949	Even-skipped homeo
C 473	7.4	35.2	10	1	ABK95840	Solute Carrier Fam
C 474	7.4	35.2	10	1	ABK95837	Solute Carrier Fam
C 475	7.4	35.2	10	1	ABL42671	Human maturation/a
C 476	7.4	35.2	10	1	ABL55362	Mint RAPD (random
C 477	7.4	35.2	10	1	ABN81467	Human HTATIP PCR p
C 478	7.4	35.2	10	1	AAS96206	Human Acetylcholin
C 479	7.4	35.2	10	1	AAS96195	Human Acetylcholin
C 480	7.4	35.2	10	1	AAD26168	Human endothelin 2
C 481	7.4	35.2	10	1	AAL48067	Human CSF3 gene al
C 482	7.4	35.2	10	1	ABT05346	Human NAGA-alpha g
C 483	7.4	35.2	10	1	ABQ72341	Human CYP2D6 gene
C 484	7.4	35.2	10	1	ABV78373	Human Th2 cell SAG
C 485	7.4	35.2	10	1	ABV78501	Human Th1 cell pre
C 486	7.4	35.2	10	1	ABV84770	Human tetranectin
C 487	7.4	35.2	10	1	ABV84449	Human heat shock p
C 488	7.4	35.2	10	1	ABV84235	Human chronic hepa
C 489	7.4	35.2	10	1	ABV84561	Human HCC underexp
C 490	7.4	35.2	10	1	ABV84764	Chronic hepatitis
C 491	7.4	35.2	10	1	ABV84221	Human tetranectin
C 492	7.4	35.2	10	1	ABV84947	Human multiple HCC
C 493	7.4	35.2	10	1	ABV84447	Human HCC overexpr
C 494	7.4	35.2	10	1	ABV84198	Human heat shock p
C 495	7.4	35.2	10	1	ABV84728	Chronic hepatitis
C 496	7.4	35.2	10	1	ABK09429	Human NPR1 gene al
C 497	7.4	35.2	10	1	ABK28551	Paraoxonase 2 (PON
C 498	7.4	35.2	10	1	ABL52050	Human SLC18A2 pref
C 499	7.4	35.2	10	1	ABK96615	Human interleukin
C 500	7.4	35.2	10	1	ABL45924	Human EDG6 gene al
C 501	7.4	35.2	10	1	ABN88032	Human SCYB14 prefe
C 502	7.4	35.2	10	1	AAS16750	Human APOA4 ASO, p
C 503	7.4	35.2	10	1	ABN86551	Streptomyces strai
C 504	7.4	35.2	10	1	AAK98593	Human enolase 3 ge
C 505	7.4	35.2	10	1	ABN81250	Oligonucleotide pr
C 506	7.4	35.2	10	1	AAS99401	Aldehyde dehydroge
C 507	7.4	35.2	10	1	AAS99388	Aldehyde dehydroge
C 508	7.4	35.2	10	1	ABK30047	Vancomycin-resista
C 509	7.4	35.2	10	1	ABK30060	Vancomycin-resista
C 510	7.4	35.2	10	1	ABK30057	Vancomycin-resista
C 511	7.4	35.2	10	1	ABL36370	Human lysosomal ac
C 512	7.4	35.2	10	1	AAL48136	Human neuropeptide
C 513	7.4	35.2	10	1	AAS95980	Human CALM1 gene a
C 514	7.4	35.2	10	1	AAS95999	Human CALM1 gene a
C 515	7.4	35.2	10	1	AAS96001	Human CALM1 gene a
C 516	7.4	35.2	10	1	AAL39774	SMOH polymorphism
C 517	7.4	35.2	10	1	ADH22211	Primer extension D
C 518	7.4	35.2	10	1	ABX79711	EST polymorphic DN
C 519	7.4	35.2	10	1	ABX79834	EST polymorphic DN
C 520	7.4	35.2	10	1	ACA94633	DNA tag from human
C 521	7.4	35.2	10	1	ACA94632	DNA tag from human
C 522	7.4	35.2	10	1	ABT14308	Nucleic acid PCR a
C 523	7.4	35.2	10	1	ABT16373	Gene therapy vecto
C 524	7.4	35.2	10	1	ABT16373	Gene therapy vecto
C 525	7.4	35.2	10	1	AAD60162	Human ARG signal t
C 526	7.4	35.2	10	1	ADC45707	DNA sequencing res
C 527	7.4	35.2	10	1	ADH62271	Signal transducing
C 528	7.4	35.2	10	1	ADI10259	Rakshit plant rand
C 529	7.4	35.2	10	1	ADH75058	Photodamage detect
C 530	7.4	35.2	10	1	ABZ96137	Human C/EBP antise
C 531	7.4	35.2	10	1	ADJ93954	Azotobacter bacter
C 532	7.4	35.2	10	1	ADJ93954	Azotobacter bacter
C 533	7.4	35.2	10	1	ADM77073	Photodamage marker
C 534	7.4	35.2	10	1	ABD20046	Human C/EBPN DNA f
C 535	7.4	35.2	10	1	ADZ99517	Human photodamage
C 536	7.4	35.2	10	1	ADH57681	Extendable oligo E
C 537	7.4	35.2	10	1	ADH57602	Extendable oligo E
C 538	7.4	35.2	10	1	ADI26552	Rat PIM1 antisense
C 539	7.4	35.2	10	1	ADI13682	Cytoplasmic tumour
C 540	7.4	35.2	10	1	ADJ95575	Equine herpesvirus
C 541	7.4	35.2	10	1	ADN89098	Hyperlipidemia tre
C 542	7.4	35.2	10	1	ADO05774	Nucleotide sequenc
C 543	7.4	35.2	10	1	ADO39888	Androgen-regulated
C 544	7.4	35.2	10	1	ADO26312	Human chondromedin

545	7.4	35.2	10	1	ADR27909	Human VE-statin ex
546	7.4	35.2	10	1	ADS76996	Breast cancer dete
C 547	7.4	35.2	10	1	ADS76954	Breast cancer dete
C 548	7.4	35.2	10	1	ADS77203	Breast cancer dete
C 549	7.4	35.2	10	1	ADS78056	Breast cancer dete
C 550	7.4	35.2	10	1	ADS77992	Breast cancer dete
C 551	7.4	35.2	10	1	ADS77293	Breast cancer dete
C 552	7.4	35.2	10	1	ADS77023	Breast cancer dete
C 553	7.4	35.2	10	1	ADS76953	Breast cancer dete
C 554	7.4	35.2	10	1	ADS76221	Breast cancer dete
C 555	7.4	35.2	10	1	ADS78162	Breast cancer dete
C 556	7.4	35.2	10	1	ADS76799	Breast cancer dete
C 557	7.4	35.2	10	1	ADS77335	Breast cancer dete
558	7.4	35.2	10	1	ADS76995	Breast cancer dete
C 559	7.4	35.2	10	1	ADS76366	Breast cancer dete
C 560	7.4	35.2	10	1	ADS78102	Breast cancer dete
C 561	7.4	35.2	10	1	ADS77022	Breast cancer dete
C 562	7.4	35.2	10	1	ADS77202	Breast cancer dete
563	7.4	35.2	10	1	ADU18767	Breast cancer dete
C 564	7.4	35.2	10	1	ADU19573	Hypoxia-related tu
C 565	7.4	35.2	10	1	ADU19354	Hypoxia-related tu
C 566	7.4	35.2	10	1	ADU19103	Hypoxia-related tu
567	7.4	35.2	10	1	ADU19820	Hypoxia-related tu
568	7.4	35.2	10	1	ADU18946	Hypoxia-related tu
C 569	7.4	35.2	10	1	ADU78581	Hypoxia-related tu
C 570	7.4	35.2	10	1	ADW73862	Rice oligonucleoti
C 571	7.4	35.2	10	1	ADY54310	Arm 1 oligo includ
572	7.4	35.2	10	1	ADZ23138	Phyllanthus amarus
573	7.4	35.2	10	1	ADZ24419	Human SNP detectio
574	7.4	35.2	10	1	ADZ23793	Human SNP detectio
575	7.4	35.2	10	1	ADZ24430	Human SNP detectio
C 576	7.4	35.2	10	1	ADZ67686	INVADER oligonucle
C 577	7.4	35.2	10	1	ADZ76869	Krishna tulsi DNA
C 578	7.4	35.2	10	1	AEA90141	Artemisia annua ar
579	7.4	35.2	11	1	ABV69801	Human skin EST 758
580	7.4	35.2	11	1	ABV62380	Human skin EST 166
581	7.4	35.2	11	1	ADX25610	5' AscI site oligo
C 582	7.2	34.3	12	1	AAX54938	C/EBP-beta antisen
C 583	7.2	34.3	12	1	AAA34385	Human adenosine re
C 584	7.2	34.3	12	1	AAF20507	Human C/EBP polynu
C 585	7.2	34.3	12	1	ABZ96201	Human C/EBP antise
C 586	7.2	34.3	12	1	AEB31299	Mouse 18S rDNA com
C 587	7.2	34.3	12	1	AEB31301	Human 18S rDNA com
C 588	7.2	34.3	12	1	AEB31300	Rat 18S rDNA compl
C 589	7.2	34.3	15	1	AAF46831	IGFBP3 oligonucleo
C 590	7.2	34.3	15	1	AAF46830	IGFBP3 oligonucleo
C 591	7.2	34.3	16	1	ADL91730	Collagen type IX a
592	7.2	34.3	20	1	AAV69995	Mouse c-jun protei
593	7	33.3	10	1	ABA06199	Human normal hepat
C 594	7	33.3	10	1	ABL45887	Human EDG6 gene al
C 595	7	33.3	10	1	AAZ85815	Metastatic breast
C 596	7	33.3	10	1	AAQ71095	Merlin exon 10 spl
C 597	7	33.3	10	1	AAQ87131	NaeI substrate oli
C 598	7	33.3	10	1	AAQ96792	HIV-1 NL4-3 nef ge
599	7	33.3	10	1	AAQ96984	HIV-1 NL4-3 nef ge
600	7	33.3	10	1	AAQ96983	HIV-1 NL4-3 nef ge
601	7	33.3	10	1	AAQ96985	HIV-1 NL4-3 nef ge
C 602	7	33.3	10	1	AAQ96793	HIV-1 NL4-3 nef ge
603	7	33.3	10	1	AAQ96986	PCR primer for the
604	7	33.3	10	1	AAQ90121	5'-primer for mamm
605	7	33.3	10	1	AAT29334	5'-primer for mamm
606	7	33.3	10	1	AAT29313	5'-primer for mamm
C 607	7	33.3	10	1	AAT29293	Hammerhead ribozym
C 608	7	33.3	10	1	AAT10090	Yeast tag for addi
609	7	33.3	10	1	AAV50187	US5912147 primer 1
C 610	7	33.3	10	1	AAX77475	US5912147 primer 2
611	7	33.3	10	1	AAX77476	US5912147 primer 2
612	7	33.3	10	1	AAZ28347	Lung cancer indica
C 613	7	33.3	10	1	AAZ28347	Primer SP4A5 for g
C 614	7	33.3	10	1	AAZ61441	Human dendritic ce
C 615	7	33.3	10	1	AAZ78750	Human dendritic ce
616	7	33.3	10	1	AAZ79591	Human dendritic ce
C 617	7	33.3	10	1	AAZ79112	Human dendritic ce
618	7	33.3	10	1	AAZ78274	Human dendritic ce
C 619	7	33.3	10	1	AAZ79074	Human dendritic ce
620	7	33.3	10	1	AAZ78343	Human dendritic ce
621	7	33.3	10	1	AAZ77871	Human dendritic ce
C 622	7	33.3	10	1	AAZ79427	Human dendritic ce
623	7	33.3	10	1	AAZ79444	Human dendritic ce
C 624	7	33.3	10	1	AAZ78099	Human dendritic ce
625	7	33.3	10	1	AAZ79480	Human dendritic ce
C 626	7	33.3	10	1	AAZ77608	Human dendritic ce
627	7	33.3	10	1	AAZ82905	Metastatic breast
C 628	7	33.3	10	1	AAZ83064	Metastatic breast
629	7	33.3	10	1	AAZ83787	Metastatic breast
630	7	33.3	10	1	AAZ85889	Metastatic breast
631	7	33.3	10	1	AAZ82125	Metastatic breast
C 632	7	33.3	10	1	AAZ82631	Metastatic breast
C 633	7	33.3	10	1	AAZ82867	Metastatic breast
634	7	33.3	10	1	AAZ81312	Metastatic breast
635	7	33.3	10	1	AAZ80814	Metastatic breast
C 636	7	33.3	10	1	AAZ81489	Metastatic breast
637	7	33.3	10	1	AAZ85240	Metastatic breast
638	7	33.3	10	1	AAZ85596	Metastatic breast
639	7	33.3	10	1	AAZ82633	Metastatic breast
640	7	33.3	10	1	AAZ85912	Metastatic breast
C 641	7	33.3	10	1	AAZ82082	Metastatic breast
C 642	7	33.3	10	1	AAZ83360	Metastatic breast
C 643	7	33.3	10	1	AAZ84570	Metastatic breast
644	7	33.3	10	1	AAZ84917	Metastatic breast
C 645	7	33.3	10	1	AAZ86247	Metastatic breast
C 646	7	33.3	10	1	AAZ81044	Metastatic breast
647	7	33.3	10	1	AAZ81638	Metastatic breast
648	7	33.3	10	1	AAZ81933	Metastatic breast
649	7	33.3	10	1	AAZ84040	Metastatic breast
650	7	33.3	10	1	AAZ86609	Metastatic breast
651	7	33.3	10	1	AAZ82698	Metastatic breast
652	7	33.3	10	1	AAZ84042	Metastatic breast
C 653	7	33.3	10	1	AAZ84284	Metastatic breast
654	7	33.3	10	1	AAZ85585	Metastatic breast
C 655	7	33.3	10	1	AAZ85958	Metastatic breast
656	7	33.3	10	1	AAZ82293	Metastatic breast
C 657	7	33.3	10	1	AAZ82945	Metastatic breast
658	7	33.3	10	1	AAZ83312	Metastatic breast
C 659	7	33.3	10	1	AAZ83464	Metastatic breast
660	7	33.3	10	1	AAZ82560	Metastatic breast
C 661	7	33.3	10	1	AAZ82992	Metastatic breast
662	7	33.3	10	1	AAZ79752	Human colon prefer
663	7	33.3	10	1	AAZ79859	Human dendritic ce
664	7	33.3	10	1	AAZ79807	Human prostate pre
665	7	33.3	10	1	AAZ79746	Human colon prefer
C 666	7	33.3	10	1	AAA73648	Probe #17 for sequ
C 667	7	33.3	10	1	AAA73647	Probe #16 for sequ
C 668	7	33.3	10	1	AAA73645	Probe #14 for sequ
C 669	7	33.3	10	1	AAA73646	Probe #15 for sequ
C 670	7	33.3	10	1	AAA70761	PCR primer #7 for
C 671	7	33.3	10	1	AAS04437	Human DAXX DNA pri
C 672	7	33.3	10	1	AAH63468	Human ubiquitously
673	7	33.3	10	1	AAH63684	Human ubiquitously
C 674	7	33.3	10	1	AAH63781	Human ubiquitously
675	7	33.3	10	1	AAH64309	Human ubiquitously
C 676	7	33.3	10	1	AAH64225	Human ubiquitously
677	7	33.3	10	1	AAH64231	Human ubiquitously
C 678	7	33.3	10	1	AAH63421	Human cancer tissu
679	7	33.3	10	1	AAH64302	Human ubiquitously
C 680	7	33.3	10	1	AAH63467	Human ubiquitously
681	7	33.3	10	1	AAH63397	Human cancer tissu
682	7	33.3	10	1	AAS57302	Human CHRN2 allele
C 683	7	33.3	10	1	AAS57283	Human CHRN2 allele
684	7	33.3	10	1	AAH25889	Nestin promoter ve
C 685	7	33.3	10	1	AAH25889	Nestin promoter ve
C 686	7	33.3	10	1	AAH32825	LPS activated huma
687	7	33.3	10	1	AAH32869	LPS activated huma
688	7	33.3	10	1	AAH32681	LPS activated huma
C 689	7	33.3	10	1	AAF75027	HTR1A gene polymor
C 690	7	33.3	10	1	AAH41713	Anti-PEP gene cons

691	7	33.3	10	1	AAF70446	Human DRD2 polymor
c 692	7	33.3	10	1	AAA91467	Human CHRM5 gene,
693	7	33.3	10	1	ABA83148	Claudin 2 ovarian
c 694	7	33.3	10	1	AAF38910	Yeast NORF gene SA
695	7	33.3	10	1	AAF33704	Yeast NORF gene SA
c 696	7	33.3	10	1	AAF36509	Yeast NORF gene SA
697	7	33.3	10	1	AAF33404	Yeast NORF gene SA
c 698	7	33.3	10	1	AAF36625	Yeast NORF gene SA
c 699	7	33.3	10	1	AAF37397	Yeast NORF gene SA
700	7	33.3	10	1	AAF40108	Yeast NORF gene SA
701	7	33.3	10	1	AAF43351	Yeast NORF gene SA
702	7	33.3	10	1	AAF33705	Yeast NORF gene SA
703	7	33.3	10	1	AAF36000	Yeast NORF gene SA
704	7	33.3	10	1	AAF42397	Yeast NORF gene SA
c 705	7	33.3	10	1	AAF43632	Yeast NORF gene SA
706	7	33.3	10	1	AAS95650	Human NPY1R gene a
c 707	7	33.3	10	1	AAD25081	Primer #8 used to
708	7	33.3	10	1	AAD26712	Human GPR31 gene p
709	7	33.3	10	1	AAD26031	Primer #33 to dete
710	7	33.3	10	1	ABL42059	C-terminal tail of
c 711	7	33.3	10	1	ABL42059	C-terminal tail of
712	7	33.3	10	1	ABL42060	Fragment of a reve
c 713	7	33.3	10	1	ABL42060	Fragment of a reve
c 714	7	33.3	10	1	ABL52166	Human PER1 prefer
c 715	7	33.3	10	1	ABL01195	Human AKR1B1 gene
716	7	33.3	10	1	AAS98854	Colony stimulating
717	7	33.3	10	1	AAS98814	Colony stimulating
718	7	33.3	10	1	ABL42674	Human maturation/a
719	7	33.3	10	1	ABL42776	Human maturation/a
720	7	33.3	10	1	ABL42840	Human maturation/a
c 721	7	33.3	10	1	ABL57664	Human SCYA24 prime
c 722	7	33.3	10	1	AAD25385	Human primer #2 to
723	7	33.3	10	1	ABN81466	Human HTATIP PCR p
c 724	7	33.3	10	1	ABN81466	Human HTATIP PCR p
725	7	33.3	10	1	ABK96027	Human LIPE gene po
726	7	33.3	10	1	AAD26186	Human endothelin 2
c 727	7	33.3	10	1	AAL48068	Human CSF3 gene al
728	7	33.3	10	1	ABQ71544	Zinc finger protei
729	7	33.3	10	1	ABQ88698	Human CFL1 primer
730	7	33.3	10	1	ABA99350	Human ALDH5 allele
c 731	7	33.3	10	1	ABN80659	Human P450(cytochr
c 732	7	33.3	10	1	ABV78586	Human Th2 cell pre
733	7	33.3	10	1	ABV78572	Human Th2 cell pre
c 734	7	33.3	10	1	ABV78572	Human Th2 cell pre
735	7	33.3	10	1	ABV78578	Human Th2 cell pre
c 736	7	33.3	10	1	ABV84533	Human liver phosph
c 737	7	33.3	10	1	ABV84789	Human gamma-glutam
c 738	7	33.3	10	1	ABV84679	Human HCC/chronic
c 739	7	33.3	10	1	ABV84371	Human MHC class II
c 740	7	33.3	10	1	ABV84732	Human liver phosph
c 741	7	33.3	10	1	ABL52041	Human SLC18A2 pref
742	7	33.3	10	1	ABQ81583	Asci linker. Synt
c 743	7	33.3	10	1	ABQ81583	Asci linker. Synt
c 744	7	33.3	10	1	ABA93362	Human ACAA1 gene p
c 745	7	33.3	10	1	ABK72402	Human HTR5A gene a
c 746	7	33.3	10	1	AAS97348	Human CRYBB1 gene
747	7	33.3	10	1	ABL45895	Human EDG6 gene al
748	7	33.3	10	1	ABL45880	Human EDG6 gene al
749	7	33.3	10	1	AAS95576	Human IL8RB gene a
c 750	7	33.3	10	1	ABK54355	Human SCYA26 gene
c 751	7	33.3	10	1	ABK72641	Leukotriene B4 rec
c 752	7	33.3	10	1	AAS99404	Aldehyde dehydroge
c 753	7	33.3	10	1	AAS99416	Aldehyde dehydroge
c 754	7	33.3	10	1	AAD26806	Primer #13 to dete
c 755	7	33.3	10	1	ABK30056	Vancomycin-resista
756	7	33.3	10	1	ABK30050	Vancomycin-resista
757	7	33.3	10	1	AAS95997	Human CALM1 gene a
c 758	7	33.3	10	1	ABK81807	Human CHRM5 gene p
759	7	33.3	10	1	ADG28070	Human Myo/V1 prote
c 760	7	33.3	10	1	ADG28070	Human Myo/V1 prote
761	7	33.3	10	1	ADG28259	Human Myo/V1 prote
c 762	7	33.3	10	1	ADG28259	Human Myo/V1 prote
c 763	7	33.3	10	1	ADH22188	Primer extension D
						Human GNB3 gene po
						DNA tag from human
						DNA tag from human
						DNA tag from human
						DNA tag from human
						Nucleic acid PCR a
						Zinc finger target
						Human ARG energy m
						Oligomer #11 which
						Oligomer #11 which
						Oligonucleotide SE
						Human CERP gene al
						Human energy metab
						6784-1-G-Tam PNA p
						Azotobacter bacter
						Synthetic zinc fin
						UCP2 primer extens
						UCP2 primer extens
						Extendable oligo E
						Extracellular tumo
						Extracellular tumo
						Androgen-regulated
						Murine VE-statin e
						Breast cancer dete
						Breast cancer dete
						Breast cancer dete
						Breast cancer dete
						Breast cancer dete
						Breast cancer dete
						Breast cancer dete
						Breast cancer dete
						Breast cancer dete
						Hypoxia-related tu
						Hypoxia-related tu
						Hypoxia-related tu
						Hypoxia-related tu
						Hypoxia-related tu
						Hypoxia-related tu
						Hypoxia-related tu
						Hypoxia-related tu
						Asti DNA linker se
						Asti DNA linker se
						NTRK1 gene polymor
						Human BACE455 cDNA
						NTRK1 gene polymor
						ALIGNMENTS
						RESULT 1
						AAV69995/c
						ID AAV69995 standard; DNA; 20 BP.
						XX
						AC AAV69995;
						XX
						DT 04-FEB-1999 (first entry)
						XX
						DE Mouse c-jun protein antisense oligonucleotide #40.
						XX
						KW Mouse; c-fos; c-jun; activating protein 1; AP-1; diagnosis; metastasis;
						KW antisense oligonucleotide; phosphorothioate; regulation;
						KW malignant tumour; cell cycle expression; hyperproliferative disease; ss.
						XX
						OS Synthetic.
						OS Mus sp.
						XX
						FH Key Location/Qualifiers

FT modified_base 1..20
FT /tag= a
FT /note= "phosphorothioate linkages"
XX
PN WO9846272-A1.
XX
PD 22-OCT-1998.
XX
PF 14-APR-1998; 98WO-US007386.
XX
PR 14-APR-1997; 97US-00837201.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM, McKay R, Miraglia L, Baker B;
XX
XX WPI; 1998-609906/51.
DR
XX
PT Antisense oligonucleotides regulating Activating Protein 1 subunits -
PT hybridise with c-fos and c-jun mRNA, used for regulating metastasis, cell
PT cycle expression and hyperproliferative disease.
XX
PS Example 7; Page 52; 120pp; English.
XX
CC AAV69993 to AAV70008 represent antisense oligonucleotides which are
CC specifically hybridisable with a region of a nucleic acid encoding mouse
CC c-Jun protein. The antisense compound regulates the expression of the c-
CC Jun protein. The present invention also describes antisense
CC oligonucleotides which regulate the c-Fos protein. The antisense
CC oligonucleotides are used for the diagnosis and treatment of diseases or
CC disorders associated with Activating Protein 1 expression, of which c-Fos
CC and c-Jun are subunits. The antisense oligonucleotides are used in
CC compositions as c-Fos and/or c-Jun together with a carrier and a
CC chemotherapeutic agent. They are used to regulate the expression of c-Fos
CC or c-Jun in cells or tissues, preferably by inhibiting metastasis. They
CC also regulate cell cycle expression and can be used to treat an animal
CC with, or being prone to, a hyperproliferative disease
XX
SQ Sequence 20 BP; 5 A; 7 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 58.6%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 CCCGGCGCGTGTGGC 21
Db 16 CCCGGCGCGTGTGC 1
RESULT 2
ADL47206/c
ID ADL47206 standard; RNA; 17 BP.
XX
AC ADL47206;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOGO receptor zinzyme substrate sequence #193.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor zinzyme; substrate; ds.
XX
OS Unidentified.
XX
PN WO200281628-A2.

(Cnt 3631-44 w/ deleted
, subst iden' to 3631-47

XX 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX WPI; 2003-058513/05.
DR
XX
PT Novel enzymatic nucleic acid that down-regulates expression of neurite
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT protein kinase PKR genes, for treating cancer and inflammatory disease.
XX
PS Claim 9; SEQ ID NO 739; 317pp; English.
XX
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC that down regulate the expression or inhibit the function of a receptor
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC invention are useful for treating: cerebrovascular accident, central
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC disease, lupus, multiple sclerosis, transplant/graft rejection,
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC nucleic acids of the invention are also useful for down-regulating the
CC expression of a target gene and as a diagnostic tool to examine genetic
CC drifts and mutations within diseased cells or to detect the presence of a
CC target RNA in a cell. The present RNA sequence represents a human NOGO
CC receptor zinzyme substrate sequence.
XX
SQ Sequence 17 BP; 4 A; 7 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 61.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 TGGCCCGCGCGCTGT 18
Db 17 TTGCCCGCGCGGCTGT 2
RESULT 3
ADM54550
ID ADM54550 standard; mRNA; 17 BP.
XX
AC ADM54550;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human GRID mRNA substrate sequence #860.
XX
KW Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNazyme; amberzyme; Inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX
OS Homo sapiens.
XX
PN US2003134806-A1.
XX
PD 17-JUL-2003.
XX
PF 23-FEB-2001; 2001US-00792818.
XX
PR 10-FEB-2000; 2000US-0181594P.
XX

PA (JARV/) JARVIS T.
PA (CARL/) CARLOWITZ I V.
PA (MCSW/) MCSWIGGEN J.
PA (HAMB/) HAMBLIN P A.
PA (ELLI/) ELLIS J H.
XX
PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX
DR WPI; 2003-829646/77.
XX
PT New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
PS Claim 4; SEQ ID NO 862; 74pp; English.
XX
CC The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNzyme,
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
SQ Sequence 17 BP; 0 A; 8 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 41;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGGCCCGCGCGCGTGT 18
Db :||||| ||||| |:|:
2 UGGCCCGCGCGCCUGU 17

RESULT 4
ADL91730
ID ADL91730 standard; DNA; 16 BP.
XX
AC ADL91730;
XX
DT 03-JUN-2004 (first entry)
XX
DE Collagen type IX alpha 3 (SYX 4) control S-oligo, SEQ ID NO:131.
XX
KW Synovial sarcoma; SYX; sarcoma-associated gene; drug screening;
KW Frizzled homologue 10; FZD10-associated disease; colorectal cancer;
KW gastric cancer; chronic myeloid leukaemia; acute myeloid leukaemia;
KW FZD10 antibody; diagnosis; prognosis; prevention; cytostatic;
KW gene therapy; control oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO2004020668-A2.
XX
PD 11-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-JP010591.
XX
PR 30-AUG-2002; 2002US-0407506P.
PR 11-JUL-2003; 2003US-0486195P.
XX

PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UYTY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T;
XX
DR WPI; 2004-239208/22.
XX
PT Use of a compound or composition for diagnosing, treating or preventing
PT synovial sarcoma or a disease associated with Frizzled homologue 10, e.g.
PT colorectal cancer, gastric cancer, chronic myeloid leukemia or acute
PT myeloid leukemia.
XX
PS Example 4; SEQ ID NO 131; 143pp; English.
XX
CC The invention relates to the use of a compound or composition for
CC diagnosing, prognosing, treating or preventing synovial sarcoma or a
CC Frizzled homologue 10 (FZD10)-associated disease in a patient. The
CC invention encompasses the use of sarcoma-associated genes designated SYX
CC 1-26 or their encoded proteins in diagnosing of synovial sarcoma and in
CC screening for compounds for treating or preventing this condition; and
CC the use of antibodies specific for FZD10 (FZD10 is also referred to as
CC SYX 1 in the specification) for diagnosing, treating or preventing FZD10-
CC associated diseases. The compound, composition and methods of the
CC invention are useful for diagnosing, treating or preventing synovial
CC sarcoma or FZD10-associated diseases, such as colorectal cancer, gastric
CC cancer, chronic myeloid leukaemia or acute myeloid leukaemia. Sequences
CC ADL91688-ADL91751 represent antisense and control S-oligonucleotides used
CC in a study of antisense-mediated inhibition of the expression of synovial
CC sarcoma-associated genes.
XX
SQ Sequence 16 BP; 1 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 59.0%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 43;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTGGCCCGCGCGCGC 15
Db | ||||| |||||
3 CCGGCCCGCGCGCGC 16

RESULT 5
ADL46910/C
ID ADL46910 standard; RNA; 17 BP.
XX
AC ADL46910;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOGO receptor inozyme substrate sequence #343.
XX
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW NOGO receptor inozyme; substrate; ds.
XX
OS Unidentified.
XX
PN WO200281628-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010512.
XX
PR 05-APR-2001; 2001US-00827395.
PR 29-MAY-2001; 2001US-0294412P.
PR 28-AUG-2001; 2001US-0315315P.

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:14:10 ; Search time 79.9111 Seconds
(without alignments)
645.083 Million cell updates/sec

Title: US-09-904-968A-3
Perfect score: 29
Sequence: 1 ccataccactgtgtgtgacctgtaaat 29

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	31571	2	US-08-323-443B-1
2	29	100.0	53526	3	US-08-658-136-2
3	29	100.0	53577	3	US-08-658-136-1
4	29	100.0	53577	3	US-08-460-215A-1
5	20.2	69.7	601	3	US-09-949-016-142117
6	20.2	69.7	601	3	US-09-949-016-142118
c 7	20.2	69.7	44064	3	US-09-949-016-12015
c 8	20.2	69.7	44072	3	US-09-949-016-15757
c 9	20	69.0	24546	3	US-09-949-016-16638
c 10	19.8	68.3	105045	3	US-09-949-002-663
c 11	19.6	67.6	378	3	US-09-621-976-10243
12	19.6	67.6	8930	3	US-09-814-915A-91
13	19.6	67.6	47787	3	US-09-949-016-11969
14	19.6	67.6	97423	3	US-09-949-016-12742
15	19.6	67.6	97424	3	US-09-949-016-15576
16	19.4	66.9	601	3	US-09-949-016-51876
c 17	19.4	66.9	22104	3	US-09-949-016-12745
c 18	19.4	66.9	22104	3	US-09-949-016-17263
19	19.4	66.9	47493	3	US-09-949-016-13241
c 20	19.4	66.9	105679	3	US-09-949-016-12360
21	19.4	66.9	150032	3	US-09-949-016-14321
22	19.4	66.9	387902	3	US-09-949-016-14543
23	19.4	66.9	421883	3	US-09-949-016-12557
c 24	19.2	66.2	1683	3	US-09-902-540-4280

c 25	19.2	66.2	20250	3	US-09-902-540-1213	Sequence 1213, Ap
c 26	19.2	66.2	95750	3	US-09-949-016-11926	Sequence 11926, A
c 27	19	65.5	601	3	US-09-949-016-95981	Sequence 95981, A
c 28	19	65.5	843	3	US-09-252-991A-5079	Sequence 5079, Ap
29	19	65.5	1530	3	US-09-252-991A-5138	Sequence 5138, Ap
c 30	19	65.5	1581	3	US-09-252-991A-5015	Sequence 5015, Ap
c 31	19	65.5	66175	3	US-09-949-016-12293	Sequence 12293, A
c 32	19	65.5	95122	3	US-09-949-016-17235	Sequence 17235, A
c 33	19	65.5	97376	3	US-09-949-016-16093	Sequence 16093, A
c 34	18.8	64.8	601	3	US-09-949-016-165692	Sequence 165692, A
35	18.8	64.8	36611	3	US-09-949-016-17287	Sequence 17287, A
c 36	18.8	64.8	107679	3	US-09-949-016-16409	Sequence 16409, A
c 37	18.6	64.1	601	3	US-09-949-016-160801	Sequence 160801, A
38	18.6	64.1	45427	3	US-09-949-016-16243	Sequence 16243, A
c 39	18.6	64.1	50186	3	US-09-949-016-14066	Sequence 14066, A
40	18.6	64.1	92581	3	US-09-949-016-12182	Sequence 12182, A
41	18.6	64.1	92581	3	US-09-949-016-16542	Sequence 16542, A
42	18.6	64.1	767677	3	US-09-949-016-12147	Sequence 12147, A
43	18.6	64.1	767677	3	US-09-949-016-17361	Sequence 17361, A
44	18.4	63.4	495	3	US-09-621-976-11554	Sequence 11554, A
c 45	18.4	63.4	601	3	US-09-949-016-19572	Sequence 19572, A

ALIGNMENTS

RESULT 1
US-08-323-443B-1
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/0A462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens


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; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match      100.0%; Score 29; DB 2; Length 31571;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
   |||||
Db 1448 CCATCCACCTGCTGTGTGACCTGGTAAAT 1476

RESULT 2
US-08-658-136-2
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match      100.0%; Score 29; DB 3; Length 53526;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
   |||||
Db 2043 CCATCCACCTGCTGTGTGACCTGGTAAAT 2071

RESULT 3
US-08-658-136-1
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
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; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match      100.0%; Score 29; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
   |||||
Db 2043 CCATCCACCTGCTGTGTGACCTGGTAAAT 2071

RESULT 4
US-08-460-215A-1
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,215A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUGAN, DEBORAH
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-17.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-460-215A-1

Query Match 100.0%; Score 29; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
|||||
Db 2043 CCATCCACCTGCTGTGTGACCTGGTAAAT 2071

RESULT 5

US-09-949-016-142117
; Sequence 142117, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142117
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142117

Query Match 69.7%; Score 20.2; DB 3; Length 601;
Best Local Similarity 88.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGT 25
|||||
Db 410 CCATCCACCTGCTGTGTGGCCAGT 434

RESULT 6

US-09-949-016-142118
; Sequence 142118, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142118
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-142118

Query Match 69.7%; Score 20.2; DB 3; Length 601;
Best Local Similarity 88.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGT 25
|||||
Db 442 CCATCCACCTGCTGTGTGGCCAGT 466

RESULT 7

US-09-949-016-12015/c
; Sequence 12015, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12015
; LENGTH: 44064
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12015

Query Match 69.7%; Score 20.2; DB 3; Length 44064;
Best Local Similarity 88.0%; Pred. No. 65;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGT 25
|||||
Db 34189 CCATCCACCTGCTGTGTGGCCAGT 34165

RESULT 8

US-09-949-016-15757/c
; Sequence 15757, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15757
; LENGTH: 44072
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15757

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Query Match      69.7%; Score 20.2; DB 3; Length 44072;
Best Local Similarity 88.0%; Pred. No. 65;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 CCATCCACCTGCTGTGTGACCTGGT 25
|||
34189 CCATCCACCTGCTGTGTGGCCAGT 34165
Db

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RESULT 9
US-09-949-016-16638/c
; Sequence 16638, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16638
; LENGTH: 24546
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(24546)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16638

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Query Match      69.0%; Score 20; DB 3; Length 24546;
Best Local Similarity 82.1%; Pred. No. 74;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Oy 1 CCATCCACTGCTGTGTGACCTGGTAAA 28
 |||||
Dδ 11856 CCATCAACTGCTGTGTGACCTGGGAA 11829

RESULT 10
US-09-949-002-663
; Sequence 663, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 663
; LENGTH: 105045
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(105045)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-663

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Query Match 68.3%; Score 19.8; DB 3; Length 105045;
Best Local Similarity 91.3%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	CCATCCACCTGCTGTGTGACCTG	23
Dβ	65085	CCCTCCACCTGCTCTGTGACCTG	65107

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RESULT 11
US-09-621-976-10243/c
; Sequence 10243, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 10243
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-10243

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Query Match 67.6%; Score 19.6; DB 3; Length 378;
Best Local Similarity 84.6%; Pred. No. 69;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTGTGACCTGGTAAAT 29
|||
Db 246 TCCACCTGCTGTGTGACCTTGGCATT 221

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RESULT 12
US-09-814-915A-91
; Sequence 91, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-1
; TITLE OF INVENTION: Thereo
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 8930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-91

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